Comprehensively Investigating the Genetic Architecture of Serum Lipids: From Identity by Descent Mapping, Transcriptome-Wide Association Study to Phenome-Wide Association Study

By

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To my beloved parents and sister,

For their unconditional support and endless love

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Table of Contents

List of Tables

Table **Page**

List of Figures

Figure **Page**

List of Abbreviation

CVD	Cardiovascular disease
EHR	Electronic Health Record
GEE	Generalized Estimating Equations
GReX	Genetically Regulated Expression
GWAS	Genome-Wide Association Study
H/L	Hispanic/ Latino
HCSC/SOL	Hispanic Community Health Study / Study of Latinos
HDL-C	High-density lipoprotein cholesterol
IBD	Identity by descent
LDSR/LDSC	Linkage disequilibrium score regression
LDL-C	Low-density lipoprotein cholesterol
LLD	Lipid-lowering drug
SNP	Single Nucleotide Polymorphism
TC	Total cholesterol
TG	Triglycerides
TWAS	Transcriptome Wide Association Study

CHAPTER I

INTRODUCTION AND SPECIFIC AIMS

In the U.S., an estimated 53% of adults have dyslipidemia[1], putting a majority of the U.S. adult population at high risk for cardiovascular diseases (CVD)[2-6]. Due to the high heritability of serum lipids (total cholesterol [TC], low-density lipoprotein cholesterol [LDL-C], triglycerides [TG], and high-density lipoprotein cholesterol [HDL-C]) and their importance as risk factors for disease, genetic studies are essential for understanding the mechanisms regulating lipid levels. Large family-based linkage studies and population-based genome-wide association studies (GWAS) have successfully identified many lipid related variants and pathways, yet despite these successes, much of the heritability remains unexplained. Because lipid-associated variants exhibit incomplete penetrance and model complexity, and most genetic datasets for lipid gene discovery do not include large, well-characterized families, linkage analysis is often underpowered or impractical. Conversely, GWAS is only well-powered to detect common variants (>0.01 minor allele frequency) of modest-to-large effect size. Taken together, these methods remain underpowered to detect a swath of potentially important low-frequency or small effect lipids associated variants.

Several emerging methods are proposed to fill the gap of unmapped genetic heritability, including association analyses using genetically-regulated expression (GReX) and identity-by-descent (IBD) mapping. GReX aggregates the effect of multiple variants in gene level models based on their association with RNA abundance. On the other hand, IBD mapping identifies regions enriched for shared segments among distant relatives to investigate disease-locus associations. In addition, the predominant focus on non-Hispanic white ancestral populations limits the global relevance and therefore translational potential of large-scale genetic studies. This is particularly true in populations that are overlooked by ongoing genetic studies, but are most burdened by dyslipidemia and its downstream consequences, such as Hispanic/Latinos (H/L).[7] For example, recent work has identified ancestry-specific genetic predictors of complex phenotypes like lipid traits, that may partially explain risk differences between racial/ethnic groups[8-12]. Particularly in understudied groups like H/L, the knowledge gap between genomics, public health, and medicine causes challenges in the genomic translational pipeline. Therefore, I aimed to discover underlying causal genes and variants for lipid traits and elucidate their biological and/or pathophysiological mechanisms with transcriptome-wide association (TWAS) and IBD mapping within H/L and a large electronic health record (EHR) linked DNA databank. Further I established evidence for the clinical utility and the impact on health outcomes of identified genes.

1. **Perform relatedness-driven genomic analyses to map the genetic regulators of lipid traits in both large EHR-linked biobank and Hispanic/Latinos.** To identify ancestry-specific genetic factors associated with serum lipids, I will conduct IBD mapping with genotyping array data in both Vanderbilt University Medical Center DNA biobank (BioVU, N=95,124) and 12,803 H/L from Hispanic Communities Health Study/Study of Latino (HCHS/SOL).

2. **Perform functionally oriented genomic analyses to map the genetic regulators of lipid traits in both large EHR-linked biobank and Hispanic/Latinos.** To identify novel genetic factors associated with serum lipids, I will conduct a TWAS in subjects with available lipid measures from the Vanderbilt University Medical Center DNA biobank (BioVU, N=95,124) and 12,803 H/L from Hispanic Communities Health Study/Study of Latino (HCHS/SOL).

3. **Evaluate the clinical significance of lipid-associated loci in a large clinical dataset.** Using phenome-wide TWAS (PredixVU), I will examine the clinical impact of lipid-associated genes phenome-wide by linking genetic factors to the full medical history captured in EHRs. These analyses will establish the constellation of clinical and health outcomes associated with lipid loci derived from diverse populations.

CHAPTER II

BACKGROUND

CVD is one of the leading causes of death in the U.S., and the leading cause of death globally[13]. According to an estimate from the World Health Organization, 17.7 million people died from CVD in 2015, comprising 31% of all deaths worldwide[14]. The total direct and indirect cost of CVD was estimated at almost 330 billion dollars in the U.S. in 2013[15], and over 800 billion dollars globally in 2010[16]. This global cost is expected to increase 22% by 2030. To improve cardiovascular health, the American Heart Association introduced seven important prognostic factors for CVD, including blood cholesterol (as measured by serum lipid levels), blood pressure, blood glucose, body mass index, physical activity, diet quality, and smoking.

The link between serum lipid levels and increased risk of CVD has been known for over half century[17,18]. Two recent studies that have explored the population attributable risk of major risk factors for myocardial infarction and heart disease are the INTERHEART study and the Framingham study. In the INTERHEART study, a case-control study across 52 countries, abnormal blood lipid measures were found to have the highest population attributable risk (49.2%) of all traits studied for myocardial infarction[19,20]. The Framingham study followed 6,860 participants for the incidence of heart failure and reported significant hazard ratios for non-HDL-C and HDL-C of 1.23 and 0.77, and reported the population attributable risks for high non-HDL-C and low HDL-C of 7.5% and 15%, respectively[21]. Studying genetic factors that regulate serum lipids will help elucidate the molecular mechanisms of CVD.

Abnormal serum lipid levels (dyslipidemia) is defined by abnormal TC, LDL-C, TG, and HDL-C. Dyslipidemia has been identified as a major risk for incidence of CVD[21,22], and treating dyslipidemia demonstrates its effectiveness on CVD prevention[23]. In a prospective cohort, the subjects with elevated TG and decreased HDL have 1.32 hazard ratio to have CVD than healthy controls[22]. In the National Health and Nutrition Examination Survey (NHANES) 2003–2006, an estimated 105.3 million (53%) of the U.S. adult population had dyslipidemia. An increase in the trend of abnormal TG is also found from NHANES III (1988-1994) to NHANES 1999-2006[24]. Also, the estimated prevalence of elevated TC (>200 mg/dL) is 39.7%, 30.3% for high LDL-C (>130 mg/dL), and 18.7% for low HDL-C (<40 mg/dL) in U.S. from NHANES 2011 to 2014[15,25]. The high prevalence of abnormal lipid profile results increased CVD risk for the majority of U.S. adults. Therefore, understanding the biological mechanisms underlying serum lipids and dyslipidemia is critical and will be helpful for treating and preventing CVD.

Serum lipid levels are highly heritable in populations; heritability estimates range from 0.46-0.57 for TC, 0.40-0.64 for LDL-C, and 0.40-0.62 for HDL-C, and 0.35-0.48 for TG[26,27]. The high heritability has motivated many genetic studies of lipid traits. Familial lipid disorders provided an early opportunity to identify genes impacting lipid regulation. Linkage analysis is a powerful approach to map causal genes by identifying genomic segments cosegregating with disease within and across families. Since the mid-1990s, linkage has been successfully applied in several rare lipid diseases, e.g. familial hypercholesterolemia[28], sitosterolemia[29], familial ligand-defective apolipoprotein B-100[30], and autosomal recessive hypercholesterolemia[31]. Although linkage analysis is well-powered to identify rare variants with strong effect, it requires a known pedigree and either a large family or several families with low genetic heterogeneity, which limits its application in common and complex disease.

GWAS, on the other hand, is typically performed on independently sampled population data and tests single variant association effects. In GWAS, participants are assumed to be unrelated, and cryptic relatedness can introduce bias and reduce power. Power in GWAS is increased as a function of increasing variant frequency, effect size, and sample size. The first large-scale meta-analysis of lipid traits was conducted with 16 European datasets, and a total sample size of 17,797-22,562, depending on the trait. They identified 22 loci significantly associated with lipid traits genome-wide, including six that had not been reported previously[32]. Another two notable, large meta-analyses of GWAS are from the Global Lipids Genetics Consortium (GLGC)[33,34]. In 2010, the GLGC collected 46 cohorts from U.S., Europe, and Australia, and reported 95 significant genetic loci related to lipid traits with over 100,000 Europeans, 59 of which were novel[33]. In 2013, Willer *et al.* published a meta-analysis with still more individuals, 188,577 Europeans and 7,898 non-Europeans, and reported 157 significant loci including 62 novel loci. However, these 62 novel loci only added 2% to the explained variance[34]. Demonstrating the importance of including ancestrally diverse populations in genomic analyses of lipids traits, an additional 118 novel loci were found in a large study with 300,000 multi-ethnic participants[35]. However, all the reported variants still only explained about 8.8-12.3% variance of lipid levels.

In the past decade, linkage analysis and GWAS have successfully identified >380 loci impacting blood lipid regulation. Although these findings have informed our understanding of lipid metabolism and furthered knowledge of causal factors of CVD[36], the disparity between explained variance and heritability leaves much to be discovered about genetic regulation of lipids and this represents an unexploited resource to treat and prevent CVD. Those variants whose effects are not well detected by linkage analysis (incompletely penetrant, or data characterized by sparse or unknown family structures) nor GWAS (low frequency, high allelic heterogeneity, or small effect size) will require novel discovery approaches.

One such approach leverages identity by descent (IBD). Identity by descent describes segments of the genome shared by two or more persons because it has been inherited from a recent common ancestor without recombination. These segments are large and enriched within close relatives, but they also exist and are detectable from distant relatives[37]. For instance, the expected length of an IBD segment from a common ancestor 25 generations ago is 2cM[38,39]. IBD mapping is an approach that attempts to locate disease genes by investigating the distribution of IBD segments in distantly related cases and controls. Because IBD segments associated with a trait may harbor one or more causal variants with low frequency, this approach enhances our ability to identify genes missed by GWAS. Also, neither close relatives nor a highly penetrant Mendelian model are required for IBD mapping, making it powered to detect variants that are undetectable by GWAS or linkage analysis. From simulations, IBD mapping has a demonstrated advantage for identifying causal genes for diseases with high allelic heterogeneity, low frequency of causal variants, and high heritability[39]. Furthermore, IBD mapping has been successfully applied in several traits, including schizophrenia[40], bipolar[40], and diastolic blood pressure[41]. Therefore, applying IBD mapping is likely to enhance our ability to identify loci which explain some of the missing heritability of serum lipids.

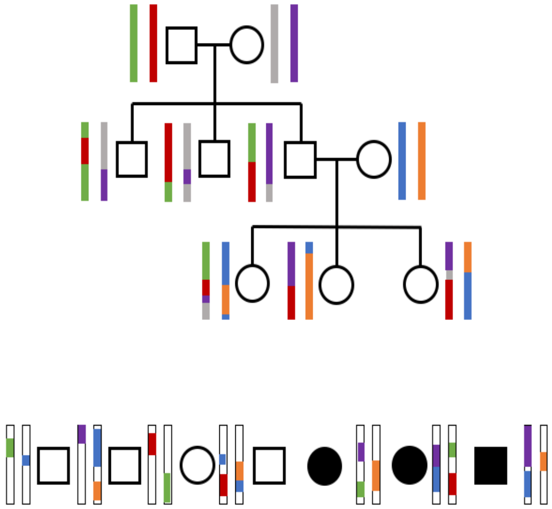

Figure 1. IBD segments infer the identical genomic segments inherited from a recent common ancestor.

Another approach to identify variants missed by GWAS and linkage leverages gene expression. Gene expression is regulated by complex mechanisms involving various factors, e.g. genetic variation, age, and environmental stimuli, and contributes to gene function and phenotype. The importance of gene expression is demonstrated by the enrichment of GWAS identified loci in expression quantitative trait loci[42]. Therefore, investigating the association between gene expression and traits of interest can be an effective way to understand the functional mechanism of GWAS loci. TWAS is a novel method that tests the effect of the imputed genetically regulated expression on phenotype. Since genetic influence on phenotype is lifelong, GReX reduces noise from temporal and environmental factors, and instead identifies the direct impact of genetic effects influencing gene expression on trait[43]. In addition, unlike single variant analysis, GReX aggregates genetic variants into a gene level functional unit, based on gene expression. As a result, TWAS results are directly biologically interpretable. This also has the effect of increasing the statistical power by reducing multiple testing burden. This powerful approach captures effects that may be too small to detect with single variant analyses and as a result TWAS complements other genomic analysis approaches such as GWAS or linkage.

Today, most cardiometabolic genetic research has been based on samples drawn from populations of European descent. Comparatively limited analyses in non-Caucasian populations have identified both novel ancestry-specific loci as well as ancestry-specific variants underlying signals previously detected in analyses of Caucasian datasets[44,45]. In an African American sample, Deo *et al.* reported both a novel common locus, which explains 1% of lipid trait variance, and diminished effects of known loci[44]. Only six GWAS have been published on lipid traits in H/L, all with limited sample sizes[7,46-50]. These studies have supported previous findings in European studies and also demonstrated evidence of H/L-specific genetic variants.

The number of published GWAS in H/Ls is in stark contrast with H/L population size. The H/L population is the most rapidly growing racial or ethnic group in the U.S. H/Ls comprised 17.7% of the U.S. population in 2015, and are projected to comprise 22.8% by 2035[51]. The prevalence of dyslipidemia in H/L is estimated at about 65%, which is higher than the general U.S. population (53%)[52]. H/L populations encompass many different ancestral and cultural backgrounds. Similarly, based on national/ethnic country of origin, distinct patterns of dyslipidemia are also observed, e.g., a higher prevalence of elevated LDL-C was found in Cubans (44.5% vs. 36% in the total H/L sample). Disparities between populations in the U.S. and within H/Ls are likely caused by both genetic and environmental factors. Genetic diversity can be beneficial to fuel discovery, e.g. improved fine mapping due to refined linkage disequilibrium or ancestry mapping. Despite these advantages, less scientific research has focused on the genetic components of lipid traits in H/Ls, compared to European-ancestry populations. Therefore, additional genetic studies in H/L populations should be prioritized to improve our understanding of the genetic etiology of lipid traits.

Serum lipid levels are not only related to future incidence of CVD, but also associated with other diseases, e.g. stoke[53,54], type 2 diabetes[55,56], and hypertension[57,58]. Several epidemiological studies have examined comorbidities of abnormal blood lipids, but the underlying reasons for their co-occurrence are still unclear. Most existing GWAS have focused on a specific phenotype, but the availability of electronic health records (EHR) now make it possible to investigate genetic effects phenome-wide. Phenome-wide association studies (PheWAS) not only attempt to reconstruct the shared genetic architecture among known comorbid diseases, but also to identify unknown related traits via genetic correlation. Previously, PheWAS has demonstrated its ability to identify eight novel SNP-disease associations for a single SNP reported associated with multiple sclerosis, e.g. cancer of rectum and anus, diabetes, and conduct disorders[59]. Therefore, applying PheWAS to genes and IBD segments associated with serum lipids will not only improve our understanding of the mechanisms by which serum lipids impact CVD, but also identify unknown risk factors and consequences of dyslipidemia.

Dyslipidemia is the most important risk factor for CVD. Because serum lipid levels are highly heritable and reliably measured, they are excellent phenotypes for investigating CVD. Although many GWAS of lipid traits have been done, IBD mapping and TWAS are novel approaches, not previously applied in genetic studies of serum lipids, that allow us to expand upon previous research. The benefits of these approaches and the large sample sizes available should result not only in replication of effects seen in previous GWAS, but also identification of novel loci related to lipid traits. Additionally, H/Ls are underrepresented in previous genetic studies. Applying IBD mapping and TWAS in H/Ls will result in identification of ancestry-specific effects that have been previously overlooked. Moreover, PheWAS will provide more evidence to understand biological mechanisms linking genetic regulation of blood lipids to other phenotypes. More comprehensive knowledge of lipid regulation pathways will lead to more effective prevention and treatment strategies for CVD. Several examples have demonstrated the benefit of genetic study to clinical practice, e.g., the discovery of mutations in *PCSK9* associated with familial hypercholesterolemia[28] has led to the development of anti-PCSK9 therapies.[60,61] In summary, both IBD mapping and TWAS of lipid traits in H/Ls and a large EHR-linked biobank will provide more evidence to understand the biological mechanisms underlying CVD.

CHAPTER III

METHODS

Overview

To explore the unidentified genetic architecture of serum lipids, I detected shared segments and performed IBD mapping and GReX based TWAS in both HCHS/SOL and BioVU. HCHS/SOL is a prospective cohort of H/L communities in the U.S., and BioVU is a DNA biorepository with linked EHR at Vanderbilt University Medical Center. Dichotomous dyslipidemia status was used as the outcome variable in the analysis of enrichment of IBD segments, and both dichotomous status and continuous serum lipids level were used in the association of GReX. Furthermore, all findings from IBD mapping and TWAS were used to identify traits that share genetic architecture with lipid regulation. The workflow for this project is summarized in Figure 2.

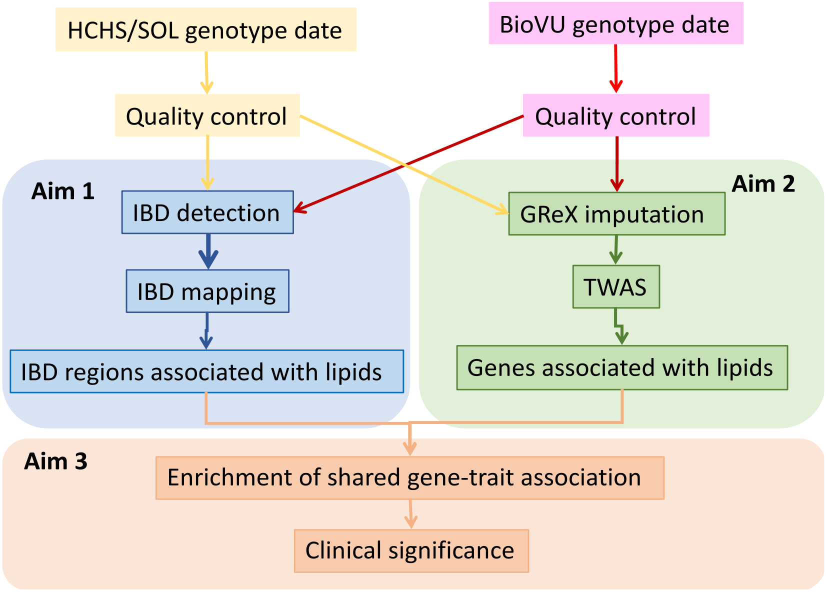

Figure 2. Flow chart of analysis

Subjects

BioVU

Vanderbilt University Medical Center (VUMC) has recruited and consented patients to join BioVU, an electronic health record linked biorepository, since February 2007[62,63]. Today, BioVU comprises 245,272 biological specimens retained from clinical testing. The EHR at VUMC offers de-identified demographic data, clinical notes, electronic orders, laboratory measurements, disease diagnosis codes, current procedures terminology (CPT) codes, and International Classification of Diseases, Ninth Revision (ICD-9). Although ICD-9 codes record patients' diagnoses, symptoms, signs and injuries, the main purpose of ICD-9 codes is billing and administration. Diagnoses with the same etiology may be covered by different ICD-9 codes. "Phenotype codes" (phecodes) are based on ICD-9 diagnostic codes and were developed for extracting phenotypes from administrative data[64]. They combine diseases or symptoms with common etiology, and develop a hierarchical structure. Today, 1,645 phecodes have been defined, each with a corresponding definition of controls for analysis. Currently in BioVU, 95,124 individuals have been genotyped, and 43,115 of which have at least one serum lipid measure, including HDL-C, LDL-C, TC and TG. Within the set of 95,124 genotyped individuals, over 75% self-report European ancestry (N=68,870), 16% self-report African ancestry (N=14,495), 3% self-report Hispanic (N=2,635), the remaining participants self-report 1% Asians ancestry, 0.1% Native American ancestry, 0.4% unknown, and 7% other. The ancestry information was also validated with genetic information, and only genetically confirmed European ancestry were carried forward into the main analyses.

HCHS/SOL

HCHS/SOL is a prospective cohort, that was designed to investigate risk and protective factors for chronic diseases and quantify morbidity and mortality due to chronic disease in Hispanic and Latino Americans[65]. From 2008 to 2011, HCHS/SOL recruited 16,415 self-identified H/L aged 18-74. The participants are from randomly selected households in four U.S. cities: Bronx, New York; Chicago, Illinois; Miami, Florida; and San Diego, California. A stratified 2-stage probability sample design was applied for sampling[66]. Census block groups were randomly selected from defined communities near recruiting centers, and households were randomly selected from selected block groups. They were asked to fast and refrain from smoking for 12 hours before clinical examination. Fasting blood samples were collected according to standard protocols during clinical examination. A total of 12,803 subjects consented for genotyping and were successfully genotyped.

Genotyping and quality control

A total of 95,124 participants in BioVU were genotyped by Illumina Multi-Ethnic Genotyping Array (MEGA), which comprises over 2 million genetic makers. Variants with >2% missingness and individuals with >3% missingness were excluded. Then, all subjects were projected with principal component analysis from all populations in 1000 Genome to determine their ancestral population. A total of 69,948 subjects are classified as European ancestry, 15,642 are African, 905 are East Asian, 416 are south Asian, and 2605 are Hispanic. Ancestry-specific quality control was conducted with following: MAF > 0.01, variant missingness < 0.05, sample missingness <0.1, heterozygosity F<0.2, Hardy-Weinberg equilibrium P-value>1×10^{-10}, and sex check. As a result, 69,819 individuals with 718,367 variants were kept in further analysis.

Participants in HCHS/SOL were genotyped on an Illumina custom array, the SOL HCHS Custom 15041502 B3, with the Illumina Omni 2.5M array (HumanOmni2.5-8v1-1) and ~150,000 custom SNPs, including ancestry-informative markers, especially for Amerindian populations. Samples were checked with annotated or genetically determined sex, missing call rate, and batch effect. Variants were filtered by missing call rate (>2%), Mendelian error, Hardy-Weinberg equilibrium ($P\text{-value}<1\times10^{-5}$). And, a total of 2,133,826 SNPs was used for further IBD detection and imputation.

Phenotyping

In BioVU, the serum lipid data were extracted from the linked EHR. All laboratory measurements were ordered for routine clinical care and measured with a standard clinical protocol. The extracted lipids data include HDL-C, LDL-C, TC, and TG. HDL-C was measured with direct magnesium/dextran sulfate method, TC was measured by cholesterol oxidase enzymatic method, and LDL-C was calculated using the Friedewald equation[67]. Lipid-lowering drugs (LLD) considered in data preparation include all statins, fibrates, bile acid sequestrants, niacin, and /or cholesterol absorption inhibitors (Appendix I). To avoid confounding by LLD, only the timepoints before medications have been taken for subjects with available naïve measurement(s), and, for subjects who have only medicated lipid measurements available, medication use was accounted for using standard adjustments[68]. In addition, extreme outlier values were excluded: HDL-C > 200 mg/dL, LDL-C > 500 mg/dL, TC > 1000 mg/dL and TG > 1200 mg/dL. Any laboratory measurements within 9 months of a pregnancy were removed.

In the Vanderbilt University linked EHR database, Synthetic Derivative (SD), over 44% of subjects had multiple lipid measures (n=2: 17%; n=3: 9%; n>=4: 18%). To determine the optimal phenotyping algorithm for genetic analyses of serum lipids in a large biobank, I evaluated the heritability of different phenotyping approaches for serum lipid measures from EHRs to identify the method with the highest proportion of phenotypic variation explained by genetic factors. The outpatient lipid measurements collected between age 18 to 75 in the absence of a LLD were extracted, resulting in 2,154,820 lipid measures from 196,263 individuals. I tested seven different phenotyping algorithms. These included two cross-sectional measures: first measurement only (after age 18), last measurement only (before age 75); and five longitudinal measures: longitudinal median (the median value among all included measurements), and the mean residuals from four different mixed-effects models (long-term average) as following:

$Model\ 1\colon\ Lipid_{ij} = \beta_0 + \gamma_{i0} + \beta_1 Sex_i + (\beta_2 + \gamma_{i1})Age_{ij} + (\beta_3 + \gamma_{i2}){Age_{ij}}^2 + \varepsilon_{ij}$

$Model\ 2\colon\ Lipid_{ij} = \beta_0 + \gamma_{i0} + \beta_1 Sex_i + (\beta_2 + \gamma_{i1})Age_{ij} + (\beta_3 + \gamma_{i2}){Age_{ij}}^2 + (\beta_4 + \gamma_{i3})Sex_i \times Age_{ij} + (\beta_5 + \gamma_{i4})Sex_i \times {Age_{ij}}^2 + \varepsilon_{ij}$

$Model\ 3\colon\ Lipid_{ij} = \beta_0 + \gamma_{i0} + \beta_1 Sex_i + (\beta_2 + \gamma_{i1})Age_{ij} + (\beta_3 + \gamma_{i2}){Age_{ij}}^2 + \beta_4 Ethnicity_i + \varepsilon_{ij}$

$Model\ 4\colon\ Lipid_{ij} = \beta_0 + \gamma_{i0} + \beta_1 Sex_i + (\beta_2 + \gamma_{i1})Age_{ij} + (\beta_3 + \gamma_{i2}){Age_{ij}}^2 + \beta_4 Ethnicity_i + \beta_5 Sex_i \times Ethnicity_i + (\beta_6 + \gamma_{i3})Sex_i \times Age_{ij} + (\beta_7 + \gamma_{i4})Sex_i \times {Age_{ij}}^2 + (\beta_8 + \gamma_{i5})Ethnicity_i \times Age_{ij} + (\beta_9 + \gamma_{i5})Ethnicity_i \times {Age_{ij}}^2 + \varepsilon_{ij}$

These algorithms were evaluated using SNP-based heritability, and were prioritized to minimize the effect of outliers and other non-genetic factors, e.g. sex and age of measurement. Two different SNP-based heritability estimation approaches were applied: restricted maximum likelihood estimation (REML) in the linear mixed model and linkage disequilibrium score regression (LDSR) methods. For the REML, I applied Genome-wide Complex Trait Analysis (GCTA)[69] to genotyped SNPs to construct the genetic relatedness matrix (GRM), and then applied the linear mixed model to determine the proportion of phenotypic variance explained by the GRM. LDSR uses summary statistics but accounts for linkage disequilibrium (LD) to estimate the heritability. The linkage disequilibrium score regression (LDSC) software package was applied to estimated LD-adjusted heritability with well-imputed SNPs ($R2\geq0.9$ and $MAF>0.01$)[70]. Covariates included in the heritability estimation included genetic principal components, sex, and either age at first measurement, age at last measurement, or median age.

The best algorithm was determined using only LLD naïve measures, and was then also applied in subjects with only drug confounded measures for further analyses. All serum lipids measurements after any record of LLD were adjusted according to the type of LLD (Appendix II), including statin[71], fibrates[71], bile acid sequestrants[72], niacin[72], and cholesterol absorption inhibitors[73]. The measures with multiple LLD were only adjusted with the largest effect. A sensitivity analysis was conducted to compare p-values from the analysis that included subjects with adjusted serum lipids v.s. the analysis that only included subjects with drug naïve measures.

Dyslipidemia cases in BioVU were defined as the diagnosis of any lipoid metabolism disorder (phecode 272) or record of LLD between age 18-75. The disorder of lipoid metabolism includes hyperlipidemia (272.1), hypercholesterolemia (272.11), hyperglyceridemia (272.12), mixed hyperlipidemia (272.13), hyperchylomicronemia (272.14), and unspecified disorder of lipoid metabolism (272.9). The dyslipidemia definition also included cases with a record of LLD including use of any kind of statin, fibrates, bile acid sequestrants, niacin, and cholesterol absorption inhibitors (full list summarized in Appendix I). The age of dyslipidemia case was determined by the earliest diagnosis or drug record. In contrast, controls were defined as having no diagnosis of lipoid metabolism disorder, no record of LLD, nor any abnormal measurements of serum lipids in the linked EHR (defined as HDL-C < 50 mg/dL for women, < 40 mg/dL for men; LDL-C > 160 mg/dL; TC > 240 mg/dL; TG > 150 mg/dL). Age of controls was defined as either age at last available serum lipid measure or age at last recorded visit. The dyslipidemia cases and controls were matched by age, sex and genetic ancestry.

In HCHS/SOL, blood samples were collected after 12 hours of fasting, and then shipped to a central laboratory for measurements. As in BioVU, HDL-C was measured with direct magnesium/dextran sulfate method, TC was measured by cholesterol oxidase enzymatic method, and LDL-C was calculated using the Friedewald equation[67]. The participants were asked about prescription and non-prescription medications taken within four weeks by interview. The subjects with LLD were retained for maximum sample size, but their lipid value was adjusted as above[50]. Dyslipidemia in HCHS/SOL was defined as any abnormal measure of serum lipids, including HDL-C < 50 mg/dL for women, < 40 mg/dL for men, LDL-C > 160 mg/dL, TC > 240 mg/dL, TG > 150 mg/dL, and/or any self-report of LLD. Controls were matched by age, sex, country of origin and genetic ancestry.

Phasing and Identity-by-Descent detection

Estimating the original allelic combinations, or haplotypes, that an individual received from his or her parents from genotypes, also called phasing, is a critical step for accurately identifying IBD segments. I applied SHAPEIT4 to establish phase in genotype data from both BioVU and HCHS/SOL. SHAPEIT4 is an rapid phasing tool for large-scale biobank data, and takes advantage of a Positional Burrows–Wheeler Transform (PBWT)[74] and the Li and Stephens model (LSM)[75] for capturing the haplotype sharing between subjects and identifying informative haplotypes efficiently. The pre-imputation genotyping data from both BioVU and HCSC/SOL were used for phasing and downstream IBD detection.

Following phasing, I performed IBD segment detection to identify identical genomic segments in pairs of individuals. GERMLINE is a robust and frequently used tool for IBD detection[76]. It uses a two-stage approach to identify the identical shared segment: first, GERMLINE detects the completely identical matched-seed of potential identical segments using a dictionary of phased haplotypes from the observed population, and, second, it extends the match-seed with a likelihood of IBD via a dynamic programming algorithm. To allow for genotyping error, a maximum number of two mismatched homozygous markers and one mismatched heterozygous marker is permitted within an identical segment. To mitigate the false positive rate in IBD detection, I restricted downstream IBD mapping analyses to utilize IBD segments with a length equal to or greater than 5 cM (false positive rate: 4.6% for 5 cM and 14.7% for 2.5 cM)[76].

Identity-by-Descent mapping

To find genes associated with serum lipids, I assessed enrichment of both individual segments and enrichment of any shared segments on dichotomous dyslipidemia status. Testing for enrichment of any shared IBD segment on dichotomous outcome is based on the rate of IBD sharing within cases and in case-control pairs[39]. Breakpoints were defined as a physical location in the genome at which any pair sharing an IBD segment changed sharing status. The difference in sharing rate for two groups, case-case pairs and case-control pairs, subtracting off the genomic average for each group is calculated for each breakpoint (see Formula 1). Since IBD segments are not independent, I performed one million random permutations to establish a null distribution and assess significance. I permuted case-control labels to create the null distribution, and then obtained empirical p-values from a one-sided test.

$$\Delta IBD = (rate_{case-case} - \overline{rate}_{case-case}) - (rate_{case-control} - \overline{rate}_{case-control}) \text{ (Formula 1)}$$

Dr. Browning has derived the suggestive genome-wide significance level for IBD mapping by comparing the IBD sharing from binomial distribution to the chance from the same ancestor based on the number of generations to common ancestor[39]. The suggested significance threshold for segments ≥5 cM is p-value$<1\times10^{-5}$. Taking the sample size and false discovery rate of IBD detection into account, the significance level was set to 4×10^{-5} in this study.

After determining genomic regions in which case-case pairs were significantly enriched with IBD segments, all individual IBD segments within this region were investigated. The previous steps only investigate the enrichment of IBD sharing status between pairs of cases, without considering the segments themselves. To determine the enrichment of a specific IBD segment, individual IBD segment clustering was done by DASH[77]. For rare IBD segments with less than ten carriers, the proportion of all case carriers and all control carriers was compared with a theoretical expectation and whole genome observation. For recurrent IBD segments with greater than ten carriers, a logistic generalized estimating equation (GEE) was applied to investigate the effect size of specific IBD. The GEE in the software package SUGEN was leveraged in this analysis as it has demonstrated stable p-values based on model-based variance estimation for rare variants with a minor allele frequency ≥0.01% (corresponding to a minor allele account 2 or 3)[78]. Genes within the identified regions were annotated with mapped genes from previous GWAS of any metabolic traits (Appendix III) from NHGRI-EBI catalog[79].

Genomic imputation and post-imputation quality control

Genomic imputation in BioVU was conducted with minimac4 on the Michigan Imputation Server[80]. The quality filter passed 69,819 individuals of European ancestry with 718,367 SNPs, which were then imputed using a reference panel of 32,470 samples from Haplotype Reference Consortium r1.1. A total number of 39,635,008 SNPs were imputed. Only the 7,167,360 SNPs with an imputation info score greater than 0.4 and MAF greater than 1% were used for further GReX imputation and GWAS.

In HCSC/SOL, 12,803 individuals and 2,232,944 SNPs passed quality filters for genomic imputation. SHAPEIT2 and IMPUTE2 were conducted with the 1000 Genome Project phase 1 multiethnic reference panel. In total, 25,568,744 variants were imputed. The indices of imputation quality included info score, masked SNP r^2, and the ratio of observed variance of imputed dosages to the expected binomial variance. Only the 11,749,707 SNPs with imputation info score greater than 0.4 and MAF greater than 1% were used for further GReX imputation and GWAS.

Genetically Regulated Expression imputation

PrediXcan was applied to the imputed the tissue-specific GReX based on genotyping data for both HCHS/SOL and BioVU[43]. PrediXcan uses an elastic net model with genotypic data to create models that predict tissue-specific and/or cross-tissue gene expression. Publicly available models were trained with the 922 whole-blood samples from Depression Genes and Networks and 49 tissues from Genotype-Tissue Expression project (GTEx v.7)[81]. GTEx comprises RNA sequencing and genotype data from 48 different tissues (see Table x) collected from as many as 635 donors. Using PrediXcan models, 11,749,707 imputed SNPs in HCHS/SOL and 7,167,360 imputed SNPs in BioVU were used for GReX imputation. Estimated GReX was computed using the following approach for each gene, g, where w_k is the weight for a single variant derived from regressing the gene expression on that variant, X_k, in the training sample.

$$\widehat{GReX}_g = \sum_k \hat{w}_{k,g} X_k \quad \text{(Formula 2)}$$

In addition to tissue-specific GReX, I also utilized cross-tissue models. Two different cross-tissue models were applied; one model across all tissues and another across metabolic tissues only (including whole blood, adrenal gland, subcutaneous and visceral momentum adipose tissues, liver, pancreas and skeletal muscle). Only genes imputed in at least five tissues were utilized in the cross all-tissue model, and at least three tissues for the cross metabolic-tissue model. Principal component analysis was conducted to reduce dimensions, and the smallest number of components which explained at least 80% variance were used. For each gene, Fisher's combined probability test was performed to combine p values from the association tests of all selected principal components[82].

$$\chi^2_{2k} \sim \sum_{i=1}^{k} -2\ln(p_i) \text{ (Formula 3)}$$

The combining statistic follows a χ^2 distribution with $2k$ degree of freedom, where k represents the total number of used PCs and p_i is the p-value of *i*th PC. The R package, *metap,* was implemented for combining p-values.

Single gene and genome-wide association test

Due to the existence of genetic relatedness in both BioVU and HCSC/SOL, I utilized a generalized estimating equations (GEE) model to investigate the association between serum lipid and imputed GReX or genetic variants. GEE applies quasi-likelihood estimation and working correlation matrix to handle the correlated or clustered observations. The covariates, age and sex, were also adjusted in the following model:

$$E[Y_{ij}] = \beta_0 + \beta_1 GReX_{ij} + \beta_2 Covariate_{ij} \text{ (Formula 4)}$$

In the model, *i* represents the *i*th family and *j* indicates the *j*th member of family$_i$. SUGEN was applied to conduct the GEE analysis[78].

The families in SOL have been identified in a previous study[78]. The genome-wide IBD information was applied to determine pairwise degree of relatedness. Then, the families were created by connecting the subjects who are related by first- or second-degree, leading to the identification of 2,789 families with at least two members[78] (Figure 3).

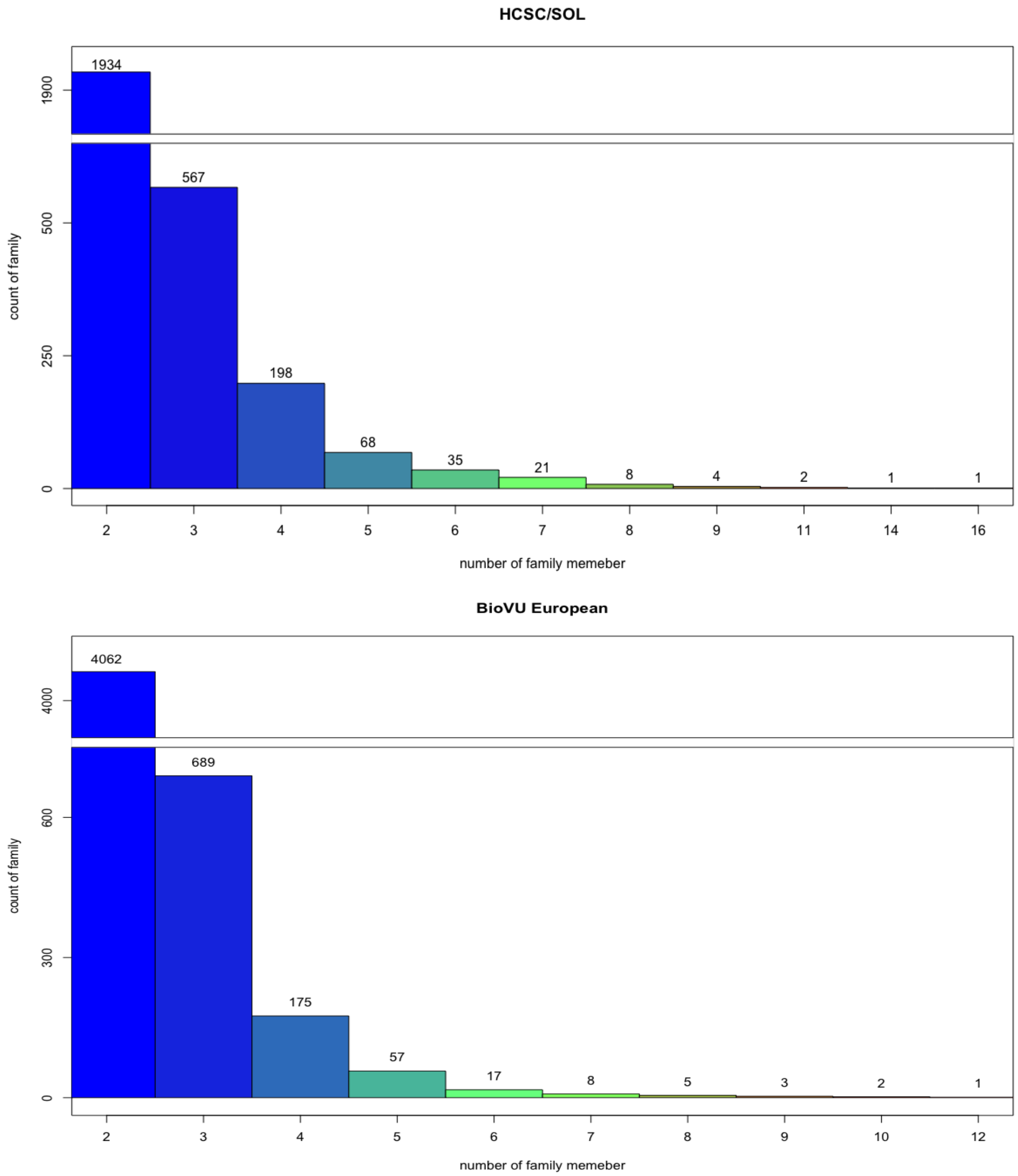

Figure 3. Bar plot of the count of families by number of family member in HCHS/SOL and BioVU

The genome-wide IBD proportion was also used to estimate the pairwise degree of relatedness in all individuals of European ancestry within BioVU, and the IBD proportion was calculated by method-of-moments estimation in PLINK after removing ancestry-informative SNPs[83]. Non-directional family networks were reconstructed based on only first- and second degree of relatedness. PRIMUS was implemented for the network reconstruction[84]. For the families with more than five members, the number and distribution of sharing IBD segments were used to verify the degree of relatedness between all the members within the family. IBD segments shared pair-wise were extracted from previous GERMLINE output, and ERSA was conducted for this validation process[85]. A total number of 5,019 families (size 2 or greater) were identified in BioVU Europeans and at least one first or second degree relative can be found in 16.4% of subjects.

Due to the multiple association tests and high correlation for the same gene across different tissues, the Benjamini-Hochberg procedure of false discovery rate (FDR) was applied to adjust the p-value[86]. The FDR adjustment was performed for the tissue-specific model and cross-tissue model for each trait, separately, and the significance threshold applied is FDR adjusted p-value less than 0.05. Genes identified by PrediXcan only were defined by a lack of GWAS significant SNP within 10 million bases in the GWAS analysis in the same dataset (GWAS significant level: p-value < 5×10^{-8}). Novel genes were defined as having no NHGRI-EBI catalog reported SNP within 1 million bases (APOE region 10 million bases)[79].

Phenome-wide association study in PredixVU

To investigate phenotypes and traits with shared genetic components, I conducted a phenome-wide association study in the DNA biobank at Vanderbilt University (BioVU). BioVU specimens are linked to participants' EHR in Vanderbilt University Medical Center, and 1,514 phecodes have been defined based on ICD9 codes. This large dataset offers a valuable opportunity to study comorbidities that share a common genetic mechanism and previously unidentified correlated diseases. Tissue-specific GReX have been imputed for over 23,000 BioVU European ancestry individuals with PrediXcan using GTEx- and DGN-trained models, and their associations with phecodes were examined via PheWAS and are stored in a readily available database, PredixVU.

All identified lipids genes were tested to characterize traits associated with their imputed expression in the electronic health records linked to BioVU samples, phenome-wide. To identify traits with shared expression architecture, I first tallied significant (p-value<0.01) PredixVU association results for each trait within the selected lipid genes. To obtain the *p*-value for each phenotype, I created an empirical distribution for each trait by first identifying the subset of selected genes expressed in a given tissue, and then randomly selecting the same number of genes and assessing the number of genes in the random set that were associated with each trait in PredixVU. The process was repeated 100,000 times to create a null distribution, and the empirical p-value was estimated based on this permutation procedure. A Bonferroni correction was performed for 1,514 PheCodes, making the significance level for determining lipids gene enrichment in GReX-trait association $P<3.3\times10^{-5}$. In addition, I also compared the direction of effect for each significant trait to the direction of effect in hyperlipidemia (Phecode 272.1). For each trait, I tallied the number of lipid genes with coordinated or opposite direction of effect in the BioVU samples. If the GReX-trait association was significant ($P<0.05$) for both hyperlipidemia and the trait in question, it was labeled as a strong coordinated or opposite effect, if not, it was labeled as a weak coordinated or opposite effect.

CHAPTER VI

RESULTS

Demographic and lipids related characteristics

Among the 69,819 genotyped European in BioVU, 27,774 individuals have at least one serum lipids measurement, 18,348 have been diagnosed with dyslipidemia (any phecode that belongs to a 272 code for lipid disorder), and 21,719 have a history of taking LLD (Appendix I). In total, 25,367 subjects have either a diagnosed phecode of dyslipidemia (13,084, 79.4%) or a history of LLD (15,496, 84.5%), and 24,382 individuals didn't have any diagnosis of dyslipidemia, history of LLD, nor abnormal serum lipid measures. Matching on age, sex and genetic ancestry, I selected 18,337 dyslipidemia cases and 18,337 matched healthy controls. Although I have matched them with age, dyslipidemia cases are still slightly older than healthy controls (cases: 52.92, control: 50.74, p-value = 7.03×10-64). The demographic and dyslipidemia related medical characteristics were summarized in Table 1.

After removing unqualified and extremely abnormal serum lipid measurements, 744,179 measures from 27,774 individuals are kept (HDL-C: 177,313, LDL-C: 191,658, TC: 189,836, and TG: 185,372). A total number of 18,420 subjects have more than one measure, and 18,839 subjects have at least one measure before any LLD treatment. The subjects with more than one drug naïve measurements are used for developing the optimal algorithm (Table 3), and the demographic information of all subjects, including those who only have LLD biased serum lipids, are summarized in Table 2.

Among the 16,415 self-identified Hispanic/Latino individuals recruited by HCHS/SOL, 12,803 subjects have been genotyped, and 12,223 of them have at least one available serum lipids

Table 1. Demographic and dyslipidemia related medical characteristics in BioVU

	Dyslipidemia		Healthy control		p-value
N	18337		18337		
Male (N, %)	7200	39.3%	7200	39.3%	1.00
Age (mean, SD)	52.92	11.38	50.74	13.32	7.0×10^{-64}
Lipid-lowering drugs history (N, %)	15496	84.5%			
Statins	13723	88.6%			
Fibrates	1849	11.9%			
Bile acid sequestrants	1769	11.4%			
Niacin	1266	8.2%			
Cholesterol absorption inhibitors	2501	16.1%			
Diagnosed dyslipidemia in EHR (N, %)	13084	71.4%			
Hyperlipidemia (x272.10)	13016	99.5%			
Hypercholesterolemia (x272.11)	5344	40.8%			
Hyperglyceridemia (x272.12)	668	5.1%			
Mixed hyperlipidemia (x272.13)	6370	48.7%			
Hyperchylomicronemia (x272.14)	59	0.5%			
Unspecified disorder of lipoid metabolism (x272.9)	167	1.3%			

Table 2. Demographic information and quantitative serum lipids in BioVU

	HDL-C		LDL-C		TC		TG	
N	25134		24762		25930		25641	
Male (N, %)	11128	44%	10993	44%	11490	44%	11424	45%
Age (mean, SD)	51.21	14.37	52.77	13.98	52.55	14.05	52.75	13.95
Measure (mg/dL)	51.18	18.04	121.55	35.78	201.47	41.68	4.84	0.54
LLD naïve measures								
N	17959		17651		18691		18370	
Male (N, %)	7004	39%	6916	39%	7338	39%	7264	40%
Age (mean, SD)	47.16	13.86	49.26	13.84	49.13	13.92	49.35	13.84
Measure (mg/dL)	54.78	17.85	113.25	33.20	193.60	39.41	4.72	0.53

Table 3. Basic demographic characteristics and estimated heritability

	HDL-C		LDL-C		TC		TG	
	mean	SD	mean	SD	mean	SD	mean	SD
N	10,777		10,559		11,276		10,940	
Male (N, %)	4,245	39.4%	4,181	39.6%	4,463	39.6%	4,367	39.9%
Age								
First measure	47.42	13.04	47.63	12.96	47.37	13.07	47.64	12.98
Median	50.55	12.93	50.64	12.90	50.51	12.95	50.63	12.93
Last measure	53.26	13.10	53.26	13.10	53.27	13.10	53.25	13.12
Measure (mg/dL)								
First measure	56.11	18.90	110.67	32.13	192.12	37.57	2.04	0.24
Last measure	55.96	18.53	116.80	34.07	197.97	40.33	2.05	0.23
Median	55.99	17.54	113.50	29.22	194.60	34.63	2.04	0.21
Long-term average								
Model 1	0.039	1.503	-0.113	3.221	0.054	4.679	0.001	0.031
Model 2	0.040	1.504	-0.103	3.218	0.069	4.702	0.002	0.031
Model 3	0.017	1.506	-0.152	3.226	-0.063	4.705	0.001	0.032
Model 4	0.010	1.514	-0.149	3.227	-0.061	4.729	0.001	0.032
REML-based heritability (GCTA)								
First measure	32.4%	3.9%	32.8%	4.0%	31.4%	3.8%	38.1%	3.8%
Last measure	35.8%	3.9%	31.9%	4.0%	28.4%	3.8%	34.7%	3.8%
Median	**41.2%**	3.9%	**38.2%**	4.0%	**34.4%**	3.8%	**45.6%**	3.8%
Model 1	39.2%	3.9%	28.6%	4.0%	27.7%	3.8%	40.5%	3.8%
Model 2	39.4%	3.9%	28.6%	4.0%	27.9%	3.8%	40.6%	3.8%
Model 3	39.3%	3.9%	28.6%	4.0%	27.8%	3.8%	40.5%	3.8%
Model 4	39.2%	3.9%	28.5%	4.0%	27.9%	3.8%	40.6%	3.8%
LD-adjusted heritability (LDSC)								
First measure	18.5%*	3.4%	18.4%	3.7%	**18.0%**$^{--}$	3.4%	26.6%*	3.6%
Last measure	23.2%	3.5%	18.2%	3.4%	14.9%	3.2%	25.7%*	3.9%
Median	**26.2%**$^{--}$	3.7%	**20.4%**$^{--}$	3.7%	17.5%	3.5%	**33.7%**$^{--}$	4.1%
Model 1	25.7%	3.4%	14.9%	3.4%	13.6%	3.4%	28.9%	3.6%
Model 2	25.8%	3.4%	14.8%	3.5%	13.5%	3.4%	28.8%	3.6%
Model 3	25.7%	3.4%	15.0%	3.4%	13.7%	3.4%	28.9%	3.6%
Model 4	25.7%	3.4%	14.7%	3.5%	13.5%	3.4%	28.8%	3.6%

* p-value<0.05, comparing to highest heritability ($^{--}$ reference heritability)

measure. In total, 1,407 (11.5%) individuals have reported at least one kind of LLD in the four months before interview, 7,025 (58.7%) have at least one abnormal lipid measures, and 7,658 (63.2%) subjects fit the dyslipidemia definition for HCHS/SOL. In contrast, 4,399 individuals have no reported history of LLD nor any abnormal serum lipids, and they are considered as controls. With matching of age, sex, country of origin, and genetic ancestry, 4,241 dyslipidemia cases and the same number of controls are selected for analysis. Their demographical and serum lipid related information are presented in Table 4. For the quantitative serum lipids, 12,223 subjects have serum lipids measures (HDL-C: n=12,222, LDL-C: n=11,967, TC: n=12,223, and TG: n=12,223), and 10,817 of them are drug naïve (Table 5)

Identity-by-Descent detection

In the European BioVU data, GERMLINE identified 3,223,024,266 total IBD segments, shared pair-wise with length equal to or greater than 5cM, among 2,437,311,471 pairs. Total IBD sharing includes 22,474,953 unique segments carried by at least three persons, and identified by DASH. On average, each cM with the autosome has 675,849.3 pairs sharing an IBD segment (0.028%). The proportion of pairs of individuals sharing IBD segments varies across the genome from 2.5×10-7 to 1.3×10-2, and are expectedly sensitive to genomic position, e.g., high sharing rate around centromere and low rate on telomere (Fig. 4).

In HCHS/SOL, 43,060,030 IBD segments, shared pair-wise with length equal to or greater than 5cM, among 81,952,003 pairs are identified by GERMLINE. These include 2,448,857 unique segments, carried by at least three persons and identified by DASH. Across the autosome, the average number of pairs sharing IBD at any given cM is 82,075.46 (0.100%), ranging from a minimum of 746 (0.0009%) to a maximum of 9,097,387 (11%) (Fig 5).

Table 4. Demographic and dyslipidemia related medical characteristics in HCSC/SOL

	Unmatched				Matched			
	Dyslipidmia		Control		Dyslipidmia		Control	
N	7568		4399		4241		4241	
Male	2966	39.2%	1917	43.6%	1795	42%	1795	42%
Age	47.87	13.37	42.99	14.31	43.79	13.92	44.10	13.66
Country of Origin								
CentralAmerican	861	11.4%	425	9.7%	425	10.0%	425	10.0%
Cuban	1400	18.5%	766	17.4%	754	17.8%	754	17.8%
Dominican	640	8.5%	491	11.2%	444	10.5%	444	10.5%
Mexican	2780	36.7%	1581	35.9%	1549	36.5%	1549	36.5%
PuertoRican	1359	18.0%	771	17.5%	741	17.5%	741	17.5%
SouthAmerican	508	6.7%	349	7.9%	313	7.4%	313	7.4%
Unknown	20	0.3%	16	0.4%	15	0.4%	15	0.4%
serum lipid measures (unadjusted)								
HDL-C	44.92	11.68	57.23	11.28	43.97	10.96	57.36	11.29
LDL-C	129.29	40.26	111.62	25.61	127.10	39.92	112.19	25.49
TC	205.37	47.15	185.95	28.24	201.71	47.18	186.76	27.96
TG	155.78	71.39	85.37	29.27	153.16	72.41	85.96	29.15
dichotomous serum lipid status	7349	97.1%			3628	85.5%		
HDL-C	5078	69.1%			2870	79.1%		
LDL-C	2178	29.6%			862	23.8%		
TC	2336	31.8%			910	25.1%		
TG	3814	51.9%			1969	54.3%		
Lipid-lowering drugs	1378	18.2%			613	14.5%		
Statins	1350	98.0%			599	97.7%		
Fibrates	145	10.5%			67	10.9%		
Bile acid sequestrants	10	0.7%			4	0.7%		
Niacin	16	1.2%			8	1.3%		
Cholesterol absorption inhibitors	41	3.0%			18	2.9%		

Table 5. Demographic information and quantitative serum lipids in HCHS/SOL

	HDL-C		LDL-C		TC		TG	
N	12222		11967		12223		12223	
Male (N, %)	5054	41%	4883	41%	5055	41%	5055	41%
Age (mean, SD)	46.11	13.87	46.07	13.92	46.12	13.87	46.12	13.87
Measure (mg/dL)	48.74	13.21	128.68	38.10	205.61	45.56	4.79	0.56
LLD naïve measures								
N	10816		10589		10817		10817	
Male (N, %)	4522	42%	4363	41%	4523	42%	4523	42%
Age (mean, SD)	44.53	13.63	44.48	13.67	44.54	13.63	44.54	13.63
Measure (mg/dL)	49.10	13.13	124.46	36.04	200.60	43.19	4.75	0.56

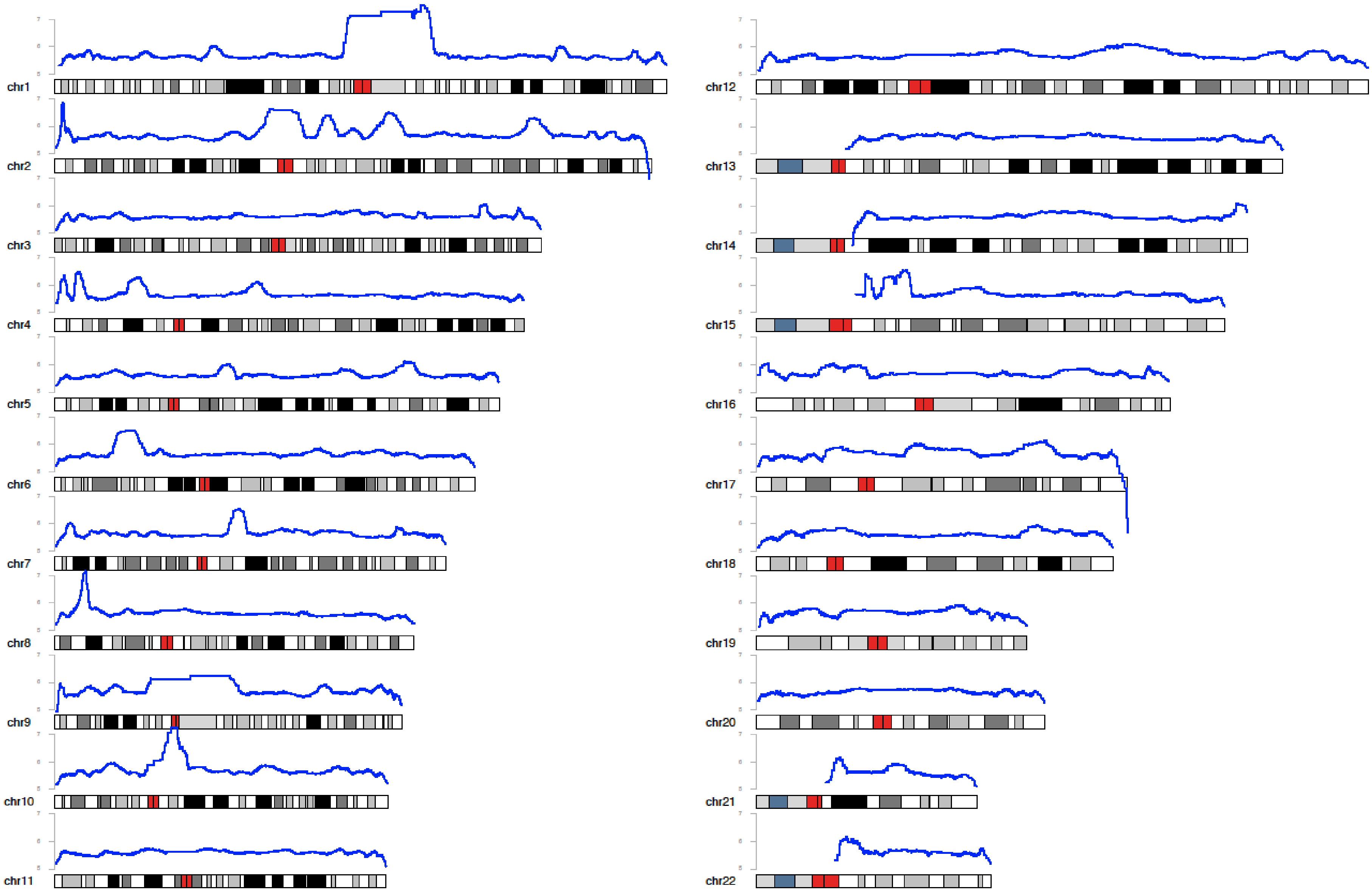

Figure 4. Number of IBD sharing pairs across whole genome in BioVU

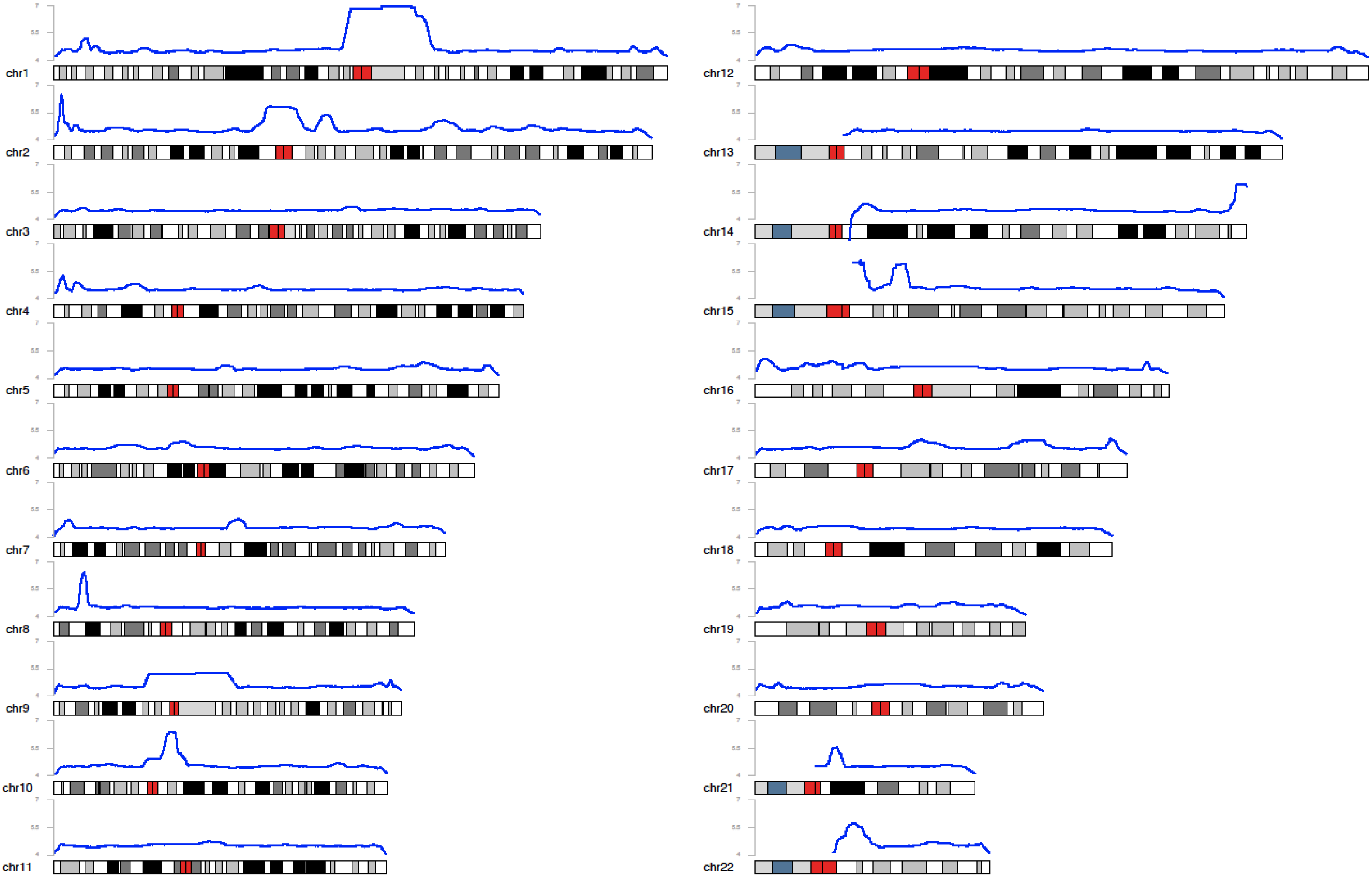

Figure 5. Number of IBD sharing pairs across whole genome in HCHS/SOL

Identity-by-Descent mapping

Among the 168,113,616 dyslipidemia case-case pairs in BioVU, 23,306,322 IBD segments are identified. On average, each case-case pair shares a total length of 18.84 cM IBD. On the other hand, 46,093,725 IBD segments are found in 336,245,569 case-control pairs, and the mean total length shared IBD is 18.42 cM for each case-control pair. Comparing the enrichment of IBD sharing between case-case pair and case-control pairs, two regions have a genome-wide significant p-value based on a null distribution derived from 1,000,000 random permutations (chr5:169,767,523-171,546,137, and chr22: 49,343,781-49,699,009, Fig 6). In addition, two other regions have a p-value close to the significance level (chr10:86,325,884-87,287,808 with p-value = 5.48×10^{-04}, and chr18:10,595,758-11,232,515 with p-value=5.25×10^{-04}). Although IBD mapping is differentially powered compared to GWAS, and therefore may detect a different set of significant regions for lipid-related traits, I annotated these regions with NHGRI-EBI Catalog genes reported as significant in published GWAS of metabolic traits (Appendix III). *RANBP17*, a gene significantly associated with HDL-C and BMI previously, is located in the identified region of chromosome 5, and *PIEZO2*, a gene within the identified region on chromosome 18, is significantly associated with diastolic blood pressure (Fig 8).

Within the two genome-wide significant regions, DASH identifies 38,381 clustered IBD segments for chromosome 5, carried by at least three individuals, and 27,771 for chromosome 22. Among the rare IBD segments (those with nine or fewer carriers), 1,480 segments (7.5%) are shared by only dislipidemia cases and 1,405 (7.2%) are only shared by controls for the identified region on chromosome 5, and there are 1,115 all-case segments (8.0%) and 977 all-control segments (7.0%) for the region on chromosome 22. The empirical expected percentage from the whole genome is 6.6% shared by only cases and 6.0% shared by only controls. As a result, both identified regions are significantly enriched with rare IBD segments exclusively shared by cases or controls (χ^2 p-value= 3.70×10^{-19} for chromosome 5, and p-value= 1.66×10^{-17} for chromosome 22). For the more common specific IBD segments, carried by ten or more subjects, 63 of 1,908 segments on chromosome 5 are found significantly associated with dyslipidemia (GEE model p-value<0.05), and 36 of 1,153 total segments are significant for the chromosome 22 region (Appendix IV).

In HCHS/SOL, IBD mapping is applied in unmatched dyslipidemia cases and controls (Table 4). In total, 15,332,912 IBD segments are identified in 28,482,378 case-case pairs, and 17,157,683 IBD segments for 33,082,884 case-control pairs. The mean IBD segment length is 3.90 cM for case-case pairs and 3.80 cM for case-control pairs. Comparing the IBD sharing rate in case-case and case-control pairs, chromosome 1 contains the only significant region (chr1:147,245,324-152,193,605, Fig 7). Several genes in the identified region of chromosome 1 have been previously linked to metabolic traits, including *ANXA9* (LDL-C) and *CERS2* (HDL-C, Fig 8). DASH identifies 7,018 specific IBD clusters in this significant region. All-case and all-control rare IBD segments are also significantly enriched in the region (679 (12.7%) for all-case and 701 (13.1%) for all-control, p-value=7.24×10^{-06}), compared to the genome-wide expected proportion (12% for all cases and 11.2% for all controls). For the 874 more common IBD segments, seventeen of them are found significantly associated with dyslipidemia (Appendix IV).

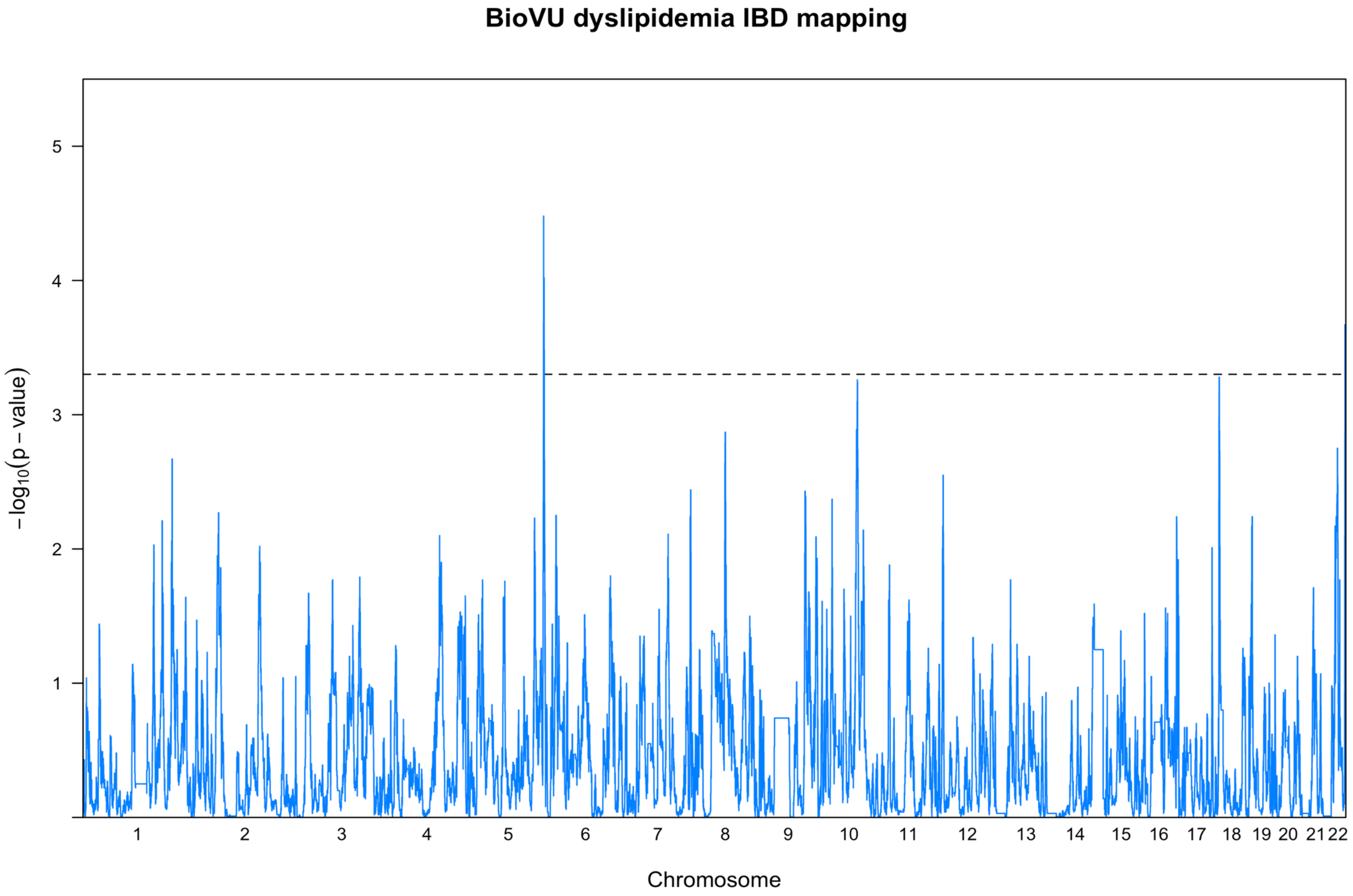

Figure 6. Manhattan plot IBD mapping on dyslipidemia status in BioVU

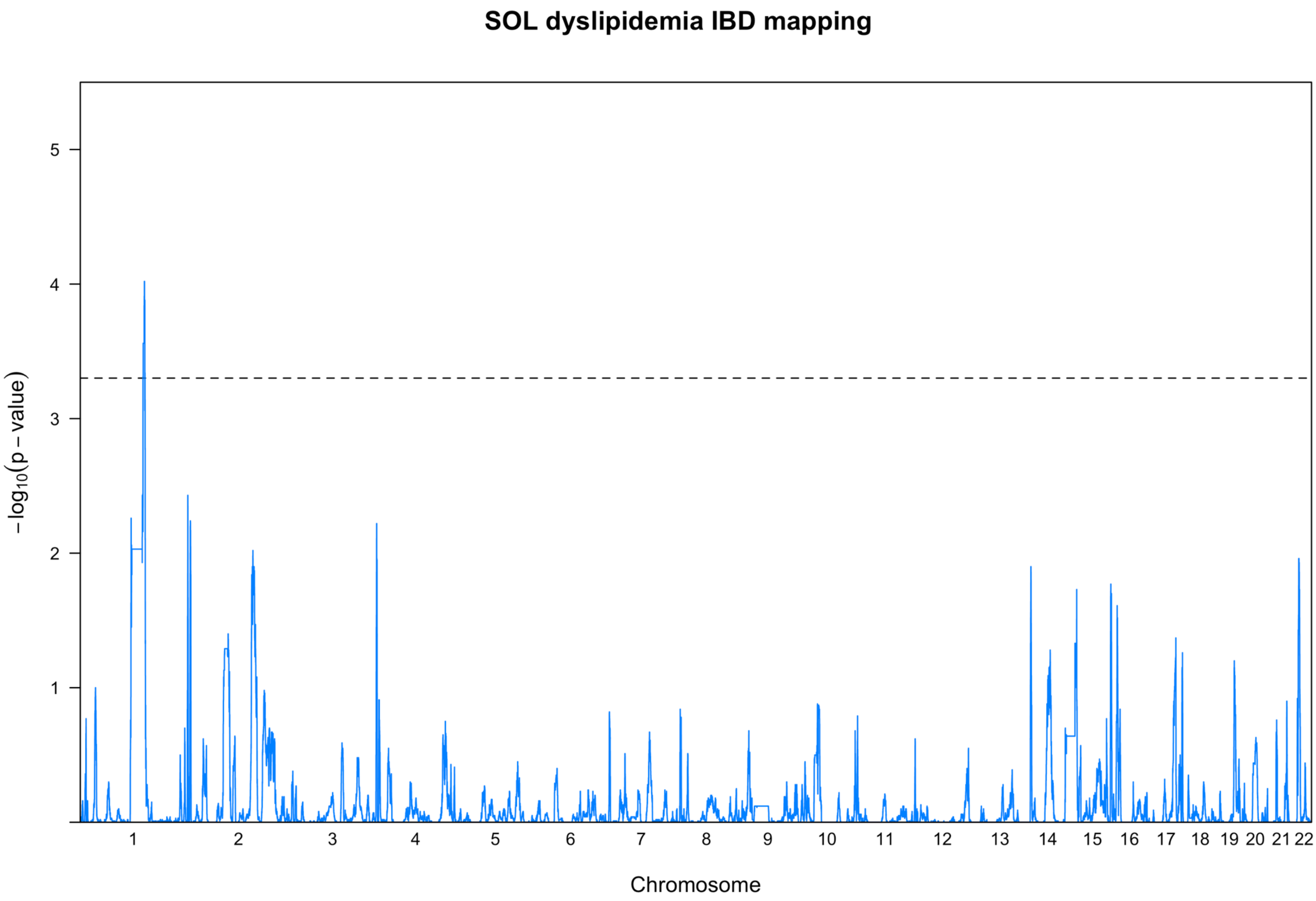

Figure 7. Manhattan plot IBD mapping on dyslipidemia status in HCHS/SOL.

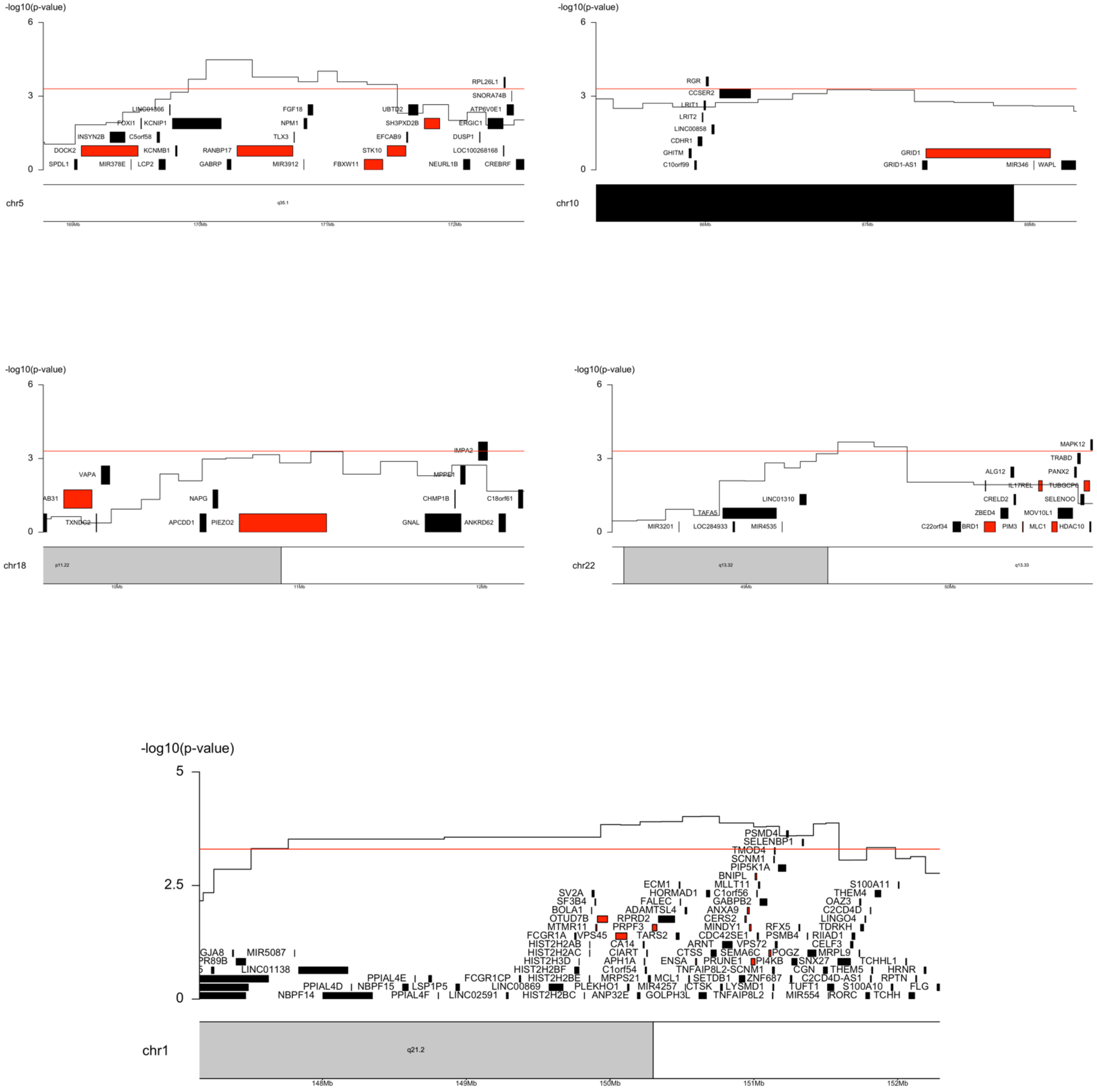

Figure 8. IBD mapping identified regions with gene annotation. Previously reported metabolic genes were labeled with red

Evaluation of optimal lipid phenotyping algorithms in Electronic Health Records

To develop the optimal serum lipid level phenotyping algorithm in large scale EHR, I tested two cross-sectional measures (first and last measurement), and five longitudinal measurements (including median, and long-term average from four different mixed effects models). The four models are all built using qualified serum lipids measures from Synthetic Derivative (SD) a de-identified version of the Vanderbilt University Medical Center EHR. In total, I extracted 2,154,820 lipid measures from 196,263 individuals. Over 44% of subjects had multiple lipid measures (n=2: 17%; n=3: 9%; n>=4: 18%). The two different SNP-based heritability estimation, REML-based and LD-adjusted, were calculated within the 11,351 unrelated subjects (≥ third degree) of genetically confirmed European-ancestry in BioVU.

Among the seven tested algorithms, the long-term averages across four models are highly correlated (R2>0.99) for all lipid measures, and longitudinal median is slightly less correlated with long-term averages (0.83-0.84 for HDL-C, and 0.87-0.89 for the other three lipids). The two cross-sectional phenotypes have the lowest correlation (0.75 for HDL-C, and 0.63-0.64 for the other three lipids), and longitudinal median have a higher correlation with cross-sectional phenotypes than the correlation between long-term average and cross-sectional phenotypes.

The estimated REML-based heritability for HDL-C is from 32.4%-41.2% across all tested algorithms, and longitudinal median captures highest heritability (41.2%). Also, longitudinal median captures highest heritability for the other three serum lipids (38.2% for LDL-C, 34.4% for TC, and 45.6% for log10 TG). LD-adjusted heritability indicates similar results. Longitudinal median resulted in the highest heritability estimate for HDL-C, LDL-C, and log10 TG. For TC, the first measurement has a slightly higher heritability than median, though this difference is not significant (18.0% for first measures and 17.5% for median, p-value=0.462). I also restricted the samples to the subjects with at least three longitudinal measures (N=8,212, a subset of the previous dataset). The results show the same trend, longitudinal median still captures the highest heritability for HDL-C, LDL-C, and TC in both REML-based and LD-adjusted estimations. For log10 TG, two different long-term averages have slightly but not significantly higher heritability than longitudinal median (model 4 for REML-based, and model 1 for LD-adjusted, Table 3). As indicated by these results, longitudinal median is applied for the subjects with multiple measurements in the following analyses (Table 2).

Tissue-specific genetically regulated expression analysis

Across 49 different tissue models, the GReX of 26,462 unique genes are imputed by PrediXcan. Their associations with both serum lipid levels and dichotomous dyslipidemia status are tested using a GEE model with adjustment for genetically identified family networks.

Adjusting the FDR to account for 49 tissue-specific models yields 134 unique genes significantly correlated with HDL-C, with *CETP* shows most significant across multiple tissues, e.g., lung (p-value=7.38×10^{-110}), esophagus mucosa (p-value=1.43×10^{-106}), and coronary artery (p-value=5.94×10^{-94}). Seventy-four unique genes from PrediXcan are not within 10Mb of the 729 genome-wide significant SNPs identified for HDL-C in BioVU. Twenty-seven of these genes are also not within 1Mb of any of the 622 reported HDL-C associated SNPs from the NHGRI-EBI Catalog, and thus are considered novel (Fig 9, Table 6 and Appendix V). For LDL-C, 164 unique genes have a significant association. The genes around rs629301 have the most significant p-values (*CELSR2* in pancreas: p-value=4.29×10^{-57}; *PSRC1* in whole blood (DGN): p-value=2.67×10^{-56}; *SORT1* in liver: p-value= 3.24×10^{-56}), and 16 of them are novel (not within 10Mb of 1,087 SNPs identified in the BioVU GWAS and not within 1Mb of 466 LDL-C SNPs from the NHGRI-EBI Catalog) (Fig 10, Table 7 and Appendix VI). Results for TC are similar to LDL-C, including 135 unique, significantly associated genes. The most significant genes fall within the ±10Mb region of rs629301, including *SORT1*, *CELSR2* and *PSRC1*. Ten novel genes fall outside of the regions of 1,032 BioVU GWAS SNPs and 580 previously reported SNPs (Fig 11, Table 8 and Appendix VII). For TG, 238 unique genes reach tissue-wide significance; *LPL* is the most significant. Filtering out any genes within the specified regions of 1,357 BioVU GWAS SNPs and 535 NHGRI-EBI Catalog SNPs, 56 unique genes are taken as novel findings. (Fig 12, Table 9 and Appendix VIII). Ten unique genes are found associated with dichotomous dyslipidemia status. One gene, *ATP5O*, has no surrounding variants identified in the BioVU GWAS or in any previously published GWAS (Fig 13 and Table 10).

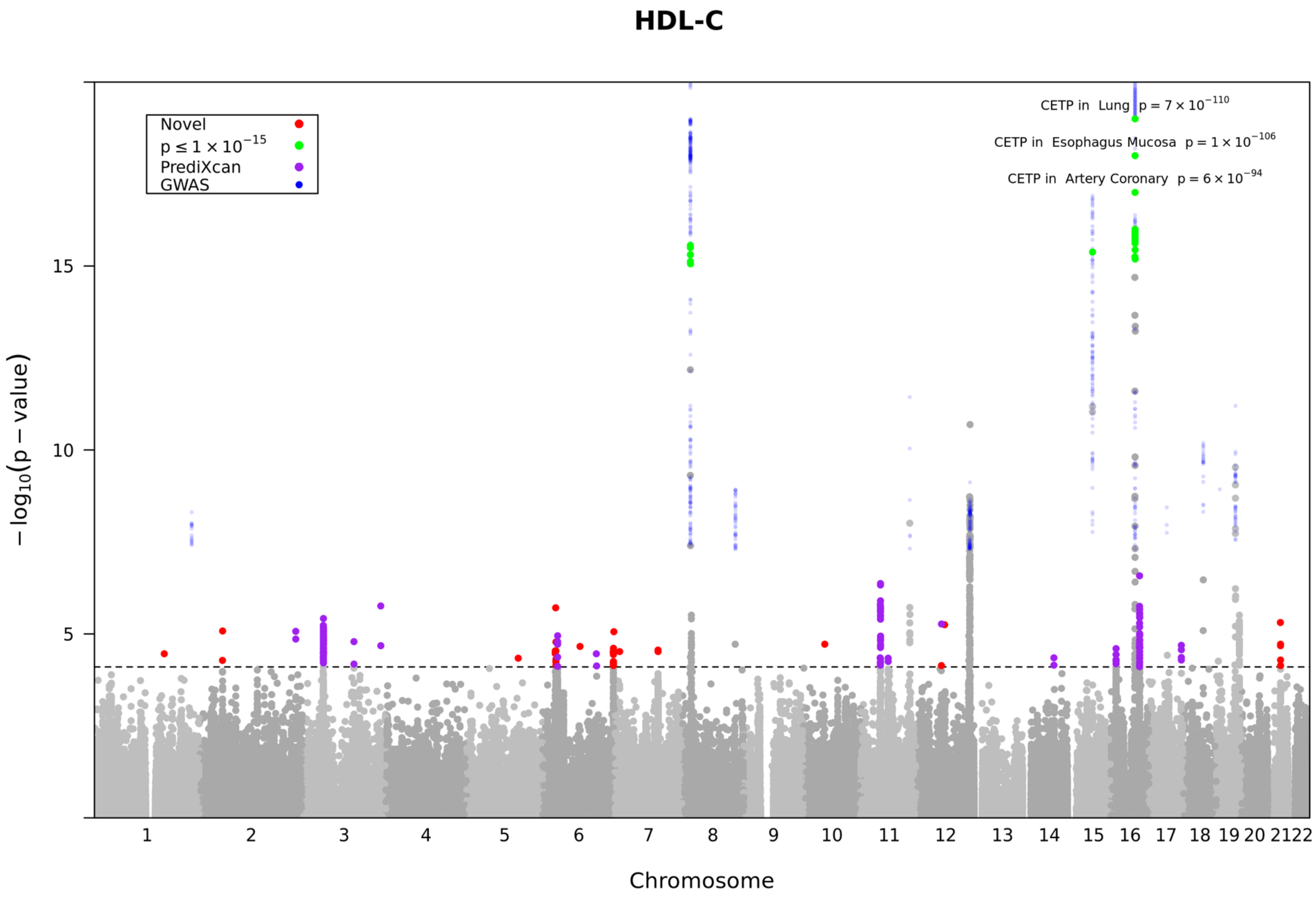

Figure 9. Manhattan plot of tissue-specific GReX association analysis on HDL-C in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 6. Novel HDL-C genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
PPP1R18	Prostate	0.11	70	-1.93	0.41	2.0×10^{-6}	3.8×10^{-3}
LINC00161	Brain Spinal cord cervical c-1	0.07	34	1.82	0.40	4.9×10^{-6}	7.7×10^{-3}
PABPC1P4	Thyroid	0.11	13	2.70	0.59	5.6×10^{-6}	8.4×10^{-3}
ACYP2	Brain Cerebellum	0.21	19	-1.43	0.32	8.4×10^{-6}	1.1×10^{-2}
FRMD1	Esophagus Gastroesophageal Junction	0.02	25	-2.28	0.51	8.7×10^{-6}	1.1×10^{-2}
XXbac-BPG248L24.12	Brain Cerebellum	0.41	45	1.42	0.33	1.7×10^{-5}	1.7×10^{-2}
N6AMT1	Muscle Skeletal	0.15	32	-1.49	0.35	1.9×10^{-5}	1.8×10^{-2}
PGBD3	Skin Sun Exposed Lower leg	0.06	52	-2.19	0.51	1.9×10^{-5}	1.8×10^{-2}
N6AMT1	Brain Caudate basal ganglia	0.07	24	-1.84	0.43	2.1×10^{-5}	1.9×10^{-2}
ORC3	Brain Frontal Cortex BA9	0.06	17	1.68	0.40	2.2×10^{-5}	2.0×10^{-2}
FGFR1OP	Skin Sun Exposed Lower leg	0.04	17	-2.87	0.68	2.5×10^{-5}	2.2×10^{-2}
SPDYE6	Testis	0.07	19	-1.72	0.41	2.7×10^{-5}	2.3×10^{-2}
IFITM4P	Small Intestine Terminal Ileum	0.18	59	1.61	0.38	2.9×10^{-5}	2.4×10^{-2}
HCG27	Adipose Subcutaneous	0.39	46	-0.91	0.22	2.9×10^{-5}	2.5×10^{-2}
FGFR1OP	Esophagus Muscularis	0.06	18	-2.37	0.57	3.0×10^{-5}	2.5×10^{-2}
POLR2J	Adipose Visceral Omentum	0.03	28	-2.16	0.52	3.0×10^{-5}	2.5×10^{-2}
PHF14	DGN-WB	0.03	12	-3.54	0.85	3.0×10^{-5}	2.5×10^{-2}
AL133458.1	Stomach	0.07	7	2.98	0.71	3.1×10^{-5}	2.5×10^{-2}
FGFR1OP	Esophagus Mucosa	0.04	10	-5.23	1.26	3.1×10^{-5}	2.6×10^{-2}
FAM103A2P	Pancreas	0.07	15	3.36	0.81	3.2×10^{-5}	2.6×10^{-2}
RPS17P1	Esophagus Mucosa	0.03	8	3.67	0.88	3.4×10^{-5}	2.7×10^{-2}
RXRG	Liver	0.04	28	-2.24	0.54	3.5×10^{-5}	2.7×10^{-2}
RNASET2	Esophagus Gastroesophageal Junction	0.12	58	1.32	0.32	3.7×10^{-5}	2.8×10^{-2}
CEP120	Skin Sun Exposed Lower leg	0.04	35	2.36	0.58	4.6×10^{-5}	3.3×10^{-2}
HLA-B	Skin Sun Exposed Lower leg	0.11	29	-1.56	0.38	4.9×10^{-5}	3.5×10^{-2}
N6AMT1	Adrenal Gland	0.04	37	-2.18	0.54	5.1×10^{-5}	3.6×10^{-2}
GPR75	Colon Transverse	0.02	4	-9.03	2.23	5.2×10^{-5}	3.7×10^{-2}
HLA-B	Skin Not Sun Exposed Suprapubic	0.06	13	-2.18	0.54	5.6×10^{-5}	3.8×10^{-2}
FGFR1OP	Thyroid	0.10	28	-1.54	0.38	5.6×10^{-5}	3.8×10^{-2}
HCG27	Brain Hypothalamus	0.11	37	-1.79	0.44	5.7×10^{-5}	3.9×10^{-2}
RNASET2	Heart Atrial Appendage	0.03	46	2.31	0.58	5.9×10^{-5}	3.9×10^{-2}
FGFR1OP	Whole Blood	0.04	10	-4.12	1.03	6.5×10^{-5}	4.3×10^{-2}
RNASET2	Thyroid	0.14	44	1.38	0.35	6.7×10^{-5}	4.4×10^{-2}
XXbac-BPG248L24.12	Brain Cerebellar Hemisphere	0.47	58	1.05	0.26	7.0×10^{-5}	4.6×10^{-2}
COQ10A	Artery Tibial	0.03	6	-5.77	1.45	7.2×10^{-5}	4.7×10^{-2}
RWDD2B	Ovary	0.10	34	1.97	0.50	7.2×10^{-5}	4.7×10^{-2}
FGFR1OP	Colon Sigmoid	0.04	9	-3.12	0.79	7.3×10^{-5}	4.7×10^{-2}

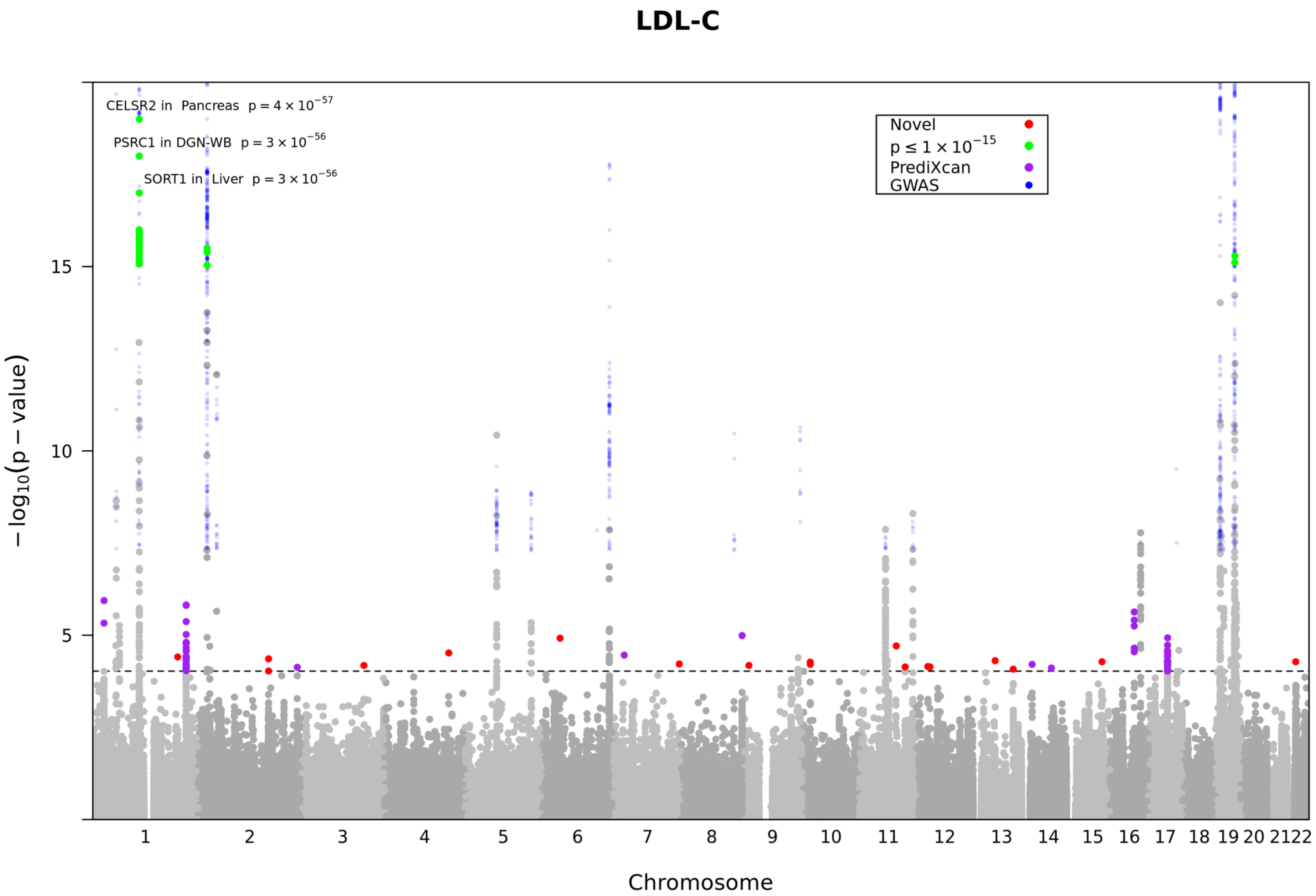

Figure 10. Manhattan plot of tissue-specific GReX association analysis on LDL-C in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

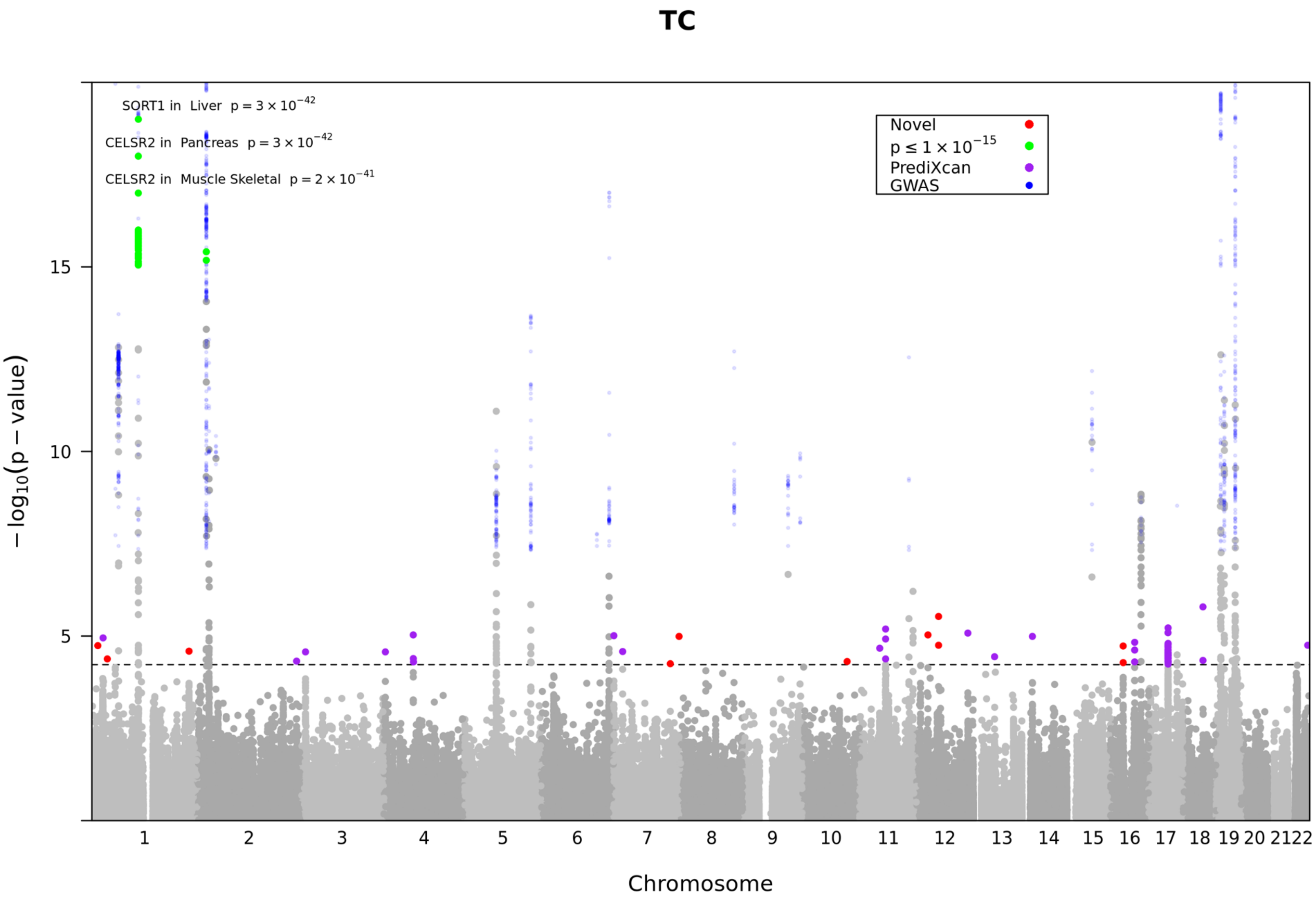

Figure 11. Manhattan plot of tissue-specific GReX association analysis on TC in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 7. Novel LDL-C genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
MRPL14	Spleen	0.06	13	-5.84	1.33	1.2×10^{-5}	1.1×10^{-2}
RP11-777F6.3	Artery Aorta	0.05	7	-7.04	1.65	2.0×10^{-5}	1.5×10^{-2}
SH3D19	Pancreas	0.02	22	-6.57	1.58	3.0×10^{-5}	2.2×10^{-2}
C1orf106	Minor Salivary Gland	0.24	35	2.25	0.55	3.9×10^{-5}	2.6×10^{-2}
TTC21B	Breast Mammary Tissue	0.07	9	-8.06	1.97	4.4×10^{-5}	2.9×10^{-2}
WDFY2	Adipose Subcutaneous	0.07	61	2.95	0.73	4.9×10^{-5}	3.1×10^{-2}
GNB1L	Brain Caudate basal ganglia	0.08	73	2.29	0.57	5.2×10^{-5}	3.3×10^{-2}
CPEB1	Brain Cerebellar Hemisphere	0.05	10	4.97	1.23	5.3×10^{-5}	3.3×10^{-2}
ARL5B	Whole Blood	0.02	33	7.08	1.75	5.4×10^{-5}	3.4×10^{-2}
AC144652.1	Brain Nucleus accumbens basal ganglia	0.08	32	2.62	0.65	6.0×10^{-5}	3.6×10^{-2}
ARL5B	Cells EBV-transformed lymphocytes	0.22	42	3.30	0.82	6.2×10^{-5}	3.7×10^{-2}
FREM1	Lung	0.28	18	2.07	0.52	6.5×10^{-5}	3.8×10^{-2}
TM4SF4	Breast Mammary Tissue	0.04	25	4.70	1.18	6.5×10^{-5}	3.8×10^{-2}
ITPR2	Brain Cerebellar Hemisphere	0.47	74	1.43	0.36	7.1×10^{-5}	4.1×10^{-2}
ACAT1	Thyroid	0.32	28	-1.69	0.43	7.2×10^{-5}	4.1×10^{-2}
H3F3C	Ovary	0.05	36	2.46	0.62	7.2×10^{-5}	4.1×10^{-2}
TGDS	Liver	0.25	13	-2.46	0.63	8.4×10^{-5}	4.6×10^{-2}
TTC21B	Adipose Subcutaneous	0.08	33	-4.43	1.14	9.3×10^{-5}	5.0×10^{-2}

Table 8. Novel TC genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
GALNT6	Whole Blood	0.19	11	-3.73	0.80	2.9×10^{-6}	4.9×10^{-3}
ITPR2	Brain Cerebellar Hemisphere	0.47	74	1.78	0.40	9.4×10^{-6}	1.3×10^{-2}
AC144652.1	Brain Nucleus accumbens basal ganglia	0.08	32	3.23	0.73	1.0×10^{-5}	1.4×10^{-2}
GALNT6	DGN-WB	0.30	23	-2.34	0.54	1.8×10^{-5}	2.2×10^{-2}
PRDM2	Stomach	0.03	18	10.99	2.56	1.8×10^{-5}	2.2×10^{-2}
MVP	Nerve Tibial	0.10	16	-3.79	0.89	1.9×10^{-5}	2.3×10^{-2}
HMGN2P19	Colon Sigmoid	0.24	95	1.77	0.42	2.6×10^{-5}	2.9×10^{-2}
ADPRHL2	Artery Aorta	0.08	36	4.37	1.07	4.1×10^{-5}	4.0×10^{-2}
ITPRIP	Brain Anterior cingulate cortex BA24	0.06	28	-4.12	1.01	4.9×10^{-5}	4.5×10^{-2}
SEZ6L2	Thyroid	0.02	27	-5.24	1.30	5.3×10^{-5}	4.7×10^{-2}
BPGM	Artery Tibial	0.03	29	-5.01	1.24	5.7×10^{-5}	4.9×10^{-2}

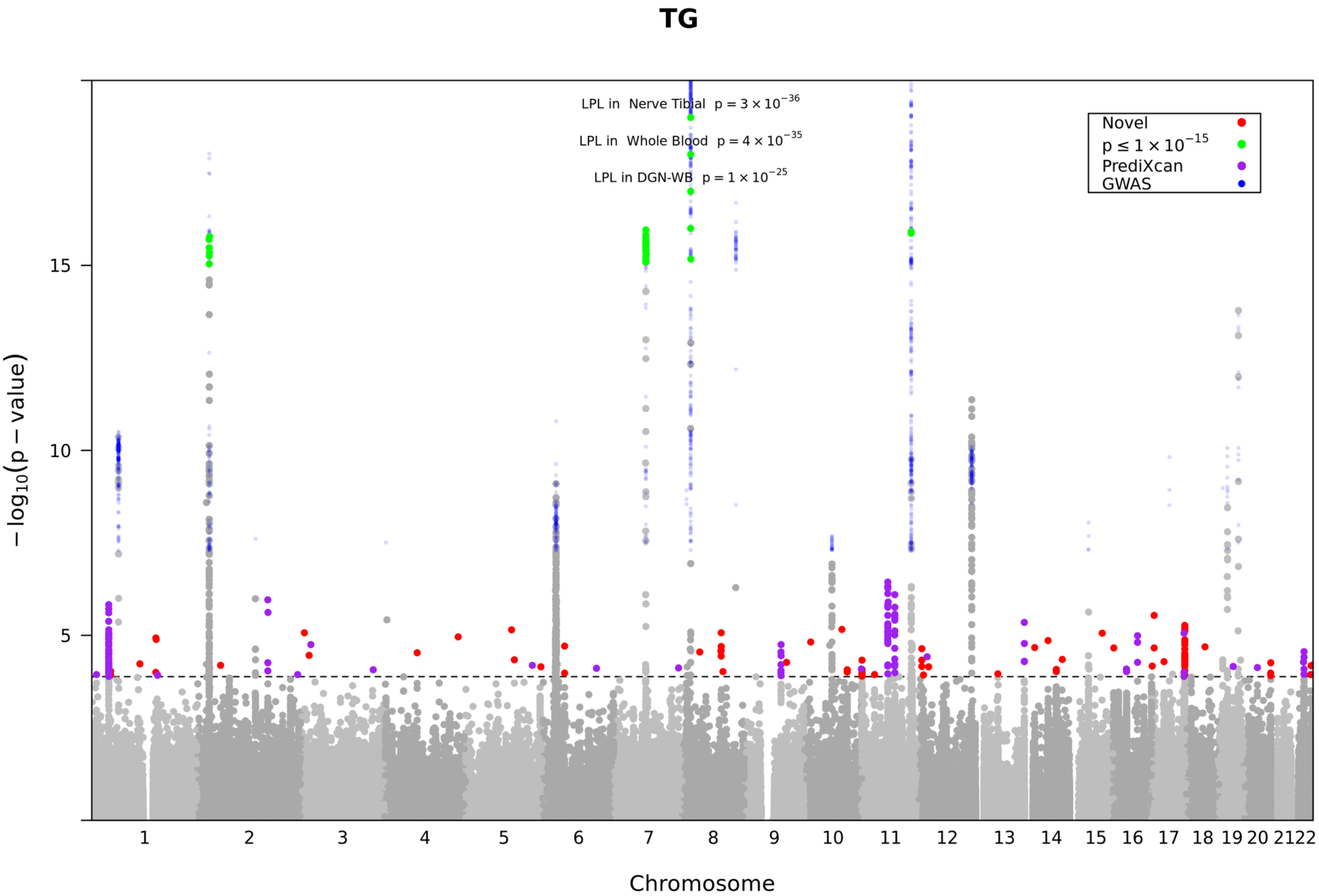

Figure 12. Manhattan plot of tissue-specific GReX association analysis on TG in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 9. Novel TG genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
WSCD1	Heart Atrial Appendage	0.03	7	-0.11	0.02	2.9×10^{-6}	2.8×10^{-3}
CCDC40	Brain Caudate basal ganglia	0.13	56	-0.04	0.01	5.3×10^{-6}	4.6×10^{-3}
CCDC40	Artery Coronary	0.30	38	-0.03	0.01	6.2×10^{-6}	5.2×10^{-3}
FAM35A	Artery Tibial	0.03	44	0.06	0.01	6.9×10^{-6}	5.8×10^{-3}
CCDC40	Small Intestine Terminal Ileum	0.33	13	-0.04	0.01	7.0×10^{-6}	5.8×10^{-3}
FER	Colon Transverse	0.03	27	0.07	0.02	7.1×10^{-6}	5.9×10^{-3}
CCDC40	DGN-WB	0.23	5	-0.04	0.01	7.6×10^{-6}	6.2×10^{-3}
SSUH2	Small Intestine Terminal Ileum	0.10	27	0.05	0.01	8.4×10^{-6}	6.7×10^{-3}
TMEM64	Skin Sun Exposed Lower leg	0.08	52	0.07	0.01	8.6×10^{-6}	6.8×10^{-3}
FBXO22	Adrenal Gland	0.12	31	-0.06	0.01	8.7×10^{-6}	6.8×10^{-3}
GALNTL6	Colon Sigmoid	0.10	27	-0.07	0.02	1.1×10^{-5}	8.2×10^{-3}
LYSMD1	Stomach	0.12	20	-0.06	0.01	1.2×10^{-5}	8.7×10^{-3}
C2CD4D	Skin Not Sun Exposed Suprapubic	0.06	37	-0.06	0.01	1.3×10^{-5}	9.2×10^{-3}
CCDC40	Spleen	0.45	9	-0.03	0.01	1.3×10^{-5}	9.5×10^{-3}
SOCS4	Nerve Tibial	0.05	39	0.08	0.02	1.4×10^{-5}	9.8×10^{-3}
CCDC40	Minor Salivary Gland	0.16	8	-0.05	0.01	1.5×10^{-5}	1.0×10^{-2}
FAM171A1	Skin Not Sun Exposed Suprapubic	0.04	33	-0.06	0.01	1.5×10^{-5}	1.1×10^{-2}
CCDC40	Brain Cerebellar Hemisphere	0.51	18	-0.03	0.01	1.8×10^{-5}	1.2×10^{-2}
GSTA2	Liver	0.32	29	0.03	0.01	2.0×10^{-5}	1.3×10^{-2}
TMEM64	Whole Blood	0.02	14	-0.12	0.03	2.0×10^{-5}	1.3×10^{-2}
KATNAL2	Heart Left Ventricle	0.03	47	-0.06	0.01	2.0×10^{-5}	1.3×10^{-2}
THTPA	Skin Sun Exposed Lower leg	0.04	61	0.06	0.01	2.1×10^{-5}	1.3×10^{-2}
LMF1	Testis	0.09	38	-0.05	0.01	2.2×10^{-5}	1.4×10^{-2}
WSCD1	DGN-WB	0.02	4	-0.14	0.03	2.2×10^{-5}	1.4×10^{-2}
COPS7A	Adipose Subcutaneous	0.05	49	-0.05	0.01	2.3×10^{-5}	1.4×10^{-2}
CCDC40	Artery Aorta	0.47	14	-0.02	0.01	2.4×10^{-5}	1.4×10^{-2}
LINC01030	Thyroid	0.02	7	0.17	0.04	2.5×10^{-5}	1.5×10^{-2}
DECR1	Pituitary	0.07	22	-0.06	0.02	2.7×10^{-5}	1.6×10^{-2}
SFRP1	Liver	0.13	27	-0.05	0.01	2.8×10^{-5}	1.7×10^{-2}
USO1	Pancreas	0.11	11	0.06	0.02	3.0×10^{-5}	1.7×10^{-2}
CCDC40	Esophagus Gastroesophageal Junction	0.25	17	-0.03	0.01	3.1×10^{-5}	1.8×10^{-2}
CCDC40	Muscle Skeletal	0.17	34	-0.04	0.01	3.2×10^{-5}	1.8×10^{-2}
CCDC40	Breast Mammary Tissue	0.35	13	-0.03	0.01	3.5×10^{-5}	2.0×10^{-2}
EFHB	Testis	0.10	74	-0.04	0.01	3.5×10^{-5}	2.0×10^{-2}
CCDC40	Brain Nucleus accumbens basal ganglia	0.30	34	-0.04	0.01	3.6×10^{-5}	2.0×10^{-2}
LINC01030	Brain Nucleus accumbens basal ganglia	0.10	62	0.04	0.01	3.7×10^{-5}	2.1×10^{-2}
CCDC40	Cells Transformed fibroblasts	0.48	12	-0.02	0.01	3.8×10^{-5}	2.2×10^{-2}
CCDC40	Whole Blood	0.19	44	-0.04	0.01	4.0×10^{-5}	2.2×10^{-2}
CCDC40	Esophagus Mucosa	0.39	13	-0.03	0.01	4.2×10^{-5}	2.3×10^{-2}
PTPN21	Heart Atrial Appendage	0.03	43	0.07	0.02	4.5×10^{-5}	2.4×10^{-2}
CCDC40	Brain Putamen basal ganglia	0.30	24	-0.03	0.01	4.5×10^{-5}	2.4×10^{-2}

Table 9. Novel TG genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
FEM1C	Adipose Subcutaneous	0.09	35	-0.05	0.01	4.6×10^{-5}	2.5×10^{-2}
MLF2	Adipose Visceral Omentum	0.08	46	0.05	0.01	4.7×10^{-5}	2.5×10^{-2}
AP006621.5	Minor Salivary Gland	0.27	56	0.02	0.01	4.7×10^{-5}	2.5×10^{-2}
CCDC40	Brain Cerebellum	0.44	13	-0.03	0.01	4.9×10^{-5}	2.6×10^{-2}
CRLF3	Ovary	0.18	26	0.04	0.01	5.2×10^{-5}	2.7×10^{-2}
ZNF782	Brain Cortex	0.05	23	-0.07	0.02	5.4×10^{-5}	2.8×10^{-2}
ZNF512B	Brain Cerebellum	0.03	11	0.08	0.02	5.5×10^{-5}	2.8×10^{-2}
CCDC40	Adipose Subcutaneous	0.51	35	-0.02	0.01	5.8×10^{-5}	2.9×10^{-2}
RP11-426L16.8	Brain Nucleus accumbens basal ganglia	0.11	45	0.03	0.01	5.9×10^{-5}	3.0×10^{-2}
CCDC40	Adipose Visceral Omentum	0.34	13	-0.03	0.01	6.1×10^{-5}	3.0×10^{-2}
MAPK11	Esophagus Muscularis	0.02	21	-0.09	0.02	6.3×10^{-5}	3.1×10^{-2}
ACYP2	Brain Cerebellum	0.21	19	0.04	0.01	6.5×10^{-5}	3.2×10^{-2}
CDPF1	Brain Anterior cingulate cortex BA24	0.06	58	0.04	0.01	6.6×10^{-5}	3.2×10^{-2}
CCDC40	Stomach	0.23	27	-0.03	0.01	6.6×10^{-5}	3.2×10^{-2}
CCDC40	Brain Cortex	0.39	29	-0.02	0.01	6.7×10^{-5}	3.2×10^{-2}
MYO1C	Nerve Tibial	0.02	68	0.04	0.01	6.7×10^{-5}	3.2×10^{-2}
COPS7A	Nerve Tibial	0.11	16	-0.06	0.02	7.0×10^{-5}	3.3×10^{-2}
ETNK1	Artery Aorta	0.05	26	-0.07	0.02	7.0×10^{-5}	3.3×10^{-2}
FAM153C	Brain Putamen basal ganglia	0.07	22	0.09	0.02	7.1×10^{-5}	3.3×10^{-2}
RPLP2	Heart Left Ventricle	0.06	11	0.07	0.02	8.3×10^{-5}	3.7×10^{-2}
NPC2	Nerve Tibial	0.07	50	-0.05	0.01	8.3×10^{-5}	3.7×10^{-2}
EBAG9P1	Pituitary	0.05	7	0.08	0.02	8.4×10^{-5}	3.7×10^{-2}
PNPLA2	Brain Cerebellar Hemisphere	0.08	26	-0.06	0.01	8.8×10^{-5}	3.9×10^{-2}
CCDC40	Liver	0.36	9	-0.03	0.01	8.9×10^{-5}	3.9×10^{-2}
IPO13	Muscle Skeletal	0.01	7	-0.16	0.04	9.4×10^{-5}	4.0×10^{-2}
RP3-449M8.6	Colon Sigmoid	0.09	14	0.05	0.01	9.5×10^{-5}	4.1×10^{-2}
CCNE2	Breast Mammary Tissue	0.04	3	-0.15	0.04	9.6×10^{-5}	4.1×10^{-2}
EBAG9P1	Esophagus Muscularis	0.11	18	0.05	0.01	9.8×10^{-5}	4.2×10^{-2}
CDC42SE1	Brain Frontal Cortex BA9	0.18	12	-0.07	0.02	9.9×10^{-5}	4.2×10^{-2}
GSTA2	Pancreas	0.06	24	0.07	0.02	1.0×10^{-4}	4.3×10^{-2}
STMN3	Esophagus Muscularis	0.07	11	0.09	0.02	1.0×10^{-4}	4.3×10^{-2}
PIDD	Adipose Visceral Omentum	0.17	31	0.03	0.01	1.1×10^{-4}	4.4×10^{-2}
AP006621.1	Brain Putamen basal ganglia	0.47	46	0.02	0.01	1.1×10^{-4}	4.4×10^{-2}
WDFY2	Nerve Tibial	0.31	22	0.03	0.01	1.1×10^{-4}	4.5×10^{-2}
WDFY2	Adipose Visceral Omentum	0.06	7	0.07	0.02	1.1×10^{-4}	4.5×10^{-2}
AP006621.1	Spleen	0.55	46	0.02	0.01	1.1×10^{-4}	4.5×10^{-2}
CCDC40	Adrenal Gland	0.38	23	-0.03	0.01	1.1×10^{-4}	4.6×10^{-2}
CTA-217C2.1	Breast Mammary Tissue	0.09	43	0.04	0.01	1.2×10^{-4}	4.6×10^{-2}
ARL14EP	Testis	0.40	30	-0.03	0.01	1.2×10^{-4}	4.6×10^{-2}
EFNA1	Thyroid	0.02	15	-0.10	0.02	1.2×10^{-4}	4.7×10^{-2}
ATP6V0B	Whole Blood	0.12	5	0.06	0.02	1.2×10^{-4}	4.7×10^{-2}

Table 9. Novel TG genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR
KLRAP1	Brain Frontal Cortex BA9	0.05	46	-0.04	0.01	1.2×10^{-4}	4.7×10^{-2}
CEND1	Heart Left Ventricle	0.14	10	0.05	0.01	1.2×10^{-4}	4.8×10^{-2}
UCKL1	Thyroid	0.06	33	-0.06	0.02	1.2×10^{-4}	4.8×10^{-2}
AP006621.1	Brain Hypothalamus	0.54	27	0.02	0.00	1.3×10^{-4}	4.9×10^{-2}

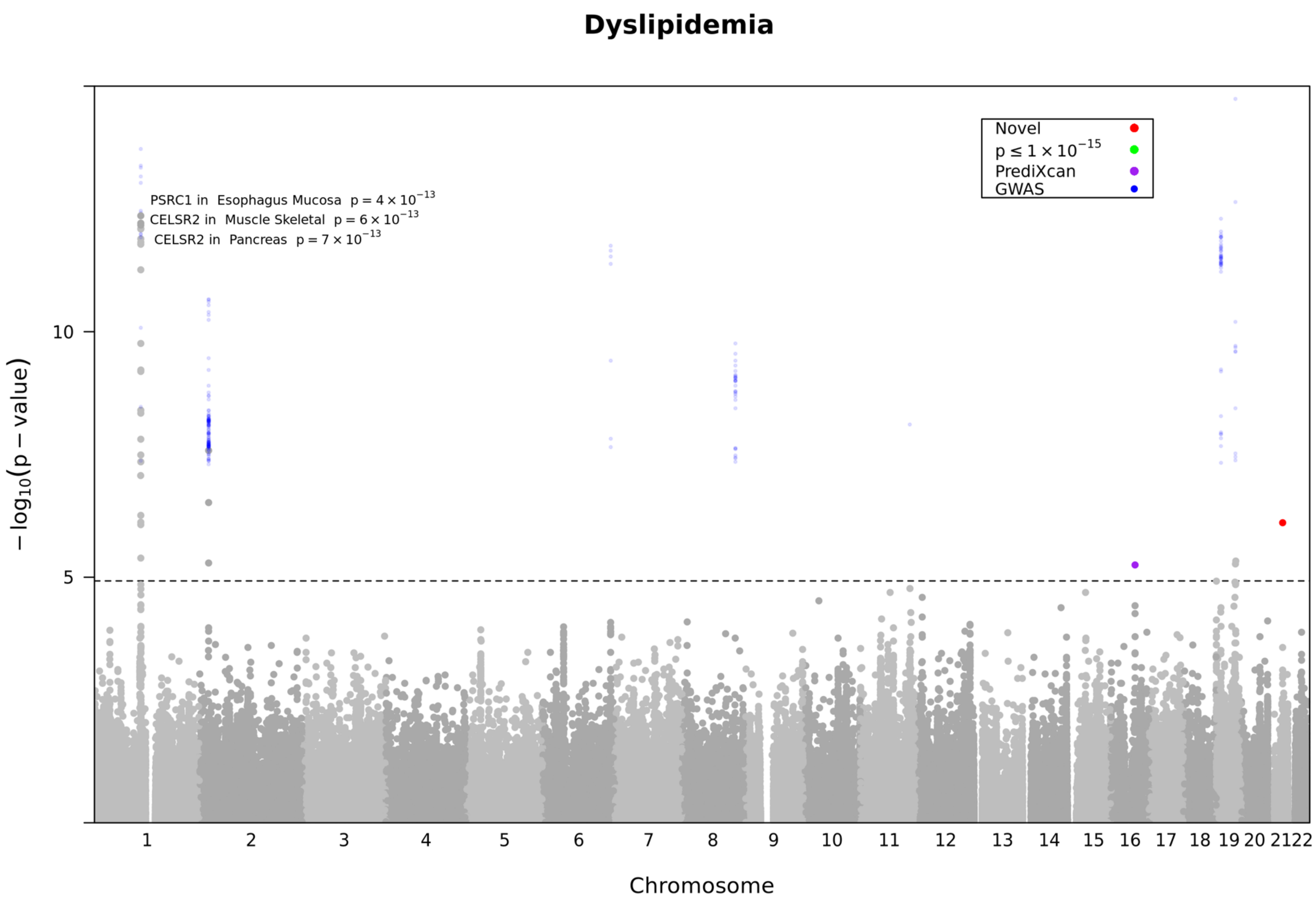

Figure 13. Manhattan plot of tissue-specific GReX association analysis on dyslipidemia in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 10. Dyslipidemia significant genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
PSRC1	Esophagus Mucosa	0.17	17	-0.22	0.03	4.3×10^{-13}	4.2×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	Muscle Skeletal	0.39	13	-0.14	0.02	6.2×10^{-13}	4.2×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	Pancreas	0.02	5	-1.04	0.14	6.8×10^{-13}	4.2×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SORT1	Liver	0.58	25	-0.13	0.02	8.0×10^{-13}	4.2×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Liver	0.48	50	-0.13	0.02	8.0×10^{-13}	4.2×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	Liver	0.45	15	-0.15	0.02	1.3×10^{-12}	5.4×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SORT1	Minor Salivary Gland	0.07	13	-0.43	0.06	1.5×10^{-12}	5.4×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	DGN-WB	0.25	11	-0.17	0.02	1.7×10^{-12}	5.4×10^{-8}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Heart Left Ventricle	0.04	7	-0.69	0.10	5.5×10^{-12}	1.6×10^{-7}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Nerve Tibial	0.02	7	-0.60	0.09	1.7×10^{-10}	4.5×10^{-6}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSMA5	Liver	0.09	33	-0.24	0.04	6.0×10^{-10}	1.4×10^{-5}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Testis	0.18	14	-0.21	0.03	6.5×10^{-10}	1.4×10^{-5}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Brain Cortex	0.13	17	-0.28	0.05	4.0×10^{-9}	8.0×10^{-5}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Muscle Skeletal	0.08	45	-0.26	0.04	4.6×10^{-9}	8.5×10^{-5}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	Brain Cerebellum	0.08	11	-0.39	0.07	1.5×10^{-8}	2.7×10^{-4}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)

Table 10. Dyslipidemia significant genes from tissue-specific GReX analysis in BioVU

Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
APOB	Colon Sigmoid	0.05	15	-0.46	0.08	2.6×10^{-8}	4.3×10^{-4}	rs515135 (pval=2.18×10^{-11})	rs577584 pval=1×10^{-229} (LDL-C, Klarin, 30275531)
PSRC1	Skin Not Sun Exposed Suprapubic	0.20	63	-0.15	0.03	3.2×10^{-8}	4.9×10^{-4}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	Esophagus Mucosa	0.15	17	-0.20	0.04	4.5×10^{-8}	6.4×10^{-4}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CLCC1	Heart Left Ventricle	0.09	36	0.21	0.04	8.5×10^{-8}	1.2×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
APOB	Esophagus Gastroesophageal Junction	0.03	10	-0.38	0.07	3.0×10^{-7}	3.9×10^{-3}	rs515135 (pval=2.18×10^{-11})	rs577584 pval=1×10^{-229} (LDL-C, Klarin, 30275531)
PSRC1	Pancreas	0.16	26	-0.15	0.03	5.5×10^{-7}	6.8×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Adipose Visceral Omentum	0.04	22	-0.34	0.07	7.6×10^{-7}	8.8×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
ATP5O	Pituitary	0.07	23	-0.24	0.05	7.8×10^{-7}	8.8×10^{-3}		
PSRC1	Colon Transverse	0.14	9	-0.22	0.05	8.6×10^{-7}	9.3×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	Whole Blood	0.04	12	-0.30	0.07	4.0×10^{-6}	4.2×10^{-2}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
DMPK	Stomach	0.06	23	-0.34	0.07	4.7×10^{-6}	4.7×10^{-2}	rs7412 (pval=1.82×10^{-15})	APOE region
APOB	Adipose Subcutaneous	0.19	18	0.14	0.03	5.1×10^{-6}	4.9×10^{-2}	rs515135 (pval=2.18×10^{-11})	rs577584 pval=1×10^{-229} (LDL-C, Klarin, 30275531)
APOC4	Brain Nucleus accumbens basal ganglia	0.11	79	-0.10	0.02	5.3×10^{-6}	5.0×10^{-2}	rs7412 (pval=1.82×10^{-15})	APOE region
CETP	Lung	0.05	10	0.33	0.07	5.6×10^{-6}	5.0×10^{-2}		rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)

In HCHS/SOL, two genes are significantly associated with HDL-C across multiple tissues, including *CETP* and *NLRC5*; both are near rs821840, a GWAS significant SNP from HCHS/SOL (Fig 14 and Table 11). Fifteen unique genes have a significant association with TG, and most of them are within 10Mb of rs1260326 (chromosome 2), except *ZNF259* which is near rs964184 (chromosome 11, Fig 17 and Table 11). However, no genes reach significance for LDL-C and TC after accounting for multiple hypothesis testing (Fig 15 & 16). For dyslipidemia, five unique genes are significantly associated, but most of them are both within 10Mb of HCHS/SOL GWAS SNPs and previously reported serum lipids SNPs, except *PDGFC* which only has only been reported as suggestively associated with HDL-C[35] (p-value=1×10^{-08}, Fig 18).

In addition, to test the effect of including medication-adjusted serum lipid measures, I also compared the log-transformed p-values of the GEE on GReX analyses to analogous results containing only drug-naïve measurements for both BioVU and HCHS/SOL. In BioVU, results containing only drug naïve measures are highly correlated with those including LLD-adjusted measures of all four serum lipids (R^2= 0.87 for HDL-C, 0.77 for LDL-C, 0.75 for TC, and 0.80 for TG, Fig 19). Similarly, the correlations between with and without LLD-adjusted lipid measures are high in HCHS/SOL (R^2= 0.84 for HDL-C, 0.79 for LDL-C, 0.79 for TC, and 0.88 for TG, Fig 20).

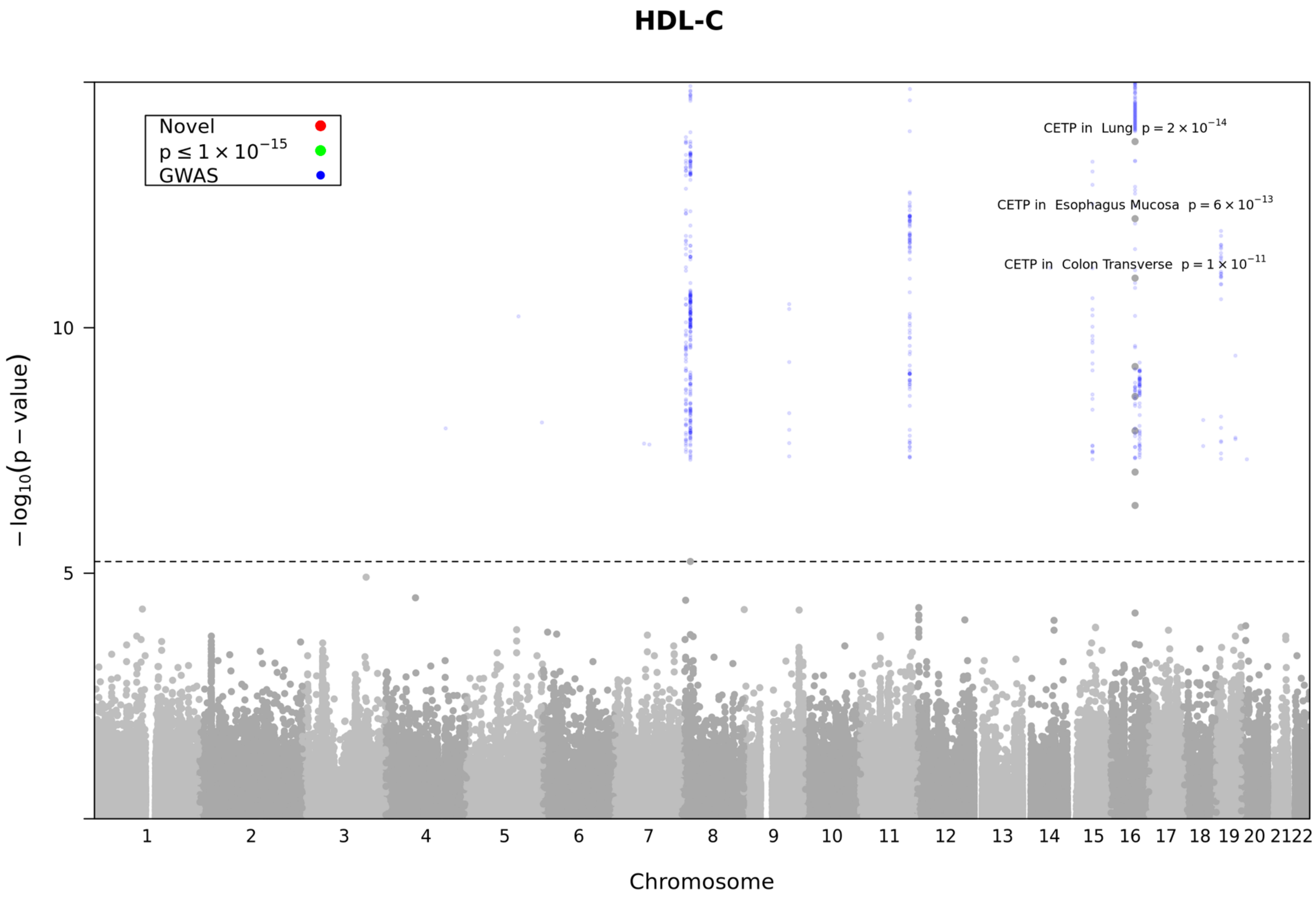

Figure 14. Manhattan plot of tissue-specific GReX association analysis on HDL-C in HCHS/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

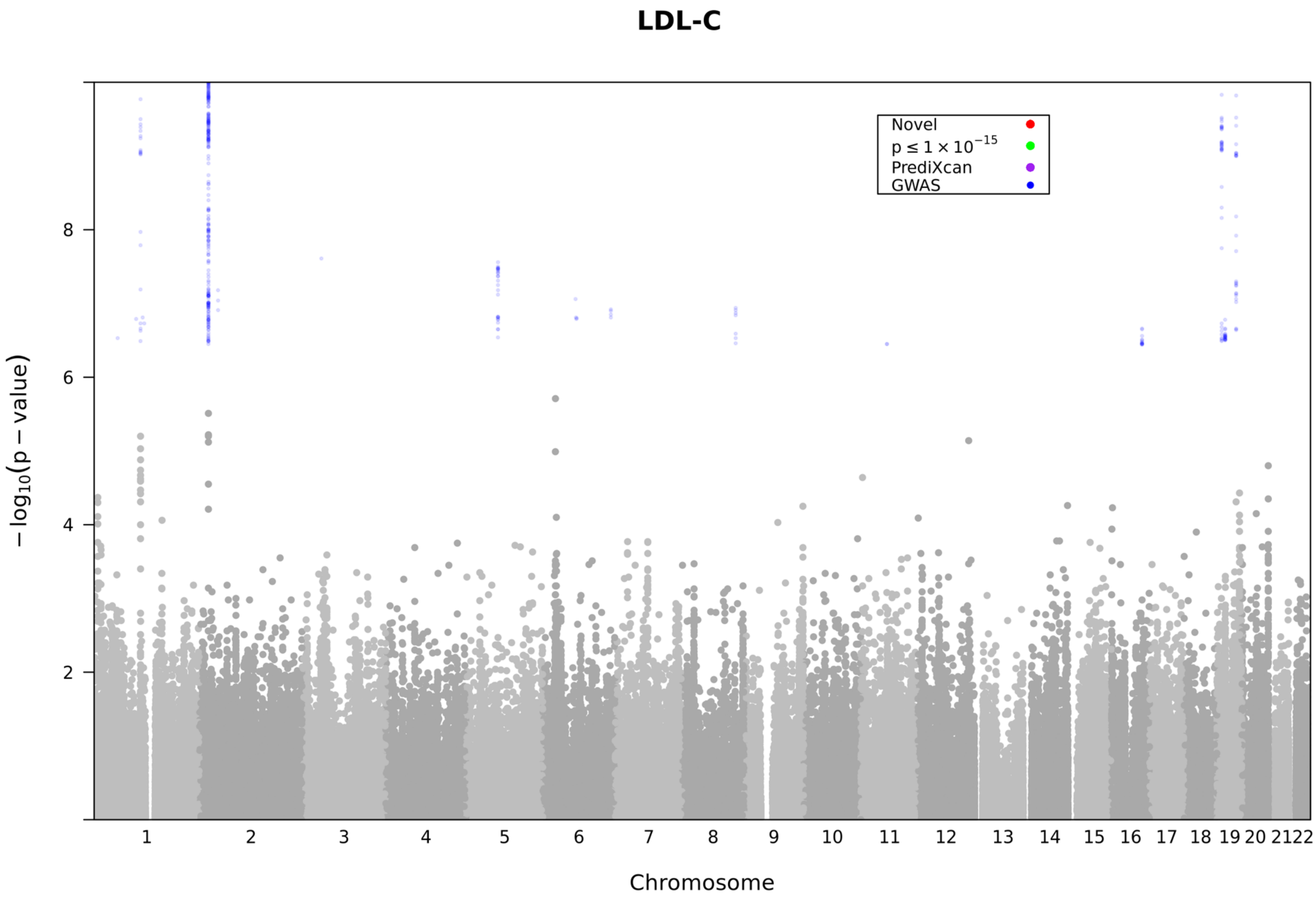

Figure 15. Manhattan plot of tissue-specific GReX association analysis on LDL-C in HCHS/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

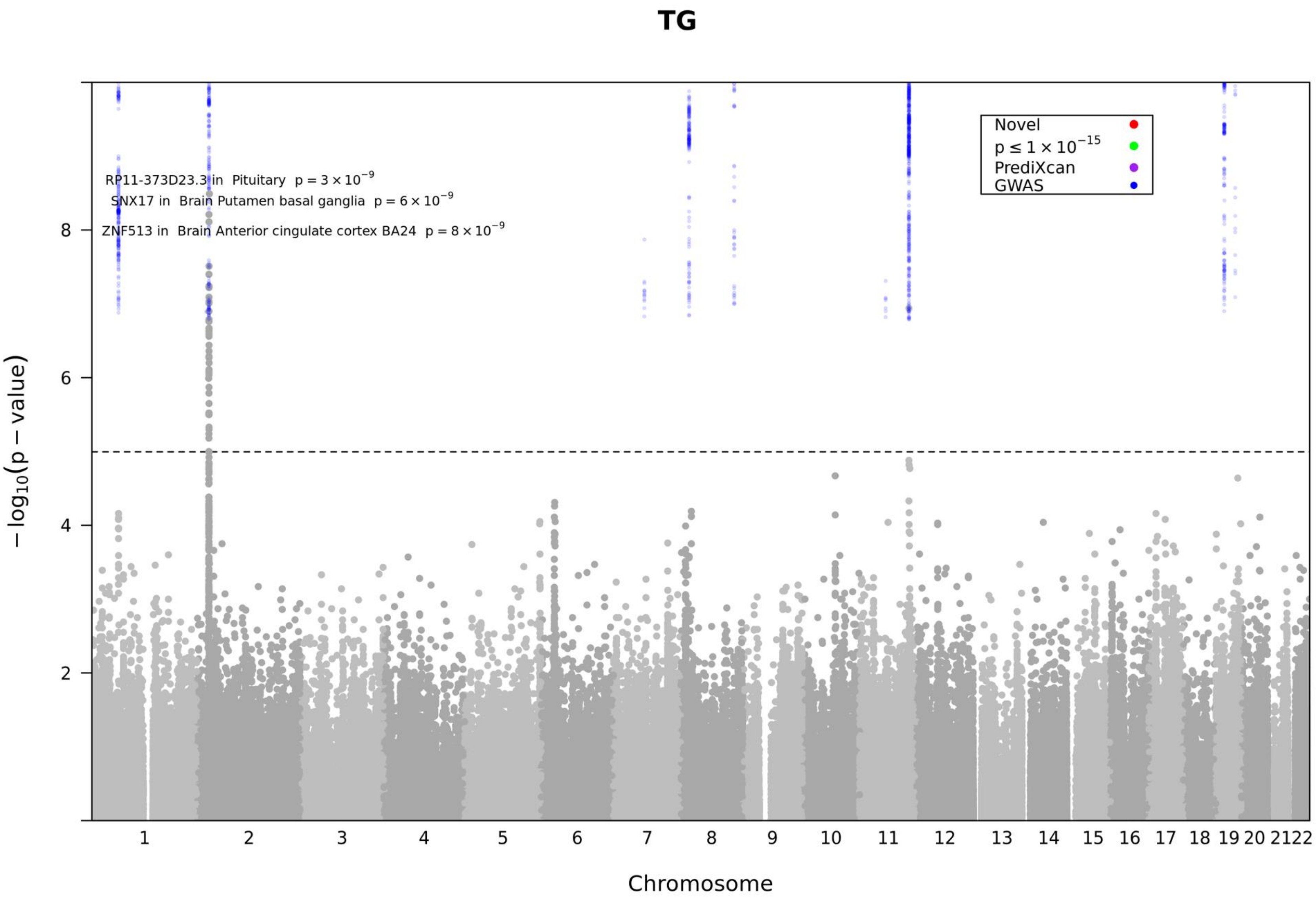

Figure 16. Manhattan plot of tissue-specific GReX association analysis on TG in HCHS/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

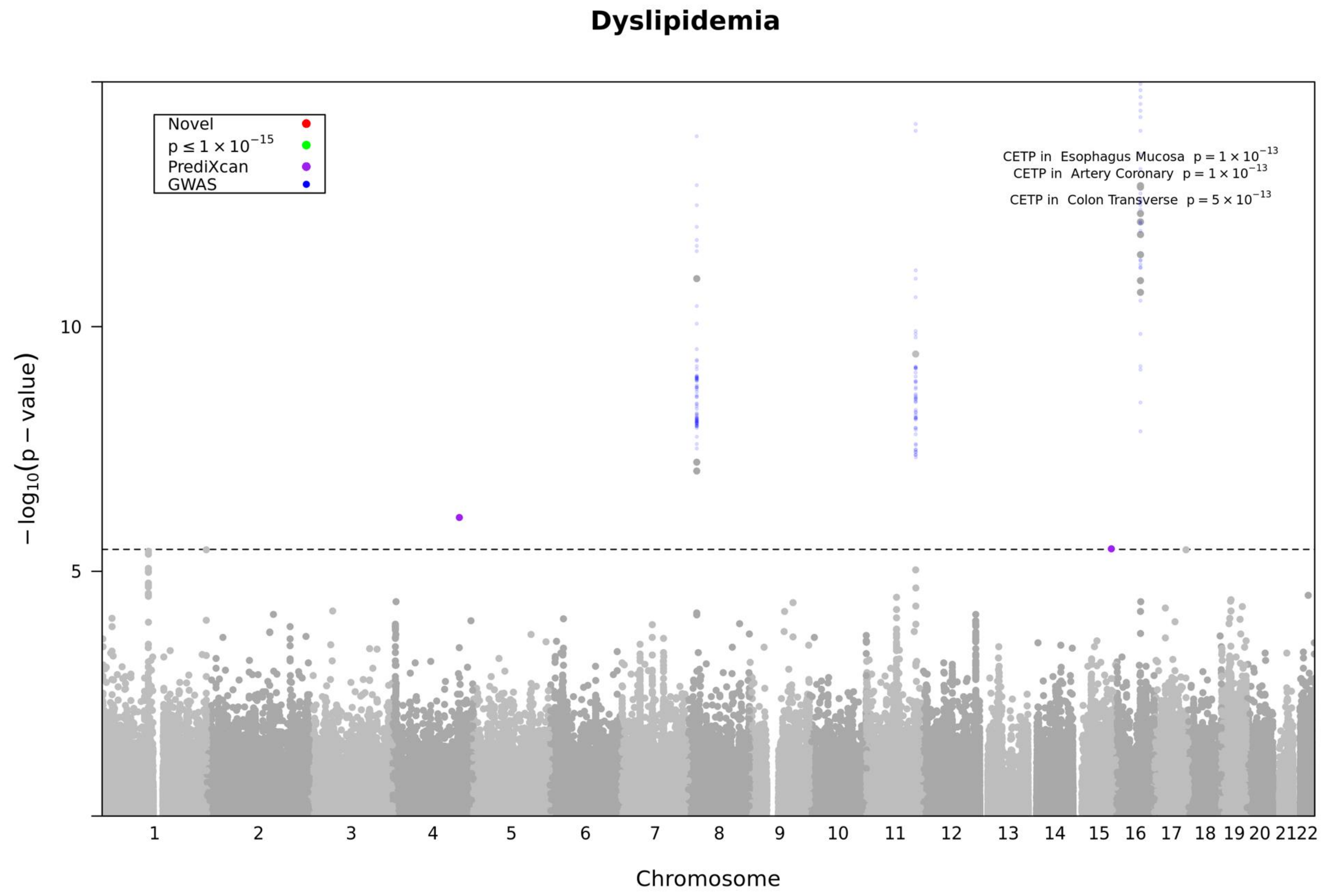

Figure 18. Manhattan plot of tissue-specific GReX association analysis on dyslipidemia in HCHS/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 11. Serum lipid significant genes from tissue-specific GReX analysis in HCHS/SOL

Trait	Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
									GWAS	NHGRI-EBI
HDL-C	CETP	Lung	0.05	10	-18.59	2.42	1.6×10^{-14}	4.3×10^{-9}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	CETP	Esophagus Mucosa	0.02	7	-29.86	4.15	6.0×10^{-13}	7.8×10^{-8}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	CETP	Colon Transverse	0.08	31	-8.72	1.28	9.8×10^{-12}	8.5×10^{-7}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	CETP	Small Intestine Terminal Ileum	0.15	19	-9.86	1.59	6.2×10^{-10}	4.0×10^{-5}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	CETP	Cells Transformed fibroblasts	0.09	10	-11.39	1.91	2.5×10^{-9}	1.3×10^{-4}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	CETP	Artery Coronary	0.10	3	-11.99	2.11	1.3×10^{-8}	5.4×10^{-4}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	NLRC5	Cells Transformed fibroblasts	0.38	33	-3.81	0.71	8.8×10^{-8}	3.3×10^{-3}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	NLRC5	Adrenal Gland	0.10	17	-8.37	1.65	4.2×10^{-7}	1.4×10^{-2}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
TG	RP11-373D23.3	Pituitary	0.06	7	0.63	0.11	3.2×10^{-9}	6.7×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	SNX17	Brain Putamen basal ganglia	0.07	9	-0.32	0.06	6.1×10^{-9}	6.7×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ZNF513	Brain Anterior cingulate cortex BA24	0.10	31	0.26	0.05	7.7×10^{-9}	6.7×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Artery Tibial	0.06	57	0.20	0.04	3.1×10^{-8}	2.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	UCN	DGN-WB	0.00	18	0.85	0.15	4.0×10^{-8}	2.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	DGN-WB	0.11	26	0.27	0.05	5.8×10^{-8}	2.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Skin Sun Exposed Lower leg	0.20	7	0.20	0.04	5.9×10^{-8}	2.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Table 11. Serum lipid significant genes from tissue-specific GReX analysis in HCHS/SOL

Trait	Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
									GWAS	NHGRI-EBI
TG	NRBP1	Skin Not Sun Exposed Suprapubic	0.24	30	0.14	0.03	6.0×10^{-8}	2.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	Muscle Skeletal	0.06	13	-0.40	0.07	8.1×10^{-8}	2.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	Brain Caudate basal ganglia	0.08	25	-0.26	0.05	8.2×10^{-8}	2.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Small Intestine Terminal Ileum	0.05	16	0.32	0.06	9.2×10^{-8}	2.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	AC074117.13	Skin Sun Exposed Lower leg	0.02	1	0.93	0.18	9.8×10^{-8}	2.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ZNF259	Skin Sun Exposed Lower leg	0.02	21	-0.50	0.09	1.2×10^{-7}	2.3×10^{-3}	rs964184 (pval=1.59×10^{-73})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
TG	KRTCAP3	DGN-WB	0.40	40	-0.12	0.02	1.3×10^{-7}	2.3×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	Skin Sun Exposed Lower leg	0.05	11	0.51	0.10	1.6×10^{-7}	2.6×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Colon Transverse	0.15	5	0.24	0.05	1.7×10^{-7}	2.6×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	Adrenal Gland	0.20	10	-0.24	0.05	1.7×10^{-7}	2.6×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Cells EBV-transformed lymphocytes	0.12	5	0.31	0.06	2.1×10^{-7}	3.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Adipose Subcutaneous	0.14	28	0.23	0.04	2.2×10^{-7}	3.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	Thyroid	0.08	8	0.34	0.07	2.4×10^{-7}	3.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Thyroid	0.01	2	0.80	0.15	2.4×10^{-7}	3.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Table 11. Serum lipid significant genes from tissue-specific GReX analysis in HCHS/SOL

Trait	Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
									GWAS	NHGRI-EBI
TG	SNX17	Muscle Skeletal	0.43	44	0.12	0.02	2.6×10^{-7}	3.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	Adipose Subcutaneous	0.04	12	0.49	0.09	2.7×10^{-7}	3.1×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Lung	0.12	19	0.26	0.05	3.6×10^{-7}	3.9×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Testis	0.08	7	0.44	0.09	4.3×10^{-7}	4.5×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Liver	0.05	1	0.49	0.10	5.1×10^{-7}	5.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	Brain Cortex	0.05	9	-0.42	0.08	5.3×10^{-7}	5.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	DGN-WB	0.00	7	1.18	0.24	5.4×10^{-7}	5.0×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	GPN1	Heart Left Ventricle	0.06	19	0.41	0.08	6.3×10^{-7}	5.7×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Cells Transformed fibroblasts	0.20	19	0.21	0.04	7.8×10^{-7}	6.8×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	SNX17	Heart Atrial Appendage	0.04	20	0.33	0.07	8.1×10^{-7}	6.8×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	TRIM54	Nerve Tibial	0.06	11	0.29	0.06	8.5×10^{-7}	6.9×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Artery Aorta	0.06	13	0.30	0.06	9.2×10^{-7}	7.2×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	C2orf70	Pancreas	0.03	11	-0.48	0.10	1.0×10^{-6}	7.8×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Breast Mammary Tissue	0.04	7	0.44	0.09	1.4×10^{-6}	1.0×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	UCN	Thyroid	0.02	2	0.75	0.16	1.6×10^{-6}	1.2×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Table 11. Serum lipid significant genes from tissue-specific GReX analysis in HCHS/SOL

Trait	Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
									GWAS	NHGRI-EBI
TG	NRBP1	Nerve Tibial	0.09	34	0.14	0.03	2.3×10^{-6}	1.6×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ATRAID	Pancreas	0.12	23	-0.30	0.06	3.0×10^{-6}	2.0×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	SNX17	Heart Left Ventricle	0.07	12	0.25	0.05	3.0×10^{-6}	2.0×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	CAD	Thyroid	0.12	21	0.22	0.05	3.1×10^{-6}	2.0×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Whole Blood	0.13	17	0.23	0.05	3.2×10^{-6}	2.0×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	C2orf28	DGN-WB	0.13	16	-0.18	0.04	3.5×10^{-6}	2.2×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	Adipose Visceral Omentum	0.06	40	-0.21	0.04	4.7×10^{-6}	2.8×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	Esophagus Muscularis	0.08	19	0.29	0.06	5.0×10^{-6}	2.9×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ATRAID	Artery Coronary	0.17	16	-0.22	0.05	5.8×10^{-6}	3.3×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ATRAID	Breast Mammary Tissue	0.07	8	-0.22	0.05	6.6×10^{-6}	3.7×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
Dyslipidemia	CETP	Esophagus Mucosa	0.02	7	2.23	0.30	1.3×10^{-13}	1.8×10^{-8}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	CETP	Artery Coronary	0.10	3	1.09	0.15	1.4×10^{-13}	1.8×10^{-8}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	CETP	Colon Transverse	0.08	31	0.65	0.09	4.9×10^{-13}	4.2×10^{-8}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)

Table 11. Serum lipid significant genes from tissue-specific GReX analysis in HCHS/SOL

Trait	Gene	Tissue	R^2	N SNPs	BETA	SE	P-value	FDR	Annotation	
									GWAS	NHGRI-EBI
Dyslipidemia	CETP	Lung	0.05	10	1.20	0.17	7.2×10^{-13}	4.7×10^{-8}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	NLRC5	Adrenal Gland	0.10	17	0.81	0.11	1.3×10^{-12}	6.9×10^{-8}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	NLRC5	Cells Transformed fibroblasts	0.38	33	0.33	0.05	3.4×10^{-12}	1.5×10^{-7}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	LPL	Nerve Tibial	0.14	33	-0.69	0.10	1.1×10^{-11}	3.7×10^{-7}	rs331 (pval=2.18×10^{-13})	rs1569209 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	CETP	Small Intestine Terminal Ileum	0.15	19	0.76	0.11	1.2×10^{-11}	3.7×10^{-7}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	CETP	Cells Transformed fibroblasts	0.09	10	0.89	0.13	2.0×10^{-11}	5.8×10^{-7}	rs711752 (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	ZNF259	Skin Sun Exposed Lower leg	0.02	21	-1.02	0.16	3.6×10^{-10}	9.4×10^{-6}	seq-rs964184 (pval=2.48×10^{-17})	rs7350481 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	LPL	Adipose Subcutaneous	0.07	24	-0.62	0.11	5.9×10^{-8}	1.4×10^{-3}	rs331 (pval=2.18×10^{-13})	rs1569209 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	LPL	Whole Blood	0.05	11	-0.82	0.15	9.0×10^{-8}	1.9×10^{-3}	rs331 (pval=2.18×10^{-13})	rs1569209 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	PDGFC	DGN-WB	0.03	18	0.78	0.16	8.0×10^{-7}	1.6×10^{-2}	NA	rs4691380 pval=1×10^{-08} (HDL-C, Klarin, 30275531)

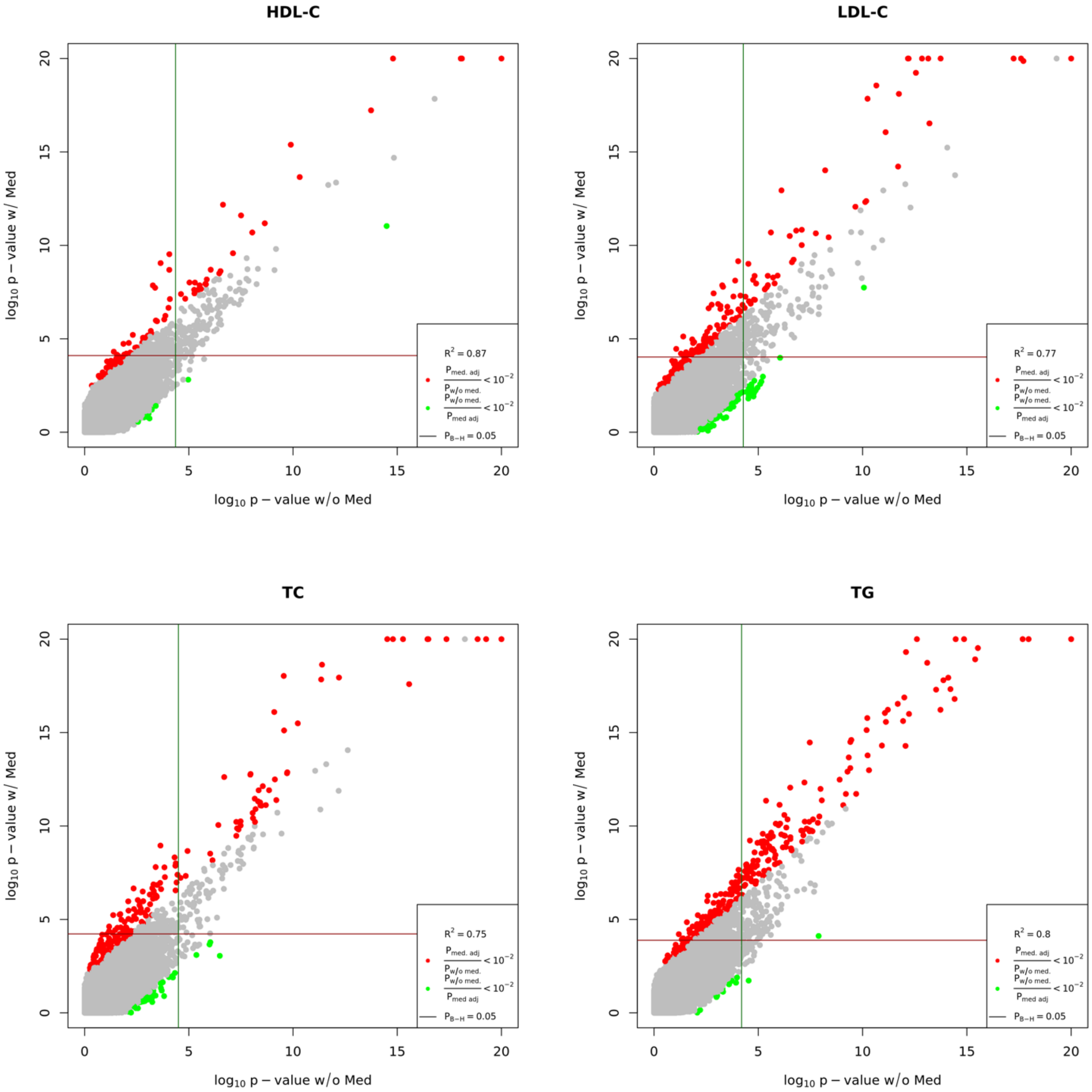

Figure 19. Log-transformed p-value comparison between drug naïve measure and LLD medicated measures in BioVU

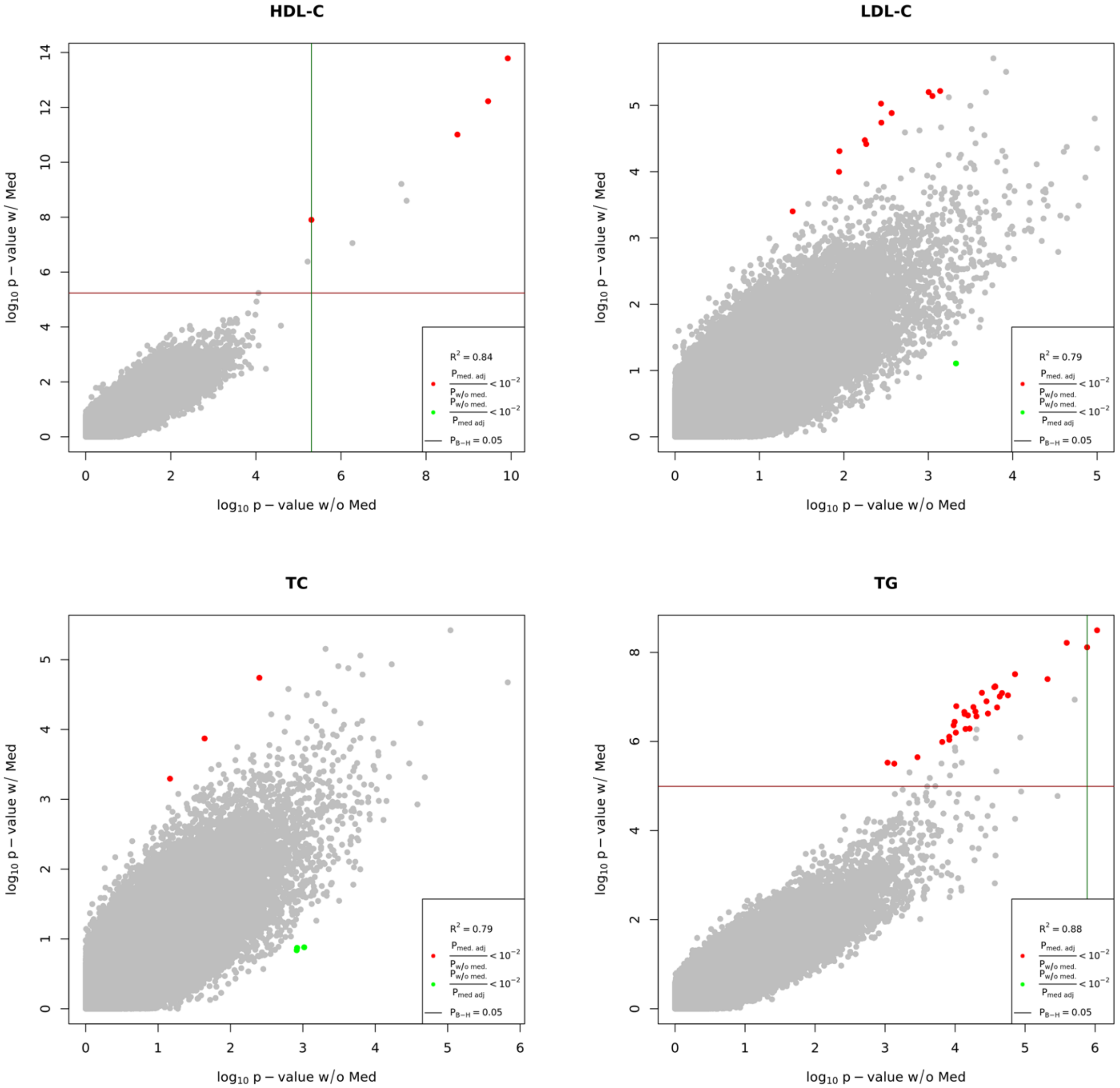

Figure 20. Log-transformed p-value comparison between drug naïve measure and LLD medicated measures in HCHS/SOL

Cross-tissue genetically regulated expression analysis

There are over 15,224 genes expressed in at least five tissues and included in the all tissues cross-tissue models, and 8,379 genes are included in the metabolic tissues cross-tissue models. Their principal components of included genes are tested separately by GEE, and then these p-values are combined using Fisher's combined probability test. The FDR correction is applied to adjust for multiple tests, and novel genes are identified as those distant from present GWAS significant SNPs and reported SNPs from NHGRI-EBI Catalog.

In BioVU, a total number of 219 unique genes are found significant for HDL-C, 149 genes for LDL-C, 159 genes for TC, 444 genes for TG, and 33 genes for dyslipidemia status. With the annotation of GWAS and reported SNPs, 83 genes are novel for HDL-C, 22 are novel for LDL-C, 31 are novel for TC, 131 are novel for TG, and 9 are novel for dyslipidemia status (Fig 21-25, Table 12-16, and Appendix IX-XII).

In HCHS/SOL, eight genes show a significant association with HDL-C, and *NRBP1* (cross all tissue model: p-value= 6.73×10^{-06}) and *RUNX2* (all tissues cross-tissue model: p-value= 1.86×10^{-05}) are novel. Twelve genes are significant for LDL-C, and three of them are novel, including *LIME1*, *PRKAB1*, and *RERE*. For TG, twenty unique genes are significant, and two genes are considered novel (*C14orf182* and *TCTEX1D2*). No genes are significant after multiple testing correction for TC. A total of 21 genes are significantly associated with dichotomous dyslipidemia status, and seven fall outside regions ±10Mb from SNPs identified in the HCHS/SOL GWAS and ±1Mb from any reported serum lipid SNPs from the NHGRI-EBI catalog (Fig 26-30 and Table 17).

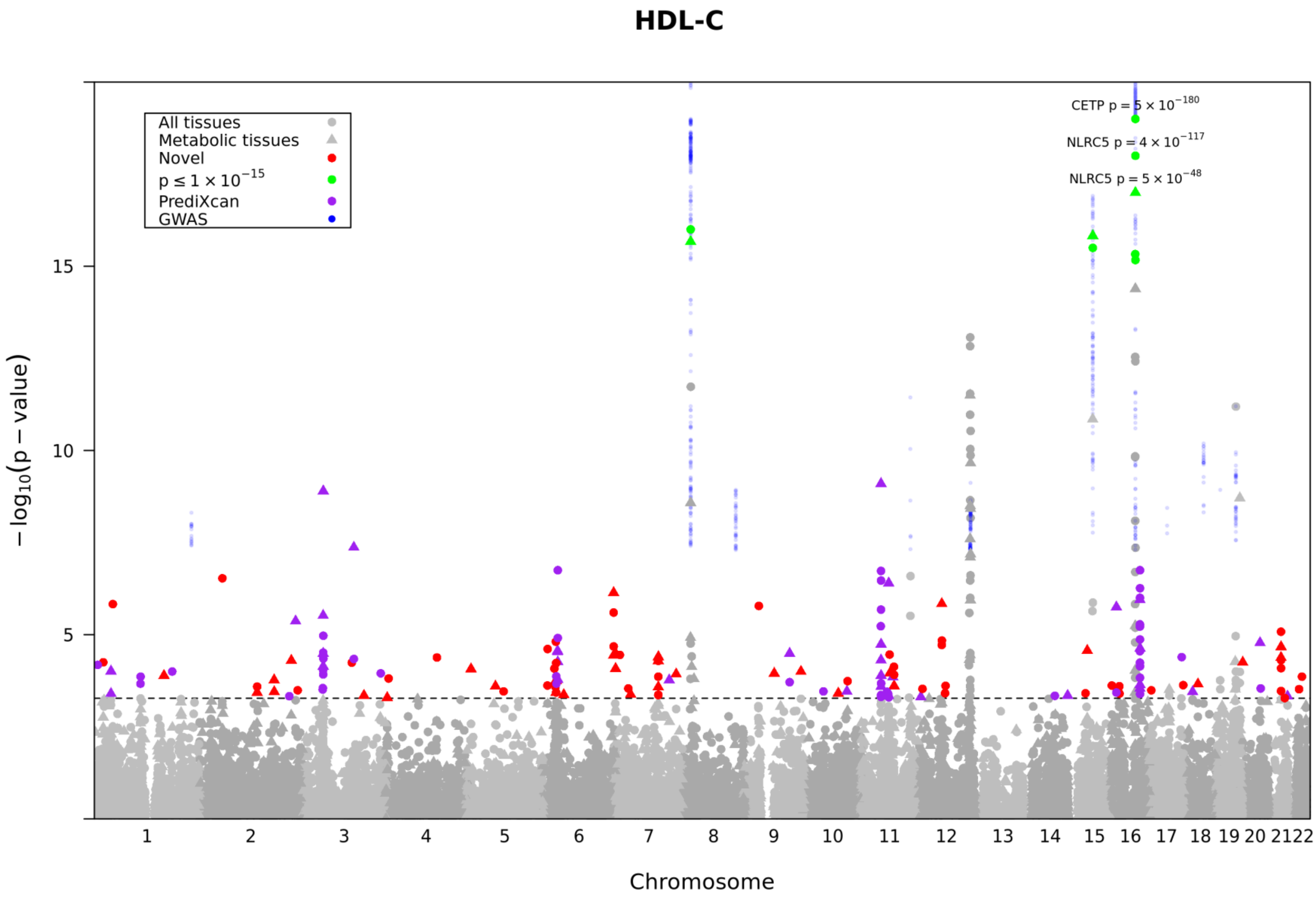

Figure 21. Manhattan plot of cross-tissue GReX association analysis on HDL-C in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 12. Novel HDL-C genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
ACYP2	cross all tissues	27	10	81%	2.9×10^{-7}	1.5×10^{-4}
RNASET2	cross metabolic tissues	6	2	86%	7.3×10^{-7}	3.3×10^{-4}
IKZF4	cross metabolic tissues	4	3	91%	1.4×10^{-6}	5.9×10^{-4}
B4GALT2	cross all tissues	6	4	88%	1.5×10^{-6}	5.9×10^{-4}
FAM205A	cross all tissues	6	3	85%	1.7×10^{-6}	6.5×10^{-4}
RNASET2	cross all tissues	23	8	82%	2.5×10^{-6}	9.1×10^{-4}
N6AMT1	cross all tissues	21	8	83%	8.2×10^{-6}	2.6×10^{-3}
COQ10A	cross all tissues	8	4	86%	1.4×10^{-5}	4.2×10^{-3}
PPP1R18	cross all tissues	16	8	81%	1.6×10^{-5}	4.5×10^{-3}
IKZF4	cross all tissues	9	4	83%	1.9×10^{-5}	5.2×10^{-3}
FGFR1OP	cross all tissues	14	5	82%	2.1×10^{-5}	5.6×10^{-3}
RWDD2B	cross metabolic tissues	6	2	87%	2.1×10^{-5}	5.7×10^{-3}
ERVFRD-1	cross all tissues	7	3	85%	2.5×10^{-5}	6.4×10^{-3}
SPATA5L1	cross metabolic tissues	7	2	83%	2.7×10^{-5}	6.9×10^{-3}
GPER1	cross metabolic tissues	4	2	81%	3.2×10^{-5}	7.7×10^{-3}
RP11-119D9.1	cross all tissues	5	3	93%	3.5×10^{-5}	8.1×10^{-3}
PHF14	cross all tissues	14	6	82%	3.5×10^{-5}	8.1×10^{-3}
AL133458.1	cross metabolic tissues	5	3	85%	3.6×10^{-5}	8.3×10^{-3}
POLR2J2	cross metabolic tissues	8	2	88%	4.0×10^{-5}	8.9×10^{-3}
POLR2J2	cross metabolic tissues	8	2	88%	4.0×10^{-5}	8.9×10^{-3}
N6AMT1	cross metabolic tissues	5	2	85%	4.1×10^{-5}	8.9×10^{-3}
MAD2L1	cross all tissues	9	5	85%	4.1×10^{-5}	8.9×10^{-3}
LTN1	cross all tissues	5	3	86%	4.9×10^{-5}	1.0×10^{-2}
IGFBP2	cross metabolic tissues	5	3	85%	5.0×10^{-5}	1.0×10^{-2}
RASA4B	cross metabolic tissues	6	3	85%	5.1×10^{-5}	1.0×10^{-2}
SPDYE6	cross all tissues	31	11	81%	5.1×10^{-5}	1.0×10^{-2}
NBPF3	cross all tissues	49	7	81%	5.6×10^{-5}	1.1×10^{-2}
NOP56	cross metabolic tissues	4	3	89%	5.6×10^{-5}	1.1×10^{-2}
RP11-384F7.2	cross all tissues	7	4	84%	5.8×10^{-5}	1.1×10^{-2}
HLA-B	cross all tissues	34	12	81%	5.9×10^{-5}	1.1×10^{-2}
USP35	cross all tissues	16	6	85%	7.4×10^{-5}	1.3×10^{-2}
RPL23P2	cross all tissues	16	7	82%	8.1×10^{-5}	1.4×10^{-2}
HIST1H2BK	cross all tissues	8	4	81%	8.4×10^{-5}	1.5×10^{-2}
PRSS16	cross all tissues	20	5	80%	8.4×10^{-5}	1.5×10^{-2}
C7orf50	cross metabolic tissues	4	2	82%	8.4×10^{-5}	1.5×10^{-2}
DAP	cross metabolic tissues	8	3	82%	8.5×10^{-5}	1.5×10^{-2}
POMT1	cross metabolic tissues	5	2	81%	9.9×10^{-5}	1.7×10^{-2}
MTL5	cross metabolic tissues	6	3	84%	1.1×10^{-4}	1.8×10^{-2}
TMEM252	cross metabolic tissues	3	2	83%	1.1×10^{-4}	1.8×10^{-2}
TPK1	cross metabolic tissues	8	3	80%	1.2×10^{-4}	1.9×10^{-2}
NARS2	cross all tissues	37	6	81%	1.2×10^{-4}	1.9×10^{-2}

Table 12. Novel HDL-C genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
RXRG	cross metabolic tissues	3	2	86%	1.3×10^{-4}	2.0×10^{-2}
POLR2J	cross all tissues	13	5	81%	1.4×10^{-4}	2.1×10^{-2}
AC005003.1	cross all tissues	6	3	86%	1.4×10^{-4}	2.1×10^{-2}
MRFAP1	cross all tissues	6	2	86%	1.6×10^{-4}	2.3×10^{-2}
KIAA1715	cross metabolic tissues	6	3	80%	1.7×10^{-4}	2.4×10^{-2}
LST1	cross metabolic tissues	4	3	89%	1.7×10^{-4}	2.4×10^{-2}
HCG27	cross metabolic tissues	8	3	85%	1.8×10^{-4}	2.5×10^{-2}
KCNIP2	cross all tissues	5	4	91%	1.8×10^{-4}	2.5×10^{-2}
ELP2	cross metabolic tissues	4	2	90%	2.2×10^{-4}	2.9×10^{-2}
RFNG	cross all tissues	10	4	81%	2.4×10^{-4}	3.1×10^{-2}
CACNA1H	cross all tissues	10	5	81%	2.4×10^{-4}	3.1×10^{-2}
MAK	cross all tissues	5	3	90%	2.4×10^{-4}	3.1×10^{-2}
NARS2	cross metabolic tissues	7	2	85%	2.4×10^{-4}	3.1×10^{-2}
RP11-766N7.3	cross all tissues	13	5	83%	2.4×10^{-4}	3.1×10^{-2}
CENPH	cross metabolic tissues	4	3	89%	2.5×10^{-4}	3.2×10^{-2}
COQ7	cross all tissues	23	7	82%	2.5×10^{-4}	3.2×10^{-2}
DARS	cross all tissues	13	5	85%	2.6×10^{-4}	3.2×10^{-2}
LRWD1	cross metabolic tissues	7	3	88%	2.6×10^{-4}	3.3×10^{-2}
IFITM4P	cross all tissues	41	12	82%	2.7×10^{-4}	3.3×10^{-2}
ADCYAP1R1	cross all tissues	8	4	84%	2.9×10^{-4}	3.5×10^{-2}
MAGOHB	cross all tissues	9	5	86%	2.9×10^{-4}	3.5×10^{-2}
UPB1	cross all tissues	27	7	81%	3.0×10^{-4}	3.5×10^{-2}
SMTNL2	cross all tissues	8	4	83%	3.2×10^{-4}	3.7×10^{-2}
PDE6D	cross all tissues	6	4	89%	3.2×10^{-4}	3.7×10^{-2}
RWDD2B	cross all tissues	36	8	81%	3.4×10^{-4}	3.9×10^{-2}
CTC-498M16.4	cross all tissues	10	4	81%	3.5×10^{-4}	3.9×10^{-2}
HOXD1	cross metabolic tissues	3	3	100%	3.5×10^{-4}	3.9×10^{-2}
HLA-C	cross metabolic tissues	8	4	84%	3.7×10^{-4}	4.0×10^{-2}
XXbac-BPG248L24.12	cross all tissues	34	13	80%	3.7×10^{-4}	4.0×10^{-2}
DARS	cross metabolic tissues	3	2	97%	3.8×10^{-4}	4.1×10^{-2}
NUTM2E	cross metabolic tissues	3	2	92%	3.8×10^{-4}	4.1×10^{-2}
PABPC1P4	cross all tissues	11	5	81%	3.9×10^{-4}	4.1×10^{-2}
OIP5	cross all tissues	15	7	81%	3.9×10^{-4}	4.1×10^{-2}
GDE1	cross all tissues	11	5	84%	4.0×10^{-4}	4.2×10^{-2}
AOAH	cross metabolic tissues	6	3	81%	4.2×10^{-4}	4.3×10^{-2}
RASA4B	cross all tissues	24	10	81%	4.3×10^{-4}	4.4×10^{-2}
CENPQ	cross metabolic tissues	6	3	83%	4.3×10^{-4}	4.4×10^{-2}
LRWD1	cross all tissues	35	8	81%	4.4×10^{-4}	4.5×10^{-2}
PLSCR1	cross metabolic tissues	5	3	90%	4.5×10^{-4}	4.5×10^{-2}
RGS12	cross metabolic tissues	3	2	81%	5.1×10^{-4}	5.0×10^{-2}
KCNJ6	cross all tissues	6	4	88%	5.2×10^{-4}	5.0×10^{-2}

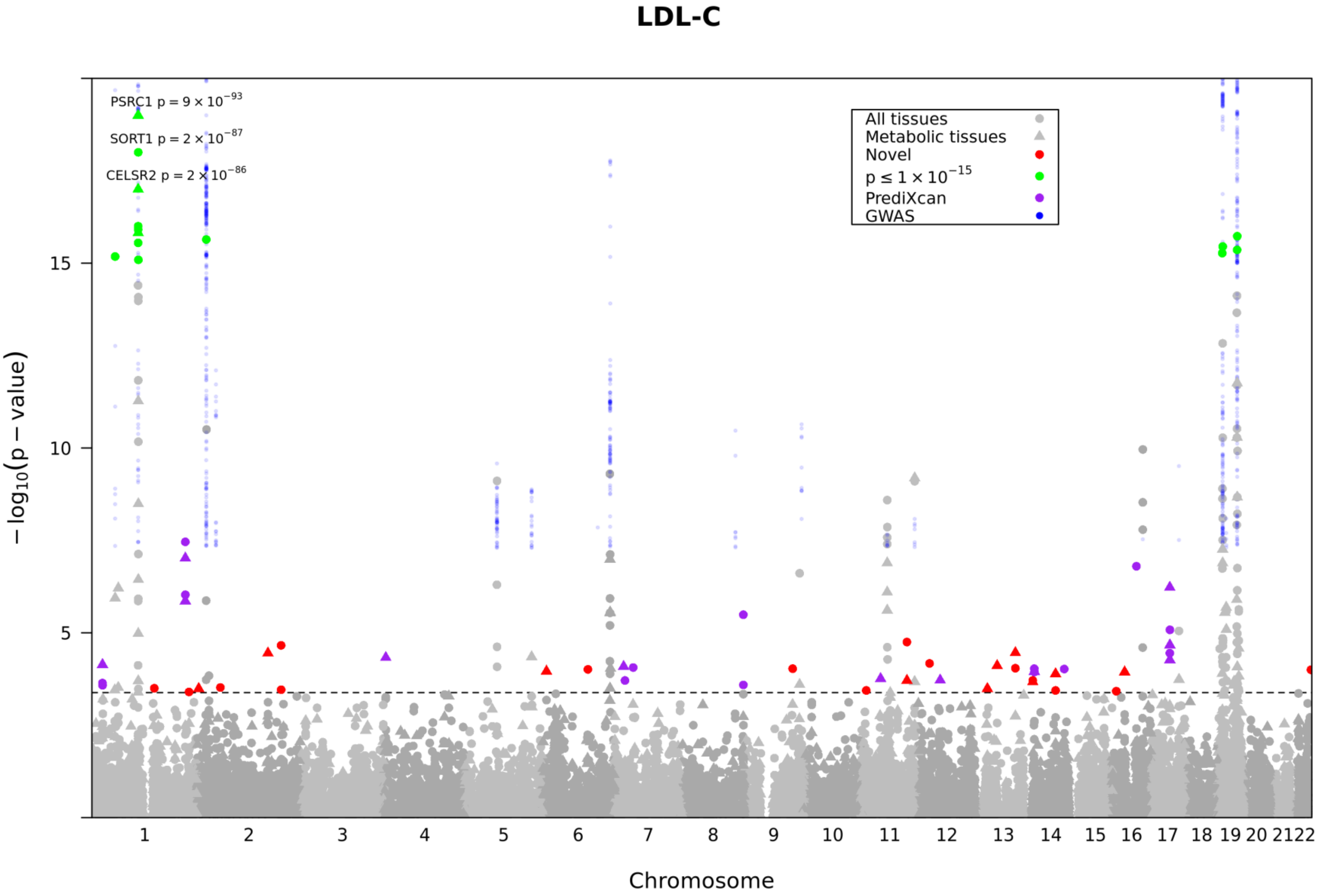

Figure 22. Manhattan plot of cross-tissue GReX association analysis on LDL-C in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 13. Novel LDL-C genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
ACAT1	cross all tissues	24	9	80%	1.8×10^{-5}	4.3×10^{-3}
GTF3C3	cross all tissues	5	3	83%	2.2×10^{-5}	5.0×10^{-3}
TGDS	cross metabolic tissues	3	2	98%	3.5×10^{-5}	7.5×10^{-3}
GALNT3	cross metabolic tissues	6	3	84%	3.5×10^{-5}	7.5×10^{-3}
ITPR2	cross all tissues	13	6	81%	6.8×10^{-5}	1.3×10^{-2}
WDFY2	cross metabolic tissues	6	3	84%	7.8×10^{-5}	1.4×10^{-2}
TGDS	cross all tissues	6	2	84%	9.2×10^{-5}	1.6×10^{-2}
PTBP3	cross all tissues	12	5	84%	9.3×10^{-5}	1.6×10^{-2}
RP1-111B22.3	cross all tissues	7	3	84%	9.9×10^{-5}	1.7×10^{-2}
WI2-81516×10^{3}.1	cross all tissues	9	6	87%	9.9×10^{-5}	1.7×10^{-2}
RP11-421M1.8	cross metabolic tissues	4	2	85%	1.1×10^{-4}	1.8×10^{-2}
RP11-426C22.6	cross metabolic tissues	4	2	81%	1.1×10^{-4}	1.9×10^{-2}
RP3-449M8.9	cross metabolic tissues	3	2	95%	1.3×10^{-4}	2.1×10^{-2}
ACAT1	cross metabolic tissues	5	2	81%	1.9×10^{-4}	2.9×10^{-2}
RNASE6	cross all tissues	12	5	83%	2.0×10^{-4}	2.9×10^{-2}
RNASE6	cross metabolic tissues	5	2	83%	2.2×10^{-4}	3.1×10^{-2}
C2orf73	cross all tissues	10	3	81%	3.0×10^{-4}	4.1×10^{-2}
RP11-495P10.3	cross all tissues	6	3	87%	3.2×10^{-4}	4.3×10^{-2}
TRAPPC12	cross metabolic tissues	5	3	86%	3.3×10^{-4}	4.3×10^{-2}
POMP	cross metabolic tissues	3	2	88%	3.3×10^{-4}	4.3×10^{-2}
PGAP1	cross all tissues	6	3	84%	3.5×10^{-4}	4.5×10^{-2}
RP13-631K18.5	cross all tissues	9	4	84%	3.6×10^{-4}	4.6×10^{-2}
ISCA2	cross all tissues	5	2	88%	3.6×10^{-4}	4.6×10^{-2}
RP11-243A14.1	cross all tissues	7	4	82%	3.8×10^{-4}	4.7×10^{-2}
HMGN2P19	cross all tissues	21	6	83%	4.0×10^{-4}	4.9×10^{-2}

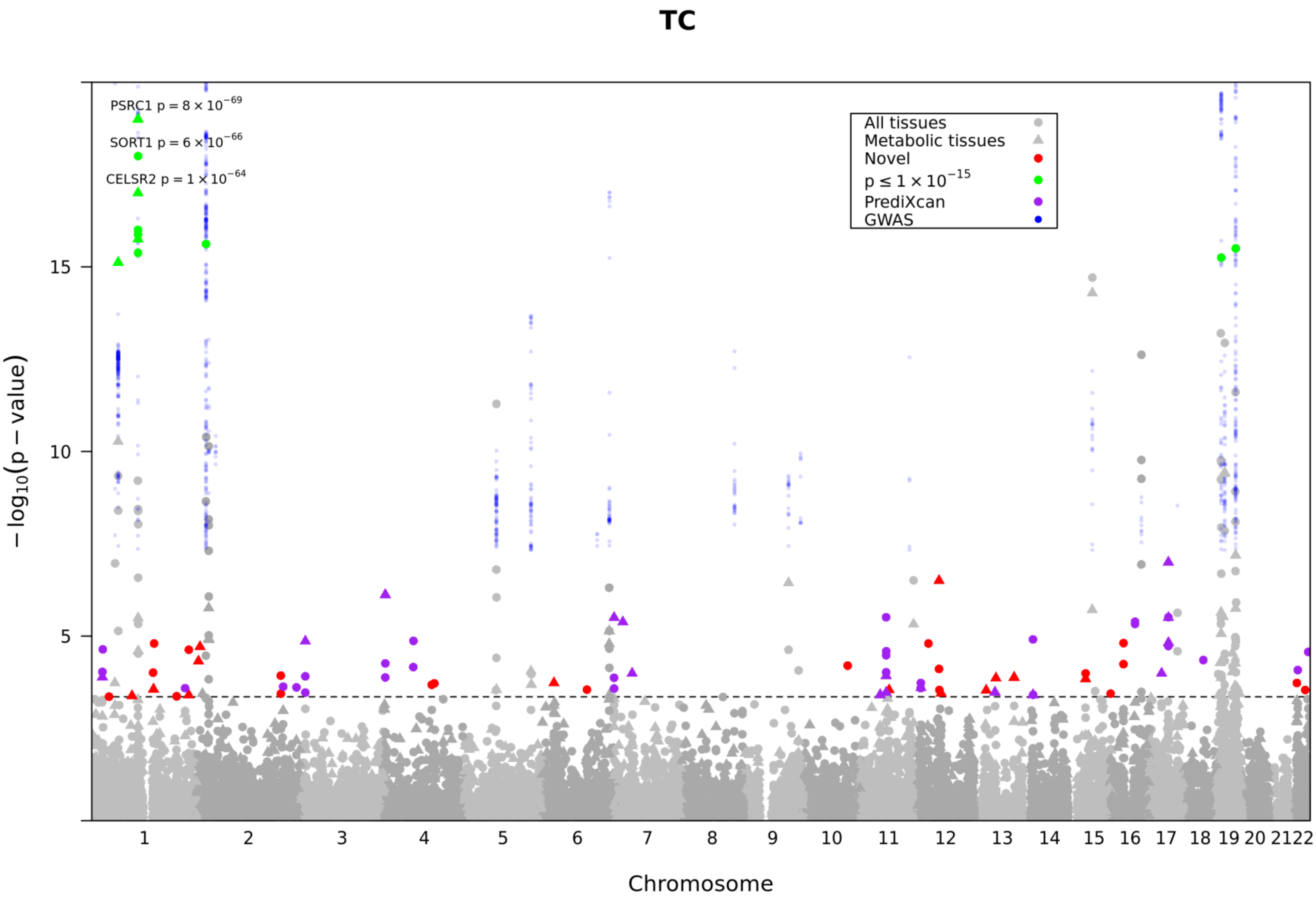

Figure 23. Manhattan plot of cross-tissue GReX association analysis on TC in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 14. Novel TC genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
GALNT6	cross metabolic tissues	3	2	92%	3.1×10^{-7}	1.4×10^{-4}
SEZ6L2	cross all tissues	8	4	88%	1.5×10^{-5}	3.9×10^{-3}
ITPR2	cross all tissues	13	6	81%	1.6×10^{-5}	3.9×10^{-3}
RP11-495P10.3	cross all tissues	6	3	87%	1.6×10^{-5}	3.9×10^{-3}
RP11-439M11.1	cross metabolic tissues	4	3	90%	1.9×10^{-5}	4.6×10^{-3}
HMGN2P19	cross all tissues	21	6	83%	2.4×10^{-5}	5.4×10^{-3}
TRAPPC12	cross metabolic tissues	5	3	86%	4.8×10^{-5}	9.6×10^{-3}
CDIPT	cross all tissues	6	4	88%	5.8×10^{-5}	1.1×10^{-2}
ITPRIP	cross all tissues	6	3	86%	6.3×10^{-5}	1.2×10^{-2}
GALNT6	cross all tissues	20	8	82%	7.8×10^{-5}	1.4×10^{-2}
RP11-458D21.1	cross all tissues	14	3	82%	9.7×10^{-5}	1.7×10^{-2}
LRRC57	cross all tissues	30	8	80%	1.0×10^{-4}	1.8×10^{-2}
GTF3C3	cross all tissues	5	3	83%	1.2×10^{-4}	1.9×10^{-2}
TGDS	cross metabolic tissues	3	2	98%	1.3×10^{-4}	2.1×10^{-2}
WDFY2	cross metabolic tissues	6	3	84%	1.4×10^{-4}	2.1×10^{-2}
LRRC57	cross metabolic tissues	6	2	88%	1.4×10^{-4}	2.2×10^{-2}
GNB1L	cross all tissues	20	10	80%	1.9×10^{-4}	2.8×10^{-2}
HCG9	cross metabolic tissues	6	3	82%	1.8×10^{-4}	2.8×10^{-2}
SNHG8	cross all tissues	35	12	81%	1.9×10^{-4}	2.8×10^{-2}
AP1AR	cross all tissues	17	3	80%	2.1×10^{-4}	3.1×10^{-2}
NBPF12	cross metabolic tissues	4	3	89%	2.7×10^{-4}	3.7×10^{-2}
APOBEC3H	cross all tissues	8	3	82%	2.9×10^{-4}	3.8×10^{-2}
KRT80	cross all tissues	10	5	82%	2.9×10^{-4}	3.8×10^{-2}
MRPL21	cross metabolic tissues	7	2	83%	2.9×10^{-4}	3.8×10^{-2}
SOBP	cross all tissues	5	3	81%	2.8×10^{-4}	3.8×10^{-2}
POMP	cross metabolic tissues	3	2	88%	3.0×10^{-4}	3.9×10^{-2}
SPRYD4	cross metabolic tissues	6	2	83%	3.6×10^{-4}	4.5×10^{-2}
PCSK6	cross all tissues	8	5	82%	3.7×10^{-4}	4.5×10^{-2}
PGAP1	cross all tissues	6	3	84%	3.7×10^{-4}	4.5×10^{-2}
HMGN2P19	cross metabolic tissues	3	1	85%	3.9×10^{-4}	4.7×10^{-2}
TMEM56	cross metabolic tissues	3	2	90%	4.1×10^{-4}	4.8×10^{-2}
C1orf106	cross all tissues	10	4	82%	4.3×10^{-4}	5.0×10^{-2}

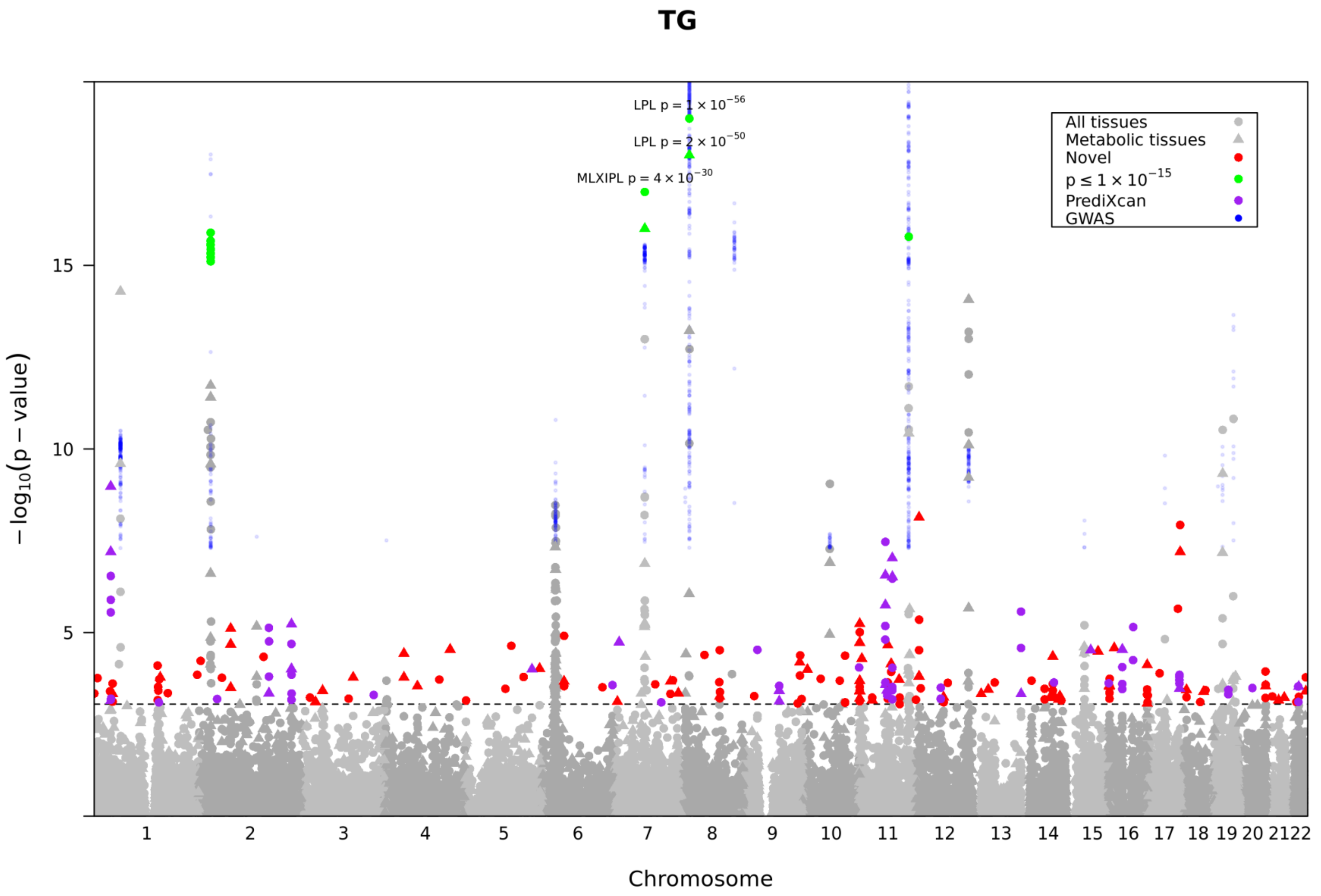

Figure 24. Manhattan plot of cross-tissue GReX association analysis on TG in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 15. Novel TG genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
MLF2	cross metabolic tissues	7	4	85%	7.3×10^{-9}	3.4×10^{-6}
CCDC40	cross all tissues	45	15	81%	1.2×10^{-8}	5.2×10^{-6}
CCDC40	cross metabolic tissues	8	4	86%	6.2×10^{-8}	2.4×10^{-5}
CD300LF	cross all tissues	10	5	86%	2.2×10^{-6}	5.9×10^{-4}
MLF2	cross all tissues	20	8	82%	4.5×10^{-6}	1.1×10^{-3}
CD151	cross metabolic tissues	8	2	84%	5.8×10^{-6}	1.3×10^{-3}
AC104135.3	cross metabolic tissues	7	2	86%	7.8×10^{-6}	1.6×10^{-3}
PNPLA2	cross all tissues	13	6	85%	9.8×10^{-6}	2.0×10^{-3}
GSTA1	cross all tissues	15	6	81%	1.2×10^{-5}	2.5×10^{-3}
AP006621.1	cross metabolic tissues	7	2	83%	1.9×10^{-5}	3.4×10^{-3}
AC104135.2	cross metabolic tissues	7	2	86%	2.1×10^{-5}	3.7×10^{-3}
DOC2GP	cross metabolic tissues	6	3	83%	2.2×10^{-5}	3.8×10^{-3}
FER	cross all tissues	9	5	83%	2.3×10^{-5}	4.0×10^{-3}
RP11-166B2.1	cross metabolic tissues	7	2	85%	2.6×10^{-5}	4.5×10^{-3}
TRIM2	cross metabolic tissues	5	3	88%	2.9×10^{-5}	4.8×10^{-3}
TMEM64	cross all tissues	7	3	85%	3.0×10^{-5}	4.9×10^{-3}
COPS7A	cross all tissues	8	5	87%	3.0×10^{-5}	4.9×10^{-3}
FBXO22	cross metabolic tissues	4	2	81%	3.2×10^{-5}	5.2×10^{-3}
GUF1	cross metabolic tissues	8	4	86%	3.7×10^{-5}	5.8×10^{-3}
RP11-56A10.1	cross all tissues	5	2	85%	4.1×10^{-5}	6.2×10^{-3}
LCN1P1	cross all tissues	7	4	82%	4.2×10^{-5}	6.3×10^{-3}
EBAG9P1	cross all tissues	24	8	81%	4.3×10^{-5}	6.4×10^{-3}
RP3-449M8.9	cross metabolic tissues	3	2	95%	4.4×10^{-5}	6.5×10^{-3}
STAM2	cross all tissues	14	5	80%	4.6×10^{-5}	6.7×10^{-3}
TRIM5	cross metabolic tissues	4	3	90%	5.1×10^{-5}	7.4×10^{-3}
AC019172.2	cross all tissues	9	5	82%	5.9×10^{-5}	8.2×10^{-3}
NTNG2	cross metabolic tissues	3	2	82%	6.5×10^{-5}	8.8×10^{-3}
SERPINH1	cross metabolic tissues	3	2	92%	7.1×10^{-5}	9.6×10^{-3}
DBNDD1	cross metabolic tissues	7	4	88%	7.6×10^{-5}	1.0×10^{-2}
CDC42SE1	cross all tissues	13	5	85%	7.9×10^{-5}	1.0×10^{-2}
THOC3	cross metabolic tissues	8	4	88%	9.6×10^{-5}	1.2×10^{-2}
NUDT5	cross metabolic tissues	3	2	89%	1.0×10^{-4}	1.2×10^{-2}
PPDPF	cross all tissues	27	12	80%	1.1×10^{-4}	1.4×10^{-2}
SERPINH1	cross all tissues	8	4	83%	1.2×10^{-4}	1.4×10^{-2}
RP11-271K11.5	cross all tissues	16	5	81%	1.3×10^{-4}	1.5×10^{-2}
COX20	cross all tissues	6	3	87%	1.4×10^{-4}	1.6×10^{-2}
GTF3C4	cross all tissues	5	2	82%	1.5×10^{-4}	1.7×10^{-2}
COPS7A	cross metabolic tissues	4	3	89%	1.6×10^{-4}	1.7×10^{-2}
NME5	cross all tissues	25	9	80%	1.6×10^{-4}	1.8×10^{-2}
RP11-85G21.3	cross metabolic tissues	3	2	88%	1.6×10^{-4}	1.8×10^{-2}
GNPDA2	cross metabolic tissues	8	3	84%	1.6×10^{-4}	1.8×10^{-2}

Table 15. Novel TG genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
CDPF1	cross all tissues	10	5	83%	1.7×10^{-4}	1.8×10^{-2}
PARP15	cross metabolic tissues	5	3	81%	1.7×10^{-4}	1.8×10^{-2}
ACYP2	cross all tissues	27	10	81%	1.7×10^{-4}	1.8×10^{-2}
RERE	cross all tissues	18	7	82%	1.7×10^{-4}	1.8×10^{-2}
RASGEF1A	cross all tissues	14	6	81%	1.8×10^{-4}	1.9×10^{-2}
CACNA1H	cross all tissues	10	5	81%	1.8×10^{-4}	1.9×10^{-2}
EFNA1	cross all tissues	9	5	86%	1.9×10^{-4}	1.9×10^{-2}
MRE11A	cross metabolic tissues	8	2	86%	1.9×10^{-4}	1.9×10^{-2}
INTU	cross all tissues	5	2	83%	1.9×10^{-4}	1.9×10^{-2}
TBXAS1	cross all tissues	5	3	84%	2.0×10^{-4}	2.0×10^{-2}
FAM35A	cross all tissues	31	10	82%	2.0×10^{-4}	2.0×10^{-2}
AP006621.5	cross metabolic tissues	7	2	84%	2.0×10^{-4}	2.0×10^{-2}
DHRS4	cross all tissues	25	12	81%	2.1×10^{-4}	2.0×10^{-2}
GSTA1	cross metabolic tissues	3	2	91%	2.1×10^{-4}	2.1×10^{-2}
LRGUK	cross metabolic tissues	8	3	83%	2.1×10^{-4}	2.1×10^{-2}
RP11-37B2.1	cross all tissues	33	13	82%	2.2×10^{-4}	2.1×10^{-2}
WDFY2	cross all tissues	19	9	82%	2.3×10^{-4}	2.2×10^{-2}
DOC2GP	cross all tissues	25	8	81%	2.3×10^{-4}	2.2×10^{-2}
ATXN7L3B	cross all tissues	7	4	84%	2.3×10^{-4}	2.2×10^{-2}
IPO13	cross all tissues	6	3	90%	2.4×10^{-4}	2.3×10^{-2}
ISCA2	cross all tissues	5	2	88%	2.5×10^{-4}	2.3×10^{-2}
BRI3	cross all tissues	18	7	83%	2.6×10^{-4}	2.3×10^{-2}
PRPF6	cross all tissues	21	10	81%	2.6×10^{-4}	2.4×10^{-2}
JMJD8	cross metabolic tissues	5	3	84%	2.8×10^{-4}	2.4×10^{-2}
GSTA2	cross all tissues	6	3	85%	2.9×10^{-4}	2.5×10^{-2}
G3BP2	cross metabolic tissues	5	3	87%	2.9×10^{-4}	2.5×10^{-2}
STMN3	cross metabolic tissues	3	2	89%	2.9×10^{-4}	2.5×10^{-2}
ARHGDIG	cross metabolic tissues	3	3	100%	2.9×10^{-4}	2.5×10^{-2}
LMF1	cross all tissues	39	15	80%	3.0×10^{-4}	2.5×10^{-2}
PIDD	cross all tissues	29	9	81%	3.0×10^{-4}	2.6×10^{-2}
FLG	cross all tissues	39	12	81%	3.1×10^{-4}	2.6×10^{-2}
AIG1	cross all tissues	11	6	84%	3.1×10^{-4}	2.6×10^{-2}
AC104135.4	cross metabolic tissues	6	3	84%	3.1×10^{-4}	2.6×10^{-2}
KLRAP1	cross all tissues	32	11	81%	3.3×10^{-4}	2.7×10^{-2}
MCTP1	cross all tissues	13	4	81%	3.4×10^{-4}	2.7×10^{-2}
MAPK1IP1L	cross all tissues	6	3	86%	3.4×10^{-4}	2.7×10^{-2}
CCNA1	cross metabolic tissues	3	2	83%	3.5×10^{-4}	2.8×10^{-2}
TUBB3	cross all tissues	8	3	82%	3.6×10^{-4}	2.8×10^{-2}
TUBB3	cross all tissues	8	3	82%	3.6×10^{-4}	2.8×10^{-2}
MPPE1	cross metabolic tissues	8	4	83%	3.6×10^{-4}	2.8×10^{-2}
SEC11C	cross all tissues	19	9	82%	3.8×10^{-4}	2.9×10^{-2}

Table 15. Novel TG genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
NPC2	cross all tissues	13	6	85%	3.8×10^{-4}	2.9×10^{-2}
KPRP	cross all tissues	5	3	84%	3.8×10^{-4}	2.9×10^{-2}
UBA7	cross metabolic tissues	4	2	94%	3.8×10^{-4}	2.9×10^{-2}
RPLP2	cross all tissues	20	8	82%	3.8×10^{-4}	2.9×10^{-2}
PIDD	cross metabolic tissues	4	2	89%	3.8×10^{-4}	2.9×10^{-2}
CHID1	cross metabolic tissues	4	3	95%	3.9×10^{-4}	2.9×10^{-2}
PKDREJ	cross metabolic tissues	6	2	80%	3.9×10^{-4}	2.9×10^{-2}
SF3A3	cross all tissues	31	8	80%	4.0×10^{-4}	3.0×10^{-2}
CCDC68	cross metabolic tissues	5	3	83%	4.0×10^{-4}	3.0×10^{-2}
SLC26A7	cross all tissues	13	5	82%	4.2×10^{-4}	3.1×10^{-2}
WDR90	cross all tissues	35	14	81%	4.3×10^{-4}	3.2×10^{-2}
RHBDL1	cross all tissues	26	9	82%	4.4×10^{-4}	3.2×10^{-2}
KIAA0040	cross all tissues	24	10	81%	4.5×10^{-4}	3.2×10^{-2}
ACTR3B	cross metabolic tissues	3	2	87%	4.5×10^{-4}	3.2×10^{-2}
C1orf159	cross all tissues	40	13	82%	4.6×10^{-4}	3.3×10^{-2}
IPO13	cross metabolic tissues	3	2	84%	4.7×10^{-4}	3.3×10^{-2}
LRGUK	cross all tissues	35	15	82%	4.7×10^{-4}	3.3×10^{-2}
MPHOSPH8	cross metabolic tissues	6	3	85%	4.7×10^{-4}	3.3×10^{-2}
DPEP1	cross all tissues	6	4	86%	5.0×10^{-4}	3.4×10^{-2}
MYO1C	cross all tissues	6	3	81%	5.1×10^{-4}	3.5×10^{-2}
RP3-449M8.9	cross all tissues	23	7	82%	5.2×10^{-4}	3.6×10^{-2}
TEK	cross all tissues	8	3	81%	5.4×10^{-4}	3.6×10^{-2}
C14orf159	cross metabolic tissues	4	3	93%	5.4×10^{-4}	3.7×10^{-2}
ANKRD20A18P	cross all tissues	5	3	93%	5.5×10^{-4}	3.7×10^{-2}
TMEM64	cross metabolic tissues	4	2	88%	5.5×10^{-4}	3.7×10^{-2}
ASCC2	cross all tissues	18	8	80%	5.6×10^{-4}	3.7×10^{-2}
IMPA2	cross all tissues	17	9	82%	5.7×10^{-4}	3.8×10^{-2}
TBK1	cross metabolic tissues	3	2	92%	5.8×10^{-4}	3.8×10^{-2}
RP13-137A17.6	cross all tissues	9	3	84%	5.8×10^{-4}	3.9×10^{-2}
TMPRSS3	cross metabolic tissues	3	2	92%	5.9×10^{-4}	3.9×10^{-2}
MTMR2	cross all tissues	9	4	82%	5.9×10^{-4}	3.9×10^{-2}
ARL14EP	cross all tissues	36	12	81%	5.9×10^{-4}	3.9×10^{-2}
EFHB	cross all tissues	49	11	81%	5.9×10^{-4}	3.9×10^{-2}
PIGH	cross metabolic tissues	5	3	87%	5.9×10^{-4}	3.9×10^{-2}
GMEB2	cross all tissues	18	7	83%	6.0×10^{-4}	3.9×10^{-2}
EPS8L2	cross metabolic tissues	6	3	81%	6.1×10^{-4}	4.0×10^{-2}
NECAB1	cross all tissues	8	5	82%	6.2×10^{-4}	4.0×10^{-2}
JMJD8	cross all tissues	28	12	82%	6.3×10^{-4}	4.0×10^{-2}
RPS6KB2	cross all tissues	27	8	82%	6.3×10^{-4}	4.0×10^{-2}
PHLDB2	cross all tissues	9	5	82%	6.3×10^{-4}	4.0×10^{-2}
EGFL7	cross all tissues	7	5	88%	6.5×10^{-4}	4.1×10^{-2}

Table 15. Novel TG genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR
GALC	cross metabolic tissues	6	3	87%	6.7×10^{-4}	4.2×10^{-2}
LGALS3	cross all tissues	13	7	80%	6.7×10^{-4}	4.2×10^{-2}
ACAD8	cross all tissues	13	7	81%	6.8×10^{-4}	4.2×10^{-2}
ARL14EP	cross metabolic tissues	5	3	90%	6.9×10^{-4}	4.2×10^{-2}
POGZ	cross all tissues	30	9	82%	6.9×10^{-4}	4.2×10^{-2}
USP16	cross metabolic tissues	3	2	94%	7.0×10^{-4}	4.3×10^{-2}
GSC	cross all tissues	11	5	83%	7.1×10^{-4}	4.3×10^{-2}
SLC12A7	cross all tissues	12	4	84%	7.1×10^{-4}	4.3×10^{-2}
EFCAB4A	cross all tissues	20	10	83%	7.4×10^{-4}	4.4×10^{-2}
ATP6V0B	cross all tissues	5	3	81%	7.6×10^{-4}	4.5×10^{-2}
GLCCI1	cross metabolic tissues	3	2	84%	7.7×10^{-4}	4.5×10^{-2}
KATNAL2	cross all tissues	20	8	81%	7.7×10^{-4}	4.6×10^{-2}
GSTT2	cross all tissues	48	13	80%	7.8×10^{-4}	4.6×10^{-2}
GLB1	cross metabolic tissues	3	2	81%	7.8×10^{-4}	4.6×10^{-2}
FAM57A	cross all tissues	32	12	81%	7.9×10^{-4}	4.6×10^{-2}
GNS	cross all tissues	17	5	80%	7.9×10^{-4}	4.6×10^{-2}
ABCC2	cross all tissues	12	6	81%	8.0×10^{-4}	4.6×10^{-2}
ENTPD7	cross all tissues	10	5	82%	8.1×10^{-4}	4.6×10^{-2}
C9orf117	cross all tissues	6	3	86%	8.5×10^{-4}	4.8×10^{-2}
GAS8	cross metabolic tissues	8	3	81%	8.5×10^{-4}	4.8×10^{-2}
AP001877.1	cross all tissues	39	10	81%	8.8×10^{-4}	5.0×10^{-2}

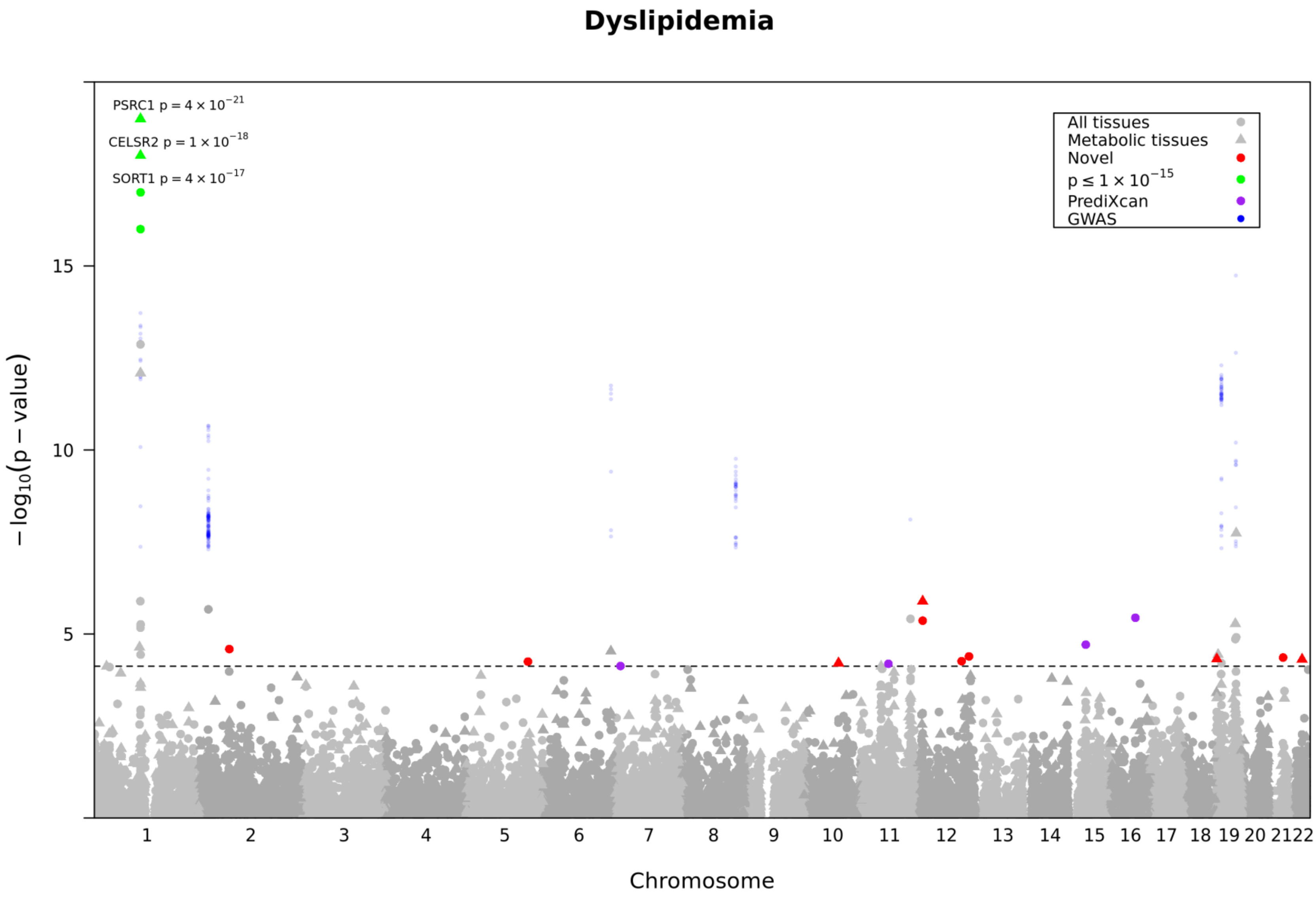

Figure 25. Manhattan plot of cross-tissue GReX association analysis on dyslipidemia in BioVU

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 16. Significant dyslipidemia genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PSRC1	cross metabolic tissues	8	3	86%	4.2×10^{-21}	9.9×10^{-17}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	cross metabolic tissues	6	3	86%	1.3×10^{-18}	1.6×10^{-14}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SORT1	cross all tissues	9	4	85%	4.3×10^{-17}	3.4×10^{-13}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
PSRC1	cross all tissues	32	11	81%	5.7×10^{-17}	3.4×10^{-13}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
CELSR2	cross all tissues	21	7	80%	1.4×10^{-13}	6.5×10^{-10}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SORT1	cross metabolic tissues	3	1	85%	8.1×10^{-13}	3.2×10^{-9}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SNRPD2	cross metabolic tissues	3	2	93%	1.8×10^{-8}	6.2×10^{-5}	rs7412 (pval=1.82×10^{-15})	APOE region
CLCC1	cross all tissues	15	4	81%	1.3×10^{-6}	3.4×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
TAS2R31	cross metabolic tissues	4	2	82%	1.3×10^{-6}	3.4×10^{-3}	NA	NA
APOB	cross all tissues	12	5	84%	2.2×10^{-6}	5.1×10^{-3}	rs515135 (pval=2.18×10^{-11})	rs577584 pval=1×10^{-229} (LDL-C, Klarin, 30275531)
CETP	cross all tissues	8	4	83%	3.6×10^{-6}	7.8×10^{-3}	NA	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
PAFAH1B2	cross all tissues	10	5	85%	3.9×10^{-6}	7.8×10^{-3}	rs964184 (pval=7.68×10^{-09})	rs7350481 pval=1×10^{-300} (TG, Klarin, 30275531)
TAS2R31	cross all tissues	16	6	81%	4.3×10^{-6}	7.9×10^{-3}	NA	NA
SMG9	cross metabolic tissues	7	2	88%	5.2×10^{-6}	8.7×10^{-3}	rs7412 (pval=1.82×10^{-15})	APOE region
GSTM3	cross all tissues	48	14	80%	5.5×10^{-6}	8.7×10^{-3}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
SARS	cross all tissues	5	3	81%	6.8×10^{-6}	1.0×10^{-2}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
DMPK	cross all tissues	20	9	82%	1.2×10^{-5}	1.7×10^{-2}	rs7412 (pval=1.82×10^{-15})	APOE region
SMG9	cross all tissues	24	7	80%	1.4×10^{-5}	1.8×10^{-2}	rs7412 (pval=1.82×10^{-15})	APOE region

Table 16. Significant dyslipidemia genes from cross-tissue GReX analysis in BioVU

Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
EHD4	cross all tissues	24	10	81%	2.0×10^{-5}	2.5×10^{-2}	NA	rs149492745 pval=3×10^{-30} (TG, Hoffmann, 29507422)
PRMT6	cross metabolic tissues	7	2	89%	2.3×10^{-5}	2.7×10^{-2}	rs660240 (pval=1.89×10^{-14})	rs1730859 pval=4×10^{-14} (LDL-C, Klarin, 30275531)
ADD2	cross all tissues	14	7	82%	2.5×10^{-5}	2.9×10^{-2}	NA	NA
SLC22A3	cross metabolic tissues	6	3	81%	2.9×10^{-5}	3.2×10^{-2}	rs74617384 (pval=1.78×10^{-12})	rs186696265 pval=3×10^{-69} (LDL-C, Hoffmann, 29507422)
NFIC	cross metabolic tissues	3	2	85%	3.6×10^{-5}	3.6×10^{-2}	rs10412048 (pval=5.05×10^{-13})	rs941408 pval=5×10^{-10} (LDL-C, Klarin, 30275531)
SYPL2	cross all tissues	29	10	81%	3.7×10^{-5}	3.6×10^{-2}	rs660240 (pval=1.89×10^{-14})	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
MSI1	cross all tissues	9	4	82%	4.1×10^{-5}	3.9×10^{-2}	NA	NA
ATP5O	cross all tissues	26	9	81%	4.3×10^{-5}	3.9×10^{-2}	NA	NA
C2CD4C	cross metabolic tissues	5	3	90%	4.8×10^{-5}	4.2×10^{-2}	NA	NA
PISD	cross metabolic tissues	3	2	81%	4.9×10^{-5}	4.2×10^{-2}	NA	NA
PAH	cross all tissues	8	4	86%	5.5×10^{-5}	4.4×10^{-2}	NA	NA
SH3RF2	cross all tissues	10	5	84%	5.6×10^{-5}	4.4×10^{-2}	NA	NA
KANK2	cross all tissues	22	9	81%	6.1×10^{-5}	4.5×10^{-2}	rs10412048 (pval=5.05×10^{-13})	rs143020224 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
RP11-137H2.6	cross metabolic tissues	6	2	84%	6.1×10^{-5}	4.5×10^{-2}	NA	NA
BATF2	cross all tissues	5	3	86%	6.5×10^{-5}	4.7×10^{-2}	NA	rs56271783 pval=1×10^{-16} (TG, Klarin, 30275531)

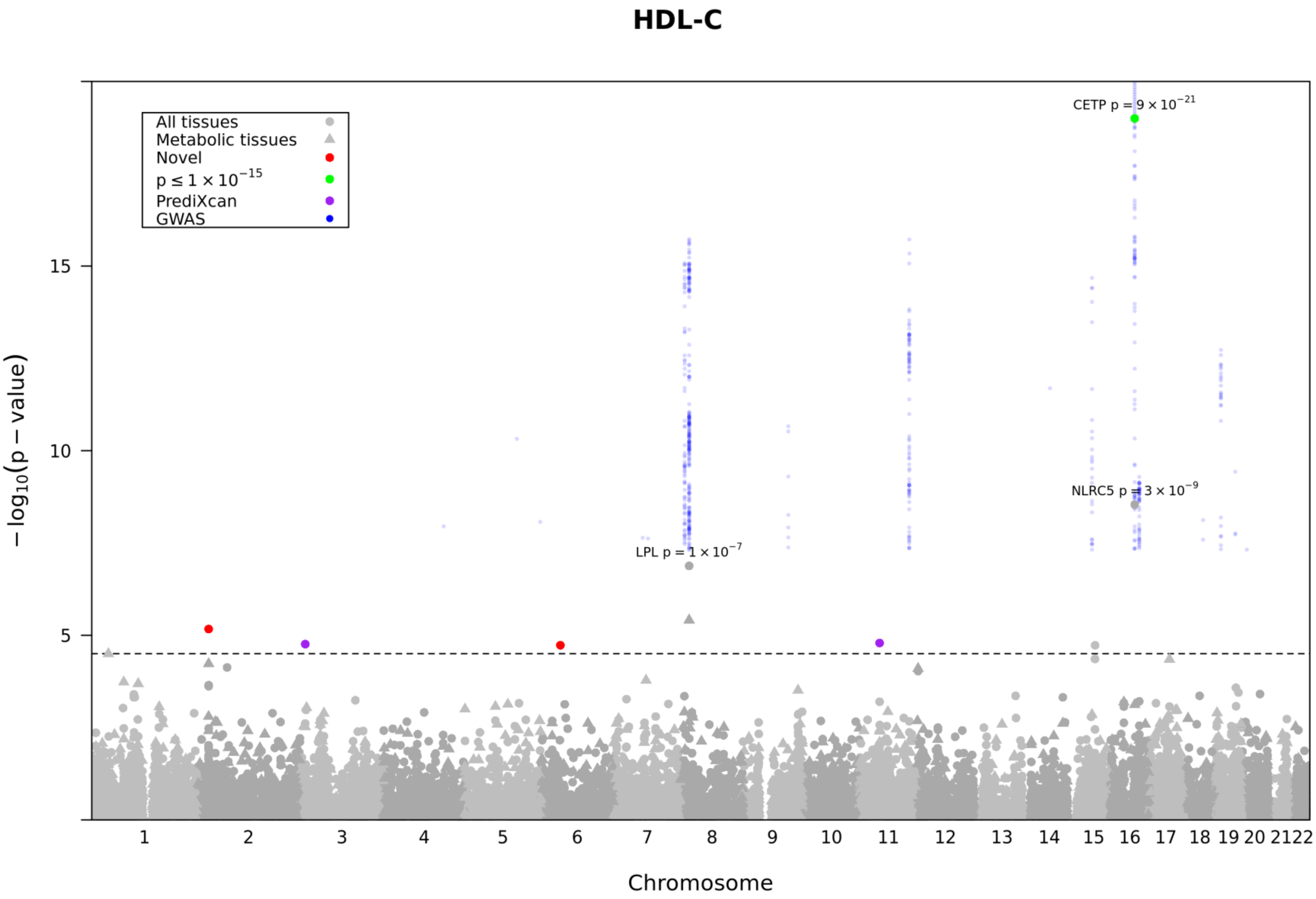

Figure 26. Manhattan plot of cross-tissue GReX association analysis on HDL-C in HCSC/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

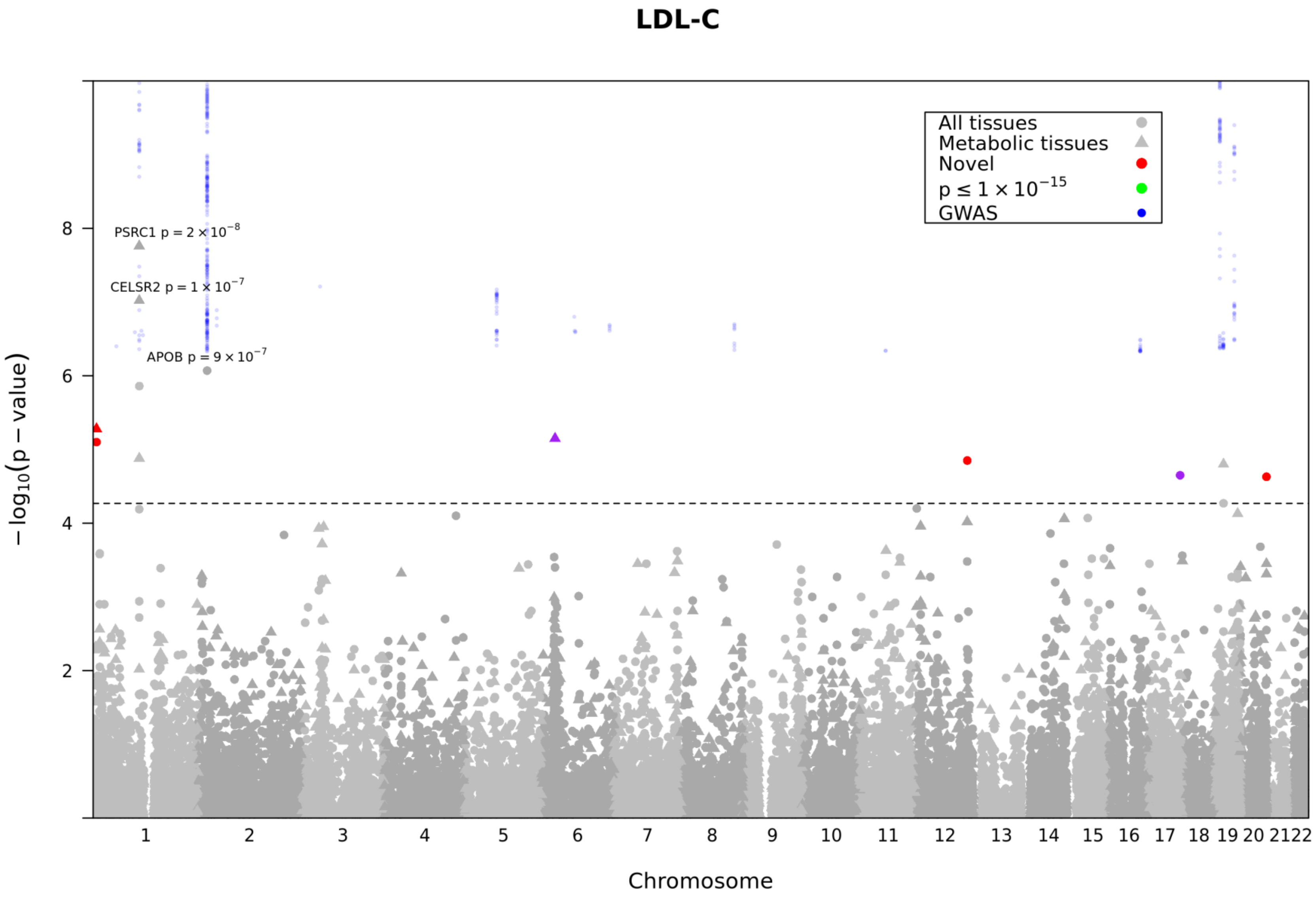

Figure 27. Manhattan plot of cross-tissue GReX association analysis on LDL-C in HCSC/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

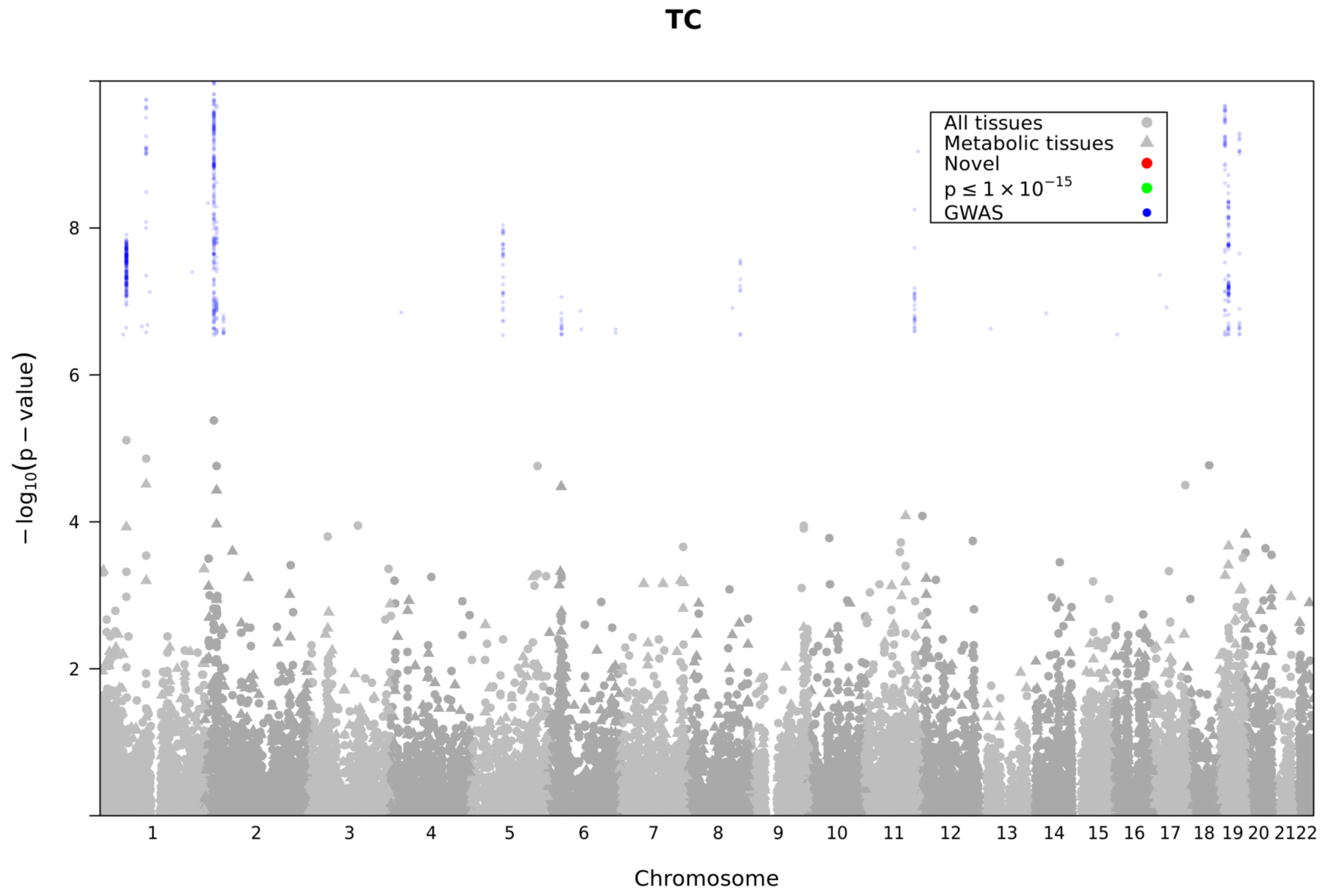

Figure 28. Manhattan plot of cross-tissue GReX association analysis on TC in HCSC/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

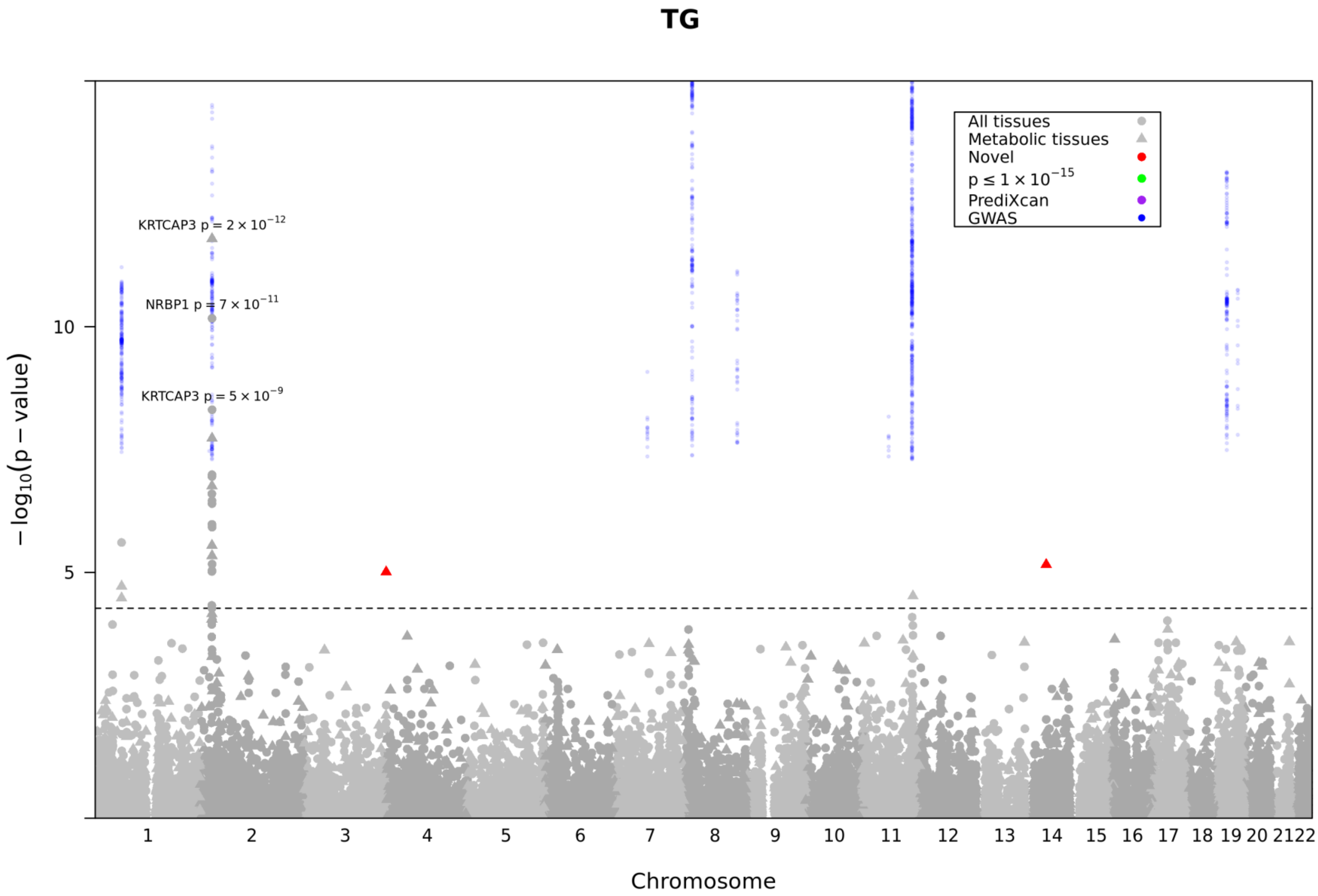

Figure 29. Manhattan plot of cross-tissue GReX association analysis on TG in HCSC/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

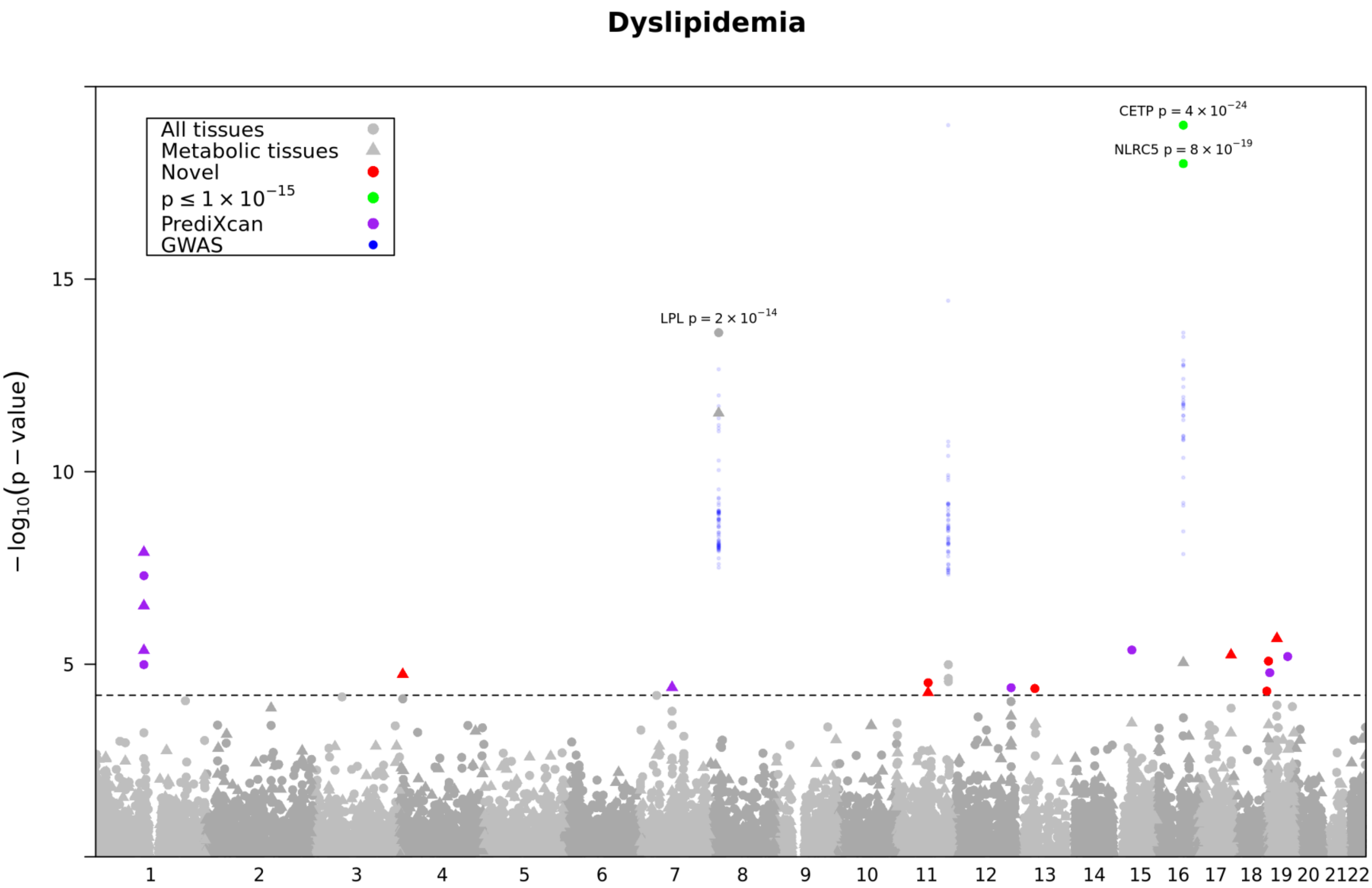

Figure 30. Manhattan plot of cross-tissue GReX association analysis on dyslipidemia in HCSC/SOL

GWAS SNPs from presented population (blue); PrediXcan only genes: no GWAS SNPs ±10MB (purple); Novel genes: no NHGRI-EBI catalog SNPs ±1MB (red)

Table 17. Serum lipid significant genes from cross-tissue GReX analysis in HCHS/SOL

Trait	Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
HDL-C	CETP	cross all tissues	8	4	81%	8.7×10^{-21}	2.1×10^{-16}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	NLRC5	cross all tissues	10	5	84%	2.9×10^{-9}	3.4×10^{-5}	rs821840 (pval=4.19×10^{-82})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HDL-C	LPL	cross all tissues	7	4	87%	1.3×10^{-7}	1.0×10^{-3}	rs3916027 (pval=1.02×10^{-21})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
HDL-C	LPL	cross metabolic tissues	4	3	92%	3.9×10^{-6}	2.3×10^{-2}	rs3916027 (pval=1.02×10^{-21})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
HDL-C	NRBP1	cross all tissues	21	5	83%	6.7×10^{-6}	3.2×10^{-2}	NA	NA
HDL-C	ZNF408	cross all tissues	11	5	82%	1.6×10^{-5}	4.9×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
HDL-C	RAF1	cross all tissues	8	5	87%	1.7×10^{-5}	4.9×10^{-2}	NA	rs35240997 pval=1×10^{-13} (Klarin, 30275531)
HDL-C	RUNX2	cross all tissues	9	5	84%	1.9×10^{-5}	4.9×10^{-2}	NA	NA
HDL-C	DENND4A	cross all tissues	6	4	87%	1.9×10^{-5}	4.9×10^{-2}	rs2070895 (pval=2.10×10^{-15})	NA
LDL-C	PSRC1	cross metabolic tissues	8	3	83%	1.7×10^{-8}	4.1×10^{-4}	rs7528419 (pval=7.25×10^{-44})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
LDL-C	CELSR2	cross metabolic tissues	6	3	84%	9.5×10^{-8}	1.1×10^{-3}	rs7528419 (pval=7.25×10^{-44})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
LDL-C	APOB	cross all tissues	12	5	84%	8.6×10^{-7}	6.8×10^{-3}	rs12997242 (pval=1.40×10^{-22})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
LDL-C	SORT1	cross all tissues	9	4	84%	1.4×10^{-6}	8.2×10^{-3}	rs7528419 (pval=7.25×10^{-44})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
LDL-C	RERE	cross metabolic tissues	6	3	81%	5.3×10^{-6}	2.5×10^{-2}	NA	NA
LDL-C	STK19	cross metabolic tissues	6	3	82%	7.0×10^{-6}	2.7×10^{-2}	NA	rs13205804 pval=3×10^{-21} (Klarin, 30275531)
LDL-C	RERE	cross all tissues	18	7	81%	8.0×10^{-6}	2.7×10^{-2}	NA	NA
LDL-C	SORT1	cross metabolic tissues	3	1	84%	1.3×10^{-5}	3.7×10^{-2}	rs7528419 (pval=7.25×10^{-44})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
LDL-C	PRKAB1	cross all tissues	18	6	80%	1.4×10^{-5}	3.7×10^{-2}	NA	NA

Table 17. Serum lipid significant genes from cross-tissue GReX analysis in HCHS/SOL

Trait	Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
LDL-C	LINC00663	cross metabolic tissues	7	4	88%	1.6×10^{-5}	3.7×10^{-2}	rs142130958 (pval=8.81×10^{-25})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
LDL-C	BIRC5	cross all tissues	14	5	81%	2.3×10^{-5}	4.7×10^{-2}	NA	rs17561950 pval=2×10^{-11} (Klarin, 30275531)
LDL-C	LIME1	cross all tissues	31	7	81%	2.4×10^{-5}	4.7×10^{-2}	NA	NA
TG	KRTCAP3	cross metabolic tissues	6	2	81%	1.6×10^{-12}	3.9×10^{-8}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	cross all tissues	21	5	83%	6.8×10^{-11}	8.1×10^{-7}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KRTCAP3	cross all tissues	17	7	82%	4.9×10^{-9}	3.8×10^{-5}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	NRBP1	cross metabolic tissues	5	2	91%	1.9×10^{-8}	1.1×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	cross all tissues	11	4	80%	1.0×10^{-7}	4.4×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	KHK	cross all tissues	31	9	81%	1.1×10^{-7}	4.4×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	CAD	cross metabolic tissues	6	3	85%	1.7×10^{-7}	5.9×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	MAPRE3	cross all tissues	11	4	82%	2.5×10^{-7}	7.5×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ZNF513	cross all tissues	6	3	92%	3.4×10^{-7}	9.0×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	SNX17	cross all tissues	9	4	82%	4.0×10^{-7}	9.5×10^{-4}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ATRAID	cross all tissues	35	11	81%	1.0×10^{-6}	2.2×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	C2orf16	cross all tissues	7	5	87%	1.2×10^{-6}	2.4×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	USP1	cross all tissues	8	4	86%	2.5×10^{-6}	4.5×10^{-3}	rs35529421 (pval=2.90×10^{-13})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)

Table 17. Serum lipid significant genes from cross-tissue GReX analysis in HCHS/SOL

Trait	Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
TG	ATRAID	cross metabolic tissues	6	3	87%	2.8×10^{-6}	4.8×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	PPM1G	cross metabolic tissues	5	3	90%	4.5×10^{-6}	7.2×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	GCKR	cross all tissues	5	3	83%	6.8×10^{-6}	9.6×10^{-3}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	C14orf182	cross metabolic tissues	3	2	80%	6.9×10^{-6}	9.6×10^{-3}	NA	NA
TG	SLC5A6	cross all tissues	23	10	81%	9.2×10^{-6}	1.1×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	ABHD1	cross all tissues	5	3	88%	9.5×10^{-6}	1.1×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TG	TCTEX1D2	cross metabolic tissues	5	2	84%	9.7×10^{-6}	1.1×10^{-2}	NA	NA
TG	DOCK7	cross metabolic tissues	4	2	81%	1.9×10^{-5}	2.2×10^{-2}	rs35529421 (pval=2.90×10^{-13})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
TG	HMBS	cross metabolic tissues	7	3	82%	3.0×10^{-5}	3.2×10^{-2}	rs964184 (pval=1.59×10^{-73})	NA
TG	USP1	cross metabolic tissues	3	2	98%	3.3×10^{-5}	3.4×10^{-2}	rs35529421 (pval=2.90×10^{-13})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
TG	DPYSL5	cross all tissues	8	4	85%	4.6×10^{-5}	4.6×10^{-2}	rs1260326 (pval=2.05×10^{-27})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
Dyslipidemia	CETP	cross all tissues	8	4	81%	3.9×10^{-24}	9.3×10^{-20}	rs711752:56996211:G:A (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	NLRC5	cross all tissues	10	5	84%	7.6×10^{-19}	9.0×10^{-15}	rs711752:56996211:G:A (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	LPL	cross all tissues	7	4	87%	2.4×10^{-14}	1.9×10^{-10}	rs331 (pval=2.18×10^{-13})	rs1569209 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	LPL	cross metabolic tissues	4	3	92%	3.0×10^{-12}	1.8×10^{-8}	rs331 (pval=2.18×10^{-13})	rs1569209 pval=1×10^{-300} (TG, Klarin, 30275531)

Table 17. Serum lipid significant genes from cross-tissue GReX analysis in HCHS/SOL

Trait	Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
Dyslipidemia	PSRC1	cross metabolic tissues	8	3	83%	1.2×10^{-8}	5.8×10^{-5}	NA	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
Dyslipidemia	SORT1	cross all tissues	9	4	84%	5.1×10^{-8}	2.0×10^{-4}	NA	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
Dyslipidemia	CELSR2	cross metabolic tissues	6	3	84%	3.0×10^{-7}	1.0×10^{-3}	NA	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
Dyslipidemia	ATP13A1	cross metabolic tissues	4	3	90%	2.1×10^{-6}	6.3×10^{-3}	NA	NA
Dyslipidemia	CDAN1	cross all tissues	13	6	86%	4.3×10^{-6}	1.0×10^{-2}	NA	rs150844304 pval=5×10^{-43} (TG, Hoffmann, 29507422)
Dyslipidemia	SORT1	cross metabolic tissues	3	1	84%	4.4×10^{-6}	1.0×10^{-2}	NA	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
Dyslipidemia	MGAT5B	cross metabolic tissues	3	1	85%	5.7×10^{-6}	1.2×10^{-2}	NA	NA
Dyslipidemia	IRGQ	cross all tissues	5	2	82%	6.3×10^{-6}	1.2×10^{-2}	NA	APOE region
Dyslipidemia	BSG	cross all tissues	18	6	82%	8.3×10^{-6}	1.5×10^{-2}	NA	NA
Dyslipidemia	NLRC5	cross metabolic tissues	3	2	91%	9.1×10^{-6}	1.5×10^{-2}	rs711752:56996211:G:A (pval=2.45×10^{-14})	rs56156922 pval=1×10^{-300} (HDL-C, Hoffmann, 29507422)
Dyslipidemia	RP11-109L13.1	cross all tissues	48	8	80%	1.0×10^{-5}	1.5×10^{-2}	seq-rs964184 (pval=2.48×10^{-17})	rs7350481 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	PSRC1	cross all tissues	32	12	82%	1.0×10^{-5}	1.5×10^{-2}	NA	rs611917 pval=1×10^{-300} (LDL-C, Klarin, 30275531)
Dyslipidemia	C19orf77	cross all tissues	5	2	82%	1.7×10^{-5}	2.3×10^{-2}	NA	rs941408 pval=5×10^{-10} (LDL-C, Klarin, 30275531)
Dyslipidemia	CRMP1	cross metabolic tissues	6	3	82%	1.8×10^{-5}	2.4×10^{-2}	NA	NA

Table 17. Serum lipid significant genes from cross-tissue GReX analysis in HCHS/SOL

Trait	Gene	Model	N tissues	N PCs	Explained variances	P-value	FDR	Annotation	
								GWAS	NHGRI-EBI
Dyslipidemia	PAFAH1B2	cross all tissues	10	5	83%	2.3×10^{-5}	2.9×10^{-2}	seq-rs964184 (pval=2.48×10^{-17})	rs7350481 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	PCSK7	cross all tissues	10	6	84%	2.8×10^{-5}	3.3×10^{-2}	seq-rs964184 (pval=2.48×10^{-17})	rs7350481 pval=1×10^{-300} (TG, Klarin, 30275531)
Dyslipidemia	NADSYN1	cross all tissues	36	9	80%	3.0×10^{-5}	3.4×10^{-2}	NA	NA
Dyslipidemia	ABHD11	cross metabolic tissues	6	3	83%	4.0×10^{-5}	4.2×10^{-2}	NA	rs13234131 pval=4×10^{-191} (TG, Klarin, 30275531)
Dyslipidemia	DNAH10OS	cross all tissues	25	8	82%	4.1×10^{-5}	4.2×10^{-2}	NA	rs10773112 pval=8×10^{-43} (HDL-C, Klarin, 30275531)
Dyslipidemia	LACC1	cross all tissues	23	9	80%	4.2×10^{-5}	4.2×10^{-2}	NA	NA
Dyslipidemia	MBP	cross all tissues	8	5	88%	5.1×10^{-5}	4.8×10^{-2}	NA	NA
Dyslipidemia	NADSYN1	cross metabolic tissues	6	2	89%	5.5×10^{-5}	5.0×10^{-2}	NA	NA

Summary of identified serum lipids related genes

Three different approaches—IBD mapping, tissue-specific GReX, and cross-tissue GReX—have been applied in two populations, BioVU and HCHS/SOL. A total of 1,079 unique genes are significantly associated with at least one lipid trait across all analyses, and 303 of them are considered novel due to no NHGRI-EBI catalog reported serum lipid SNP within 1Mb of the gene (Appendix XII). In BioVU, 969 unique genes are identified; in SOL, 152 genes are identified; 42 genes replicate in both populations. GReX of ten genes is associated with at least one lipid trait in both GReX models for both populations: *CAD, CETP, NRBP1, SNX17, PPM1G, ATRAID, NLRC5, KRTCAP3, ZNF513,* and *LPL* (Appendix XIII). Eight genes fall within the four genome-wide significant or suggestive IBD regions and also replicate in any model of GReX association. These genes include *LINC01310* (within the IBD region on chromosome 22 and cross-tissue GReX model for LDL-C), *FLG*, *CDC42SE1*, *LYSMD1*, *C2CD4D*, and *POGZ* (within the IBD region on chromosome 1 and tissue-specific and/or cross-tissue GReX model for TG), *IMPA2* and *MAPPE1* (identified IBD region of chromosome 18 and cross-tissue GReX model for TG). *LINC01310*, *FLG*, *IMPA2* and *MAPPE1* have not been reported in previous GWAS (Appendix XIII).

Phenome-wide association study

A large EHR-linked DNA databank, such as BioVU, provides an opportunity to explore the broader clinical consequences of genetic dysregulation in the 1,079 unique genes associated with serum lipid levels in the present study. I evaluated the enrichment of phenotypes associated with lipid genes using GReX association statistics in PredixVU. To determine empirical p-values for enrichment, I created a null distribution using 100,000 permutations. Sixty-eight phecodes are significantly enriched for GReX association with identified serum lipid genes after Bonferroni correction (p-value $< 3.3\times10^{-5}$) (Table 18). Twelve phecodes related to diabetes, ischemic heart disease and varicose veins are enriched for association with lipid genes. In addition, twelve phenotypes from the neurological and mental disorder categories, six genitourinary diseases, seven digestive diseases, seven different neoplasms, and fifteen other traits are enriched for GReX association in the identified lipid genes.

Table 18. Significant phenotypes enriched with serum lipid genes

					Empirical null distribution					
Phecode	Description	Category	Count	p-value	1%	5%	50%	95%	99%	max
250.2	Type 2 diabetes	endocrine/metabolic	145	$<1\times10^{-5}$	68	74	88	102	109	128
250	Diabetes mellitus	endocrine/metabolic	141	$<1\times10^{-5}$	68	73	87	102	108	130
250.3	Insulin pump user	endocrine/metabolic	130	$<1\times10^{-5}$	60	65	78	92	98	115
250.13	Type 1 diabetes with ophthalmic manifestations	endocrine/metabolic	129	$<1\times10^{-5}$	63	68	81	96	102	120
557.1	Celiac disease	digestive	126	$<1\times10^{-5}$	57	62	75	89	94	111
562	Diverticulosis and diverticulitis	digestive	123	$<1\times10^{-5}$	57	62	75	88	94	112
250.1	Type 1 diabetes	endocrine/metabolic	122	$<1\times10^{-5}$	60	65	79	93	99	114
335	Multiple sclerosis	neurological	122	$<1\times10^{-5}$	55	60	73	87	92	111
740	Osteoarthrosis	musculoskeletal	120	$<1\times10^{-5}$	59	64	77	91	97	115
250.11	Type 1 diabetes with ketoacidosis	endocrine/metabolic	119	$<1\times10^{-5}$	59	64	77	91	97	117
250.12	Type 1 diabetes with renal manifestations	endocrine/metabolic	119	$<1\times10^{-5}$	58	63	76	90	96	114
250.7	Diabetic retinopathy	endocrine/metabolic	119	$<1\times10^{-5}$	59	64	77	91	97	117
272.1	Hyperlipidemia	endocrine/metabolic	119	$<1\times10^{-5}$	56	62	74	88	94	113
580.1	Glomerulonephritis	genitourinary	118	$<1\times10^{-5}$	51	56	69	82	88	106
244.4	Hypothyroidism NOS	endocrine/metabolic	117	$<1\times10^{-5}$	55	60	73	86	92	109
250.23	Type 2 diabetes with ophthalmic manifestations	endocrine/metabolic	116	$<1\times10^{-5}$	57	62	75	89	95	115
272	Disorders of lipoid metabolism	endocrine/metabolic	116	$<1\times10^{-5}$	56	61	74	88	94	113
284	Aplastic anemia	hematopoietic	115	$<1\times10^{-5}$	57	62	75	89	95	114
530.2	Esophageal bleeding (varices/hemorrhage)	digestive	115	$<1\times10^{-5}$	58	63	76	90	96	113
593	Hematuria	genitourinary	114	$<1\times10^{-5}$	56	62	75	88	94	114
250.14	Type 1 diabetes with neurological manifestations	endocrine/metabolic	113	$<1\times10^{-5}$	57	62	75	89	94	113
358.1	Myasthenia gravis	neurological	113	$<1\times10^{-5}$	51	55	68	81	86	105
709	Diffuse diseases of connective tissue	dermatologic	112	$<1\times10^{-5}$	54	59	71	85	90	106
172.3	Carcinoma in situ of skin	neoplasms	111	$<1\times10^{-5}$	52	57	70	83	89	102
182	Malignant neoplasm of uterus	neoplasms	111	$<1\times10^{-5}$	53	58	70	83	89	105
550.5	Ventral hernia	digestive	111	$<1\times10^{-5}$	52	57	70	83	89	105
250.22	Type 2 diabetes with renal manifestations	endocrine/metabolic	110	$<1\times10^{-5}$	54	59	72	85	91	108
411.2	Myocardial infarction	circulatory system	110	$<1\times10^{-5}$	57	62	75	89	95	109

Table 18. Significant phenotypes enriched with serum lipid genes

					Empirical null distribution					
Phecode	Description	Category	Count	p-value	1%	5%	50%	95%	99%	max
585.3	Chronic renal failure [CKD]	genitourinary	110	$<1\times10^{-5}$	50	55	67	80	86	103
696.41	Psoriasis vulgaris	dermatologic	110	$<1\times10^{-5}$	53	58	70	84	89	105
180	Cervical cancer and dysplasia	neoplasms	109	$<1\times10^{-5}$	51	56	68	81	87	104
571.6	Primary biliary cirrhosis	digestive	109	$<1\times10^{-5}$	53	58	70	83	89	106
411.9	Other acute and subacute forms of ischemic heart disease	circulatory system	107	$<1\times10^{-5}$	48	53	65	78	84	103
341	Other demyelinating diseases of central nervous system	neurological	107	$<1\times10^{-5}$	49	54	66	79	84	101
149.3	Cancer of hypopharynx	neoplasms	106	$<1\times10^{-5}$	53	58	70	83	89	106
110	Dermatophytosis / Dermatomycosis	infectious diseases	105	$<1\times10^{-5}$	53	58	70	83	89	105
151	Cancer of stomach	neoplasms	105	$<1\times10^{-5}$	49	54	67	80	85	101
187.2	Malignant neoplasm of testis	neoplasms	105	$<1\times10^{-5}$	51	56	68	81	87	105
251.1	Hypoglycemia	endocrine/metabolic	104	$<1\times10^{-5}$	50	54	67	79	85	102
585.33	Chronic Kidney Disease, Stage III	genitourinary	103	$<1\times10^{-5}$	50	55	67	80	86	99
70.4	Chronic hepatitis	infectious diseases	103	$<1\times10^{-5}$	51	56	69	82	87	103
790.6	Other abnormal blood chemistry	symptoms	101	$<1\times10^{-5}$	50	55	67	80	85	100
535.2	Atrophic gastritis	digestive	100	$<1\times10^{-5}$	49	54	66	79	84	100
369	Infection of the eye	sense organs	99	$<1\times10^{-5}$	48	53	65	78	83	99
382	Otalgia	sense organs	97	$<1\times10^{-5}$	48	53	65	78	83	97
317.11	Alcoholic liver damage	mental disorders	109	1×10^{-5}	55	60	73	86	92	111
802	Fracture of pelvis	injuries & poisonings	104	1×10^{-5}	52	57	70	83	88	108
327	Sleep disorders	neurological	104	1×10^{-5}	53	58	71	84	90	107
536.3	Gastroparesis	digestive	103	1×10^{-5}	51	56	68	81	87	104
357	Inflammatory and toxic neuropathy	neurological	98	1×10^{-5}	50	55	67	80	85	99
587	Kidney replaced by transpant	genitourinary	107	2×10^{-5}	55	60	73	87	92	113
296.1	Bipolar	mental disorders	106	2×10^{-5}	53	58	71	84	89	108
244.1	Secondary hypothyroidism	endocrine/metabolic	106	2×10^{-5}	54	59	72	86	91	108
198	Secondary malignant neoplasm	neoplasms	103	2×10^{-5}	52	57	70	83	89	105
656.6	Perinatal disorders of digestive system	pregnancy complications	102	2×10^{-5}	52	56	69	82	88	103

Table 18. Significant phenotypes enriched with serum lipid genes

					Empirical null distribution					
Phecode	Description	Category	Count	p-value	1%	5%	50%	95%	99%	max
X509.3	Pulmonary insufficiency or respiratory failure following trauma and surgery	respiratory	101	2×10^{-5}	51	56	68	81	87	102
X714.1	Rheumatoid arthritis	musculoskeletal	101	2×10^{-5}	50	55	67	80	86	104
X747.13	Congenital anomalies of great vessels	congenital anomalies	100	2×10^{-5}	50	55	67	80	86	101
X358	Myoneural disorders	neurological	100	2×10^{-5}	50	55	67	80	86	109
X454	Varicose veins	circulatory system	98	2×10^{-5}	48	53	65	78	84	104
X479	Other upper respiratory disease	respiratory	97	2×10^{-5}	49	54	66	79	84	106
X411	Ischemic Heart Disease	circulatory system	112	3×10^{-5}	60	65	78	92	98	115
X297.1	Suicidal ideation	mental disorders	104	3×10^{-5}	53	58	71	84	90	105
X297	Suicidal ideation or attempt	mental disorders	103	3×10^{-5}	53	58	71	84	90	108
X352.2	Facial nerve disorders [CN7]	neurological	101	3×10^{-5}	51	56	69	82	87	108
X292.6	Hallucinations	mental disorders	98	3×10^{-5}	48	53	65	78	84	99
X288.3	Eosinophilia	hematopoietic	98	3×10^{-5}	48	53	65	78	83	104
X580.2	Nephrotic syndrome without mention of glomerulonephritis	genitourinary	97	3×10^{-5}	49	53	66	78	84	101

CHAPTER V

DISCUSSION

Although hundreds of genetic variants have been identified in GWAS of lipid phenotypes, only about 10% of the trait variance is explained by previously associated SNPs. This may be due to several factors limiting GWAS-based SNP discovery. First, GWAS are well-powered to identify modest to large effects at loci with low allelic heterogeneity and at variants with low to common allele frequencies. Effects at very rare alleles, variants with low effect size, and loci with allelic heterogeneity are likely to be missed in GWAS. Second, most well-powered GWAS to-date have been performed in samples drawn from European ancestry populations. Therefore, variants with differential minor allele frequencies in other race/ethnic groups or population-specific effects may be poorly characterized in the literature.

In this study, I investigated the missing heritability of serum lipids with two novel but emerging approaches, IBD mapping and GReX-based association analysis, in two populations, BioVU and HCSC/SOL. These approaches address the limitations of GWAS in several ways. IBD mapping leverages distant relatedness and is well-powered to detect effects of very rare (even family-specific) alleles, as well as loci with high allelic heterogeneity. Transcription-based association analyses, such as PrediXcan, aggregate SNP effects at the gene level, reducing the burden of multiple test correction, improving detection of genes implicated by a number of SNPs of small effect, and providing a natural functional interpretation of results. To begin to address the translational relevance of the findings from these methods across populations, both methods were applied in both a large Hispanic/Latino dataset, HCSC/SOL, as well as a large European ancestry clinical dataset within BioVU, an EHR-linked biobank. The genetic architecture of serum lipid traits in H/L is of particular importance because not only is this population chronically underrepresented in genomic analyses, but this population is disproportionately affected by cardiometabolic disease. I then examined the broader clinical consequences of the set of serum-lipid-associated genes I identified in these analyses via a phenome-wide transcription-based association study in BioVU.

With the advantages of these two methods and two datasets, I identified 303 novel genes and also replicated 776 previously reported genes. From IBD mapping, I identified three genome-wide significant regions and two genome-wide suggestive regions, which may harbor inherited rare variants that affect the regulation of serum lipids. I used PrediXcan to impute gene expression due to eQTL variants, and performed an association analysis to link gene function to lipid phenotype, identifying 237 novel serum lipid genes. Furthermore, my biobank enrichment analysis using the total set of 1,079 unique genes identified in any analysis brought insight to the diverse consequences and comorbidities of serum lipid levels, including several cardiovascular, neurological and psychiatric disorders, and implied they may be linked by shared causal genes.

Identify-by-descent describes genomic sharing due to inheritance from a recent common ancestor. I used both genome-wide IBD proportions and the distribution of the number and length of IBD segments to reconstruct family networks in BioVU. A total of 5,019 families were identified in BioVU, meaning that 16.4% subjects have at least one close relative (2nd degree or closer) in BioVU. Cryptic relatedness has long been a concern for GWAS, and inappropriate assumption of unrelatedness may lead to false discoveries[87,88]. Determining the correct family structures allows us to make suitable model assumptions and decrease bias in association analysis. In addition to signifying relatedness, IBD segments also can give insight to the population history[89]. I observed a lower IBD sharing rate in HCHS/SOL (82,075.5 pairs/cM) compared to BioVU

(675,849.3 pairs/cM), which could be due to differences in the ancestral populations of each dataset, or may come from use of different sampling strategies, genotyping arrays, or phasing methods. In BioVU, I restricted the analysis to individuals of European ancestry, and most participants were from the local middle Tennessee community. In contrast, HCHS/SOL recruited participants from four different metropolitan areas in the US, and the subjects were from six different countries/areas of origin[2]. In addition, recent admixture in these populations could have decreased phasing accuracy, which could lead to identification of fewer IBD segments. However, the household-based ascertainment of HCHS/SOL and the recent admixture in Hispanic/Latino populations offered a unique opportunity to investigate patterns of IBD sharing and their association with dyslipidemia.

Since there remains a substantial gap between estimated lipid trait heritability and that explained by GWAS-identified SNPs, much attention has recently been given to rare variants[90]. According to estimates by Wainschtein et al., relatively rare variants (MAF from 0.0001 to 0.1) can explain over half of heritability of BMI and body height[91]. My IBD mapping analysis detects the aggregate enrichment of all shared segments in a region. Investigating enrichment of sharing of any segment rather than association with a specific segment results in power to detect effects in a region with allelic heterogeneity. In my results, three regions reached genome-wide significance and two were suggestive. In my GWAS of the same populations, no variants reached genome-wide significance in these regions, which may indicate that IBD mapping is better powered than traditional GWAS to detect the effects at these loci. In addition, some genes located in the identified regions have been previously reported to be associated with lipid metabolism. *RANBP17* is a gene located in the genome-wide significant region on chromosome 5, and encodes a RAN transporter protein. It has been reported to be associated with several metabolic traits in GWAS, including HDL-C[35], visceral fat[92], and BMI[93]. However, molecular mechanisms underlying this gene's regulation of serum lipids are still unknown

In addition to the enrichment of IBD sharing by disease status, I also investigated the specific IBD segments shared by at least ten individuals. A total of 114 specific segments are found significantly associated with dichotomous dyslipidemia status after correcting for close relatedness. The highest odds ratio for a specific IBD segment was 14.01 (14/15 carriers are dyslipidemia cases), demonstrating that IBD segments offer an opportunity to identify private and rare causal variants with large effect size. This approach narrows the potential regions and possible carriers, and makes follow-up sequencing more efficient and affordable.

Electronic health records contain rich patient-centered data, and linking them with genetic data provides a largely untapped resource to investigate disease-relevant genetic mechanisms. However, a major difficulty is determining the optimal measure from the EHR, especially when deriving a single phenotype from multiple measures. A previous study suggested that using the long-term average from longitudinal measurements could improve power by 20% relative to using single time measures[94]. In this study, I evaluated the heritability of several different cross-sectional and longitudinal phenotyping algorithms for serum lipids in BioVU. The results indicate that the longitudinally derived phenotypes have higher heritability than those from cross-sectional methods, and the longitudinal median has the best performance over other long-term average models. However, due to low sample sizes of non-European populations in BioVU, only European ancestry individuals were included in this analysis, which could limit extrapolation of this finding to other race/ethnic groups. Similarly, the utility of this approach for other clinical measures in biobanks may differ because of different biological regulation. In addition, use of LLD is common in the general population, and this may bias genetic association results. My sensitivity analysis suggests that power can be increased and results will remain unbiased by including medicated measurements with appropriate adjustments; a finding that is consistent with previous GWAS[50].

Genetically regulated expression is an increasingly popular approach to study the association between genetic factors and phenotypes[95]. GReX aggregates individual variant effects into a functional unit, a single gene, by imputing gene expression level, and lends a natural, functional interpretation to findings[43]. My GReX association analyses in HCHS/SOL produced fewer significant genes for serum lipids compared to BioVU, which could be caused by some combination of several factors. First, the smaller sample size may limit the statistical power. Second, a difference in target population ancestry from that of the reference population used to train the GReX models may be another explanation. The PrediXcan models are trained on GTEx RNA-Seq data, and v7 models only included individuals of European ancestry. Reduced discovery in a discordant target population may indicate that some unique haplotypes in H/L are not well captured in the European GTEx data, causing an inaccurate GReX imputation, which in turn may bias the association test. However, previous research has demonstrated imputing GReX from PrediXcan using models built in a different population often performs well, especially in highly heritable genes[96].

Serum lipid levels affect and are affected by multiple tissues and organs in the human body. In addition to applying tissue-specific GReX prediction models, I also used two cross-tissue models. In general, cross-tissue models demonstrate a better power to identify novel serum-lipid-related genes due to a reduced multiple testing burden but only capture relatively concordant patterns of GReX effects across tissues. In BioVU, cross-tissue models identify 190 novel genes and tissue-specific models find 74 novel genes, with 33 genes identified by both models. *WDFY2*, *PKN3*, and *ACYP2* are the only three novel genes that were implicated for multiple lipid traits.

WDFY2 has a significant association with LDL-C, TC and TG, and has never been reported in any previous lipid GWAS. This gene encodes a protein with two WD domains and an FYVE zinc finger region, and overexpression has been reported to inhibit cancer cell's growth and migration[97]. *PKN3* encodes a protein kinase N3, and the *PKN3* knout out mice showed impairment of angiogenesis[98]. *ACYP2* encodes an acylphosphatase, and it has been reported to be associated with drug-induced hearing loss from GWAS[99]. In HCHS/SOL, all eight novel genes were identified using one of the cross-tissue models, including *CRMP1, BSG, NADSYN1, LACC1, MBP, RUNX2, PRKAB1,* and *LIME1,* and each was only associated with one lipid trait.

Four novel genes in or near the significant and suggestive IBD mapping regions were also replicated in GReX association, including *LINC01310, FLG, IMPA2* and *MAPPE1. LINC01310* is the nearest coding region to the IBD mapping segment on chromosome 22 and is significantly associated with LDL-C in the all-tissues cross-tissue GReX model in BioVU. *LINC01310* encodes a long non-coding RNA of unknown function. *FLG* is located within the IBD mapping region of chromosome 1 identified in HCSC/SOL, and is also significantly associated with TG in the all-tissues cross-tissue model in BioVU. *FLG* encodes filaggrin, also called filament-aggregating protein, and it is a major component of mammalian epidermis[100]. This gene has been reported in genetic studies of ichthyosis vulgaris[101], atopic dermatitis[102], and asthma[103]. In addition, a loss-of-function mutation in *FLG* is found to increase vitamin D concentration 10% in serum[104], and vitamin D supplementation has been reported to improve serum lipid profiles[105,106]. Therefore, *FLG* may affect UV protection of skin, in turn impacting vitamin D levels and ultimately affecting serum lipid levels[107,108].

Using a large-scale DNA biobank with linked EHR, I investigated the broader consequences of dysregulation of serum-lipid-associated genes by testing for enrichment of shared

GReX associations of these genes with any phecode. Sixty-eight phecodes are significantly enriched for association with the set of all significant and suggestive genes implicated in my analyses, including a total of 1,079 genes. Among the 68 significant phecodes is one lipid-related phecode, disorder of lipoid metabolism (phecode 272), and several known comorbidities, including hypoglycemia (251.1), and eleven other diabetes-related phecodes. The co-occurrence of diabetes and dyslipidemia has been observed in previous epidemiological studies[109,110]. The reason for this is likely multifactorial; changes in free fatty acid release in liver resulting from diabetes may be a possible explanation[111,112]. However, my finding of shared GReX association provides additional evidence of this comorbidity, and further study of shared genes may give insight into pathogenic mechanisms common to the two diseases. In addition, I observed significant enrichment of shared GReX association for myocardial infarction (411.2) and ischemic heart disease (411). Lipid profiles are known to be a major risk for cardiovascular disease[113,114], and my significant finding may indicate that shared genetic factors underlie the full progression of disease, from abnormal serum lipids to incidence of heart disease. Suicide attempt (297), bipolar disorder (296.1), and other psychiatric phecodes are also identified in the PheWAS enrichment analysis. Abnormal serum lipid levels in psychiatric patients who have attempted suicide has been observed in a prior meta-analysis[115]; the proposed explanation is through lipids' effect on serotonin production[116].

There are some limitations in this study. First, since the subjects in BioVU are from a hospital-based biobank, the definition of a control is without any diagnosis of dyslipidemia, history of LLD, or any abnormal lipid profiles from EHR laboratory records. Therefore, my dyslipidemia controls may include some undiagnosed dyslipidemia cases or those diagnosed at a non-Vanderbilt provider, potentially reducing our power to detect effects. However, age at last visit and number of visits were used to match controls to cases, and this process controlled for imbalanced periods of observation. Second, I only investigated IBD segments longer than 5 cM because of a high false discovery rate for smaller segments, which may limit my power to detect novel regions relevant to serum lipids shared by very distant relatives. Recently, several new IBD detection methods have been developed, e.g., iLASH[117], RaPID[118], and hap-IBD[119], if these methods have lower false positive detection rates for smaller segments, this could improve the resolution and power of IBD mapping in future studies. Third, the GReX imputation models are based on GTEx data, and though this is the most comprehensive and largest publicly available RNA-Seq dataset, model accuracy is still limited by the relatively low sample size[120]. Also, as noted previously, applying European-ancestry-derived models in non-European populations may reduce the power of GReX association because it will not reflect the effect of eQTLs of low frequency in Europeans that are higher frequency in non-European populations. Finally, my PheWAS enrichment analysis is based on EHR from Vanderbilt University Medical Center, and the results may be limited or biased by misdiagnosis or lack of diagnosis of the dataset. Despite these limitations, which primarily impact power rather than introducing sources of bias, I identified many findings of previous genetic analyses of serum lipids traits as well as numerous novel genes and regions warranting further follow-up via future replication and functional validation.

CHAPTER VI

CONCLUSION

Given that several large-scale GWAS of serum lipid traits have previously been published, the potential for further gene discovery in smaller sample size datasets may seem limited. However, by utilizing emerging methods that can increase power for discovery of common variant effects, like GReX association, and that can probe unobserved rare variation that GWAS is not able to detect, like IBD mapping, I was able to discover novel genes that impact these traits. Furthermore, applying these methods in a non-European population leveraged differences in genetic variation that can further increase discovery, highlighted areas of needed improvement to account for population history differences between ancestry groups, and helped to ensure that methodological advances do not perpetuate racial disparities in precision medicine efforts. Finally, using an innovative approach to catalog the effect of dysregulation of lipid genes on the medical phenome, I described novel comorbidities and consequences of genetic variation underlying dyslipidemia.

In short, using two novel approaches, IBD mapping and GReX association analysis, improved our understanding of the genetic mechanism of serum lipid regulation. Also, both a large-scale biobank with linked EHR, BioVU, and an epidemiological study of an underrepresented population, HCHS/SOL, were used. IBD mapping identified two significant regions on chromosome 5 and chromosome 22 in BioVU, and one region on chromosome 1 was found in HCHS/SOL. All three regions were not present in a traditional GWAS of each population. In total, these approaches identified 303 novel serum lipid related genes in the two populations studied. In my analysis of HCHS/SOL, I identified 42 genes that were also found in the BioVU analysis, and 22 genes that only reached genome-wide significance in HCHS/SOL. In the set of all 1,079 novel and known genes that reached genome-wide significance in my analyses, I found enriched GReX associations with various diabetes-related phenotypes, heart disease, psychiatric disorders, and others. Together, these findings extended our knowledge of the genetic etiology of serum lipid traits, highlight the importance of innovative statistical strategies, especially in historically underrepresented and disproportionately disease-burdened populations, and enrich our understanding of the phenotypic consequences of regulatory variation within the genetic architecture of serum lipids.

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Appendices

Appendix I. Lipid-lowering drugs in BioVU

Medicine	Type
colesevelam	Bile acid sequestrants
colesevelam 0.9 gm	Bile acid sequestrants
colesevelam 1 packet	Bile acid sequestrants
colesevelam 3.75 g	Bile acid sequestrants
colesevelam 3.75gm pkt	Bile acid sequestrants
colesevelam 3.75 gram oral powder packet	Bile acid sequestrants
colesevelam 625 mg tablet	Bile acid sequestrants
colesevelam hcl	Bile acid sequestrants
colesevelam hcl 625mg	Bile acid sequestrants
colesevelam hcl (welchol)	Bile acid sequestrants
colesevelam powder 0.9gm	Bile acid sequestrants
colesevelam powder; welchol	Bile acid sequestrants
colesevelam : welchol	Bile acid sequestrants
colesevelam (welchol)	Bile acid sequestrants
colesevelam: welchol	Bile acid sequestrants
colesevelam (welchol) granules for suspension	Bile acid sequestrants
welchol (colesevelam)	Bile acid sequestrants
cholestyramine	Bile acid sequestrants
cholestyramine 1 gm	Bile acid sequestrants
cholestyramine 1 scoop	Bile acid sequestrants
cholestyramine 20% in aquaphor cream	Bile acid sequestrants
cholestyramine-aspartame	Bile acid sequestrants
cholestyramine-aspartame 4 gram oral powder	Bile acid sequestrants
cholestyramine-aspartame 4 gram oral powder for susp in a packet	Bile acid sequestrants
cholestyramine (bulk)	Bile acid sequestrants
cholestyramine (bulk) misc	Bile acid sequestrants
cholestyramine (bulk) powder	Bile acid sequestrants
cholestyramine (bulk) powder	Bile acid sequestrants
cholestyramine light	Bile acid sequestrants
cholestyramine light 4 gram oral powder	Bile acid sequestrants
cholestyramine light 4 gram powder for susp in a packet	Bile acid sequestrants
cholestyramine light oral	Bile acid sequestrants
cholestyramine light (prevalite)	Bile acid sequestrants
cholestyramine packet	Bile acid sequestrants
cholestyramine packets	Bile acid sequestrants
cholestyramine : questran	Bile acid sequestrants
cholestyramine (questran)	Bile acid sequestrants
cholestyramine: questran	Bile acid sequestrants
cholestyramine resin	Bile acid sequestrants
cholestyramine-sucrose	Bile acid sequestrants
cholestyramine with sucrose	Bile acid sequestrants
cholestyramine (with sugar)	Bile acid sequestrants
cholestyramine (with sugar) 4 gram oral powder	Bile acid sequestrants
cholestyramine (with sugar) 4 gram powder for susp in a packet	Bile acid sequestrants
cholestyramine (with sugar) oral	Bile acid sequestrants
prevalite (cholestyramine)	Bile acid sequestrants
questran (cholestyramine)	Bile acid sequestrants
questran light (cholestyramine)	Bile acid sequestrants
stomahesive powder-cholestyramine-zinc oxide (happy hiney) topical ointment	Bile acid sequestrants
welchol (cholestyramine)	Bile acid sequestrants
cholestyramine light (prevalite)	Bile acid sequestrants
prevalite	Bile acid sequestrants
prevalite 4 gram oral powder	Bile acid sequestrants
prevalite 4 gram powder for susp in a packet	Bile acid sequestrants
prevalite (cholestyramine)	Bile acid sequestrants
prevalite oral	Bile acid sequestrants

Medicine	Type
prevalite packets	Bile acid sequestrants
prevalite powder	Bile acid sequestrants
prevalite (questran light)	Bile acid sequestrants
bile acid sequestrants	Bile acid sequestrants
cholestyramine : questran	Bile acid sequestrants
cholestyramine (questran)	Bile acid sequestrants
cholestyramine: questran	Bile acid sequestrants
prevalite (questran light)	Bile acid sequestrants
questran	Bile acid sequestrants
questran 4 gram powder for susp in a packet	Bile acid sequestrants
questran (cholestyramine)	Bile acid sequestrants
questran light	Bile acid sequestrants
questran light (cholestyramine)	Bile acid sequestrants
questran light oral	Bile acid sequestrants
questran light packets	Bile acid sequestrants
questran oral	Bile acid sequestrants
questran packets	Bile acid sequestrants
colesevelam hcl (welchol)	Bile acid sequestrants
colesevelam powder; welchol	Bile acid sequestrants
colesevelam : welchol	Bile acid sequestrants
colesevelam (welchol)	Bile acid sequestrants
colesevelam: welchol	Bile acid sequestrants
colesevelam (welchol) granules for suspension	Bile acid sequestrants
welchol	Bile acid sequestrants
welchol 1/4 packet	Bile acid sequestrants
welchol 3.75 gram oral powder packet	Bile acid sequestrants
welchol 3.75 grams	Bile acid sequestrants
welchol 625 mg	Bile acid sequestrants
welchol 625 mg tablet	Bile acid sequestrants
welchol (cholestyramine)	Bile acid sequestrants
welchol (colesevelam)	Bile acid sequestrants
welchol for oral suspension	Bile acid sequestrants
welchol oral	Bile acid sequestrants
welchol packet	Bile acid sequestrants
welchol pkts 1/4 pkt	Bile acid sequestrants
colestid / colestipol	Bile acid sequestrants
colestid (colestipol)	Bile acid sequestrants
colestipol	Bile acid sequestrants
colestipol 1 gram tablet	Bile acid sequestrants

Medicine	Type
colestipol 5 gram oral granules	Bile acid sequestrants
colestipol 5 gram oral packet	Bile acid sequestrants
colestipol 7.5 gram oral packet	Bile acid sequestrants
colestipol (colestid)	Bile acid sequestrants
colestipol hcl	Bile acid sequestrants
colestipol hydrochloride	Bile acid sequestrants
colestipol;micronized	Bile acid sequestrants
colestipol oral	Bile acid sequestrants
colestipol packet	Bile acid sequestrants
colestipol tablet: colestid	Bile acid sequestrants
colestid	Bile acid sequestrants
colestid 1 gram tablet	Bile acid sequestrants
colestid / colestipol	Bile acid sequestrants
colestid (colestipol)	Bile acid sequestrants
colestid flavored	Bile acid sequestrants
colestid granules	Bile acid sequestrants
colestid oral	Bile acid sequestrants
colestipol (colestid)	Bile acid sequestrants
colestipol tablet: colestid	Bile acid sequestrants
ezetimibe	Cholesterol absorption inhibitors
ezetimibe 10 mg tablet	Cholesterol absorption inhibitors
ezetimibe oral	Cholesterol absorption inhibitors
ezetimibe : zetia	Cholesterol absorption inhibitors
ezetimibe / zetia	Cholesterol absorption inhibitors
ezetimibe (zetia)	Cholesterol absorption inhibitors
ezetimibe: zetia	Cholesterol absorption inhibitors
zetia (ezetimibe)	Cholesterol absorption inhibitors
ezetimibe : zetia	Cholesterol absorption inhibitors
ezetimibe / zetia	Cholesterol absorption inhibitors
ezetimibe (zetia)	Cholesterol absorption inhibitors
ezetimibe: zetia	Cholesterol absorption inhibitors
samp-zetia	Cholesterol absorption inhibitors

Medicine	Type
zetia	Cholesterol absorption inhibitors
zetia 10mg	Cholesterol absorption inhibitors
zetia 10 mg tablet	Cholesterol absorption inhibitors
zetia (ezetimibe)	Cholesterol absorption inhibitors
zetia oral	Cholesterol absorption inhibitors
zetia (zetia)	Cholesterol absorption inhibitors
antara / fenofibrate	Fibrates
antara (fenofibrate)	Fibrates
antara (fenofibrate micronized)	Fibrates
bezafibrate	Fibrates
clofibrate	Fibrates
cor (fenofibrate)	Fibrates
fenofibrate	Fibrates
fenofibrate 120 mg tablet	Fibrates
fenofibrate 130mg	Fibrates
fenofibrate 134 mg	Fibrates
fenofibrate 145mg	Fibrates
fenofibrate 145 mg	Fibrates
fenofibrate 145 mg	Fibrates
fenofibrate 150 mg capsule	Fibrates
fenofibrate 160mg	Fibrates
fenofibrate 160 mg tablet	Fibrates
fenofibrate 40 mg tablet	Fibrates
fenofibrate 48 mg	Fibrates
fenofibrate 50 mg capsule	Fibrates
fenofibrate 54 mg tablet	Fibrates
fenofibrate (antara)	Fibrates
fenofibrate (fenofibrate)	Fibrates
fenofibrate (fenofibrate ; micronized)	Fibrates
fenofibrate (fenoglide)	Fibrates
fenofibrate (lofibra)	Fibrates
fenofibrate micronized	Fibrates
fenofibrate micronized 130 mg capsule	Fibrates
fenofibrate micronized 134 mg capsule	Fibrates
fenofibrate micronized 200 mg capsule	Fibrates
fenofibrate micronized 43 mg capsule	Fibrates
fenofibrate micronized 67 mg capsule	Fibrates
fenofibrate micronized oral	Fibrates
fenofibrate micronized (tricor)	Fibrates
fenofibrate nanocrystallized	Fibrates
fenofibrate nanocrystallized 145 mg tablet	Fibrates
fenofibrate nanocrystallized 160 mg tablet	Fibrates
fenofibrate nanocrystallized 48 mg tablet	Fibrates
fenofibrate oral	Fibrates
fenofibrate : tricor	Fibrates
fenofibrate / tricor	Fibrates
fenofibrate (tricor)	Fibrates
fenofibrate: tricor	Fibrates
fenofibrate (trilipix)	Fibrates
fibrates	Fibrates
lofibra (fenofibrate)	Fibrates
phenofibrate	Fibrates
tricor / fenofibrate	Fibrates
tricor (fenofibrate)	Fibrates
tricor (fenofibrate nanocrystallized)	Fibrates
triglide (fenofibrate)	Fibrates
trilipix (fenofibrate)	Fibrates
gemfibrozil	Fibrates
gemfibrozil 600 mg tablet	Fibrates
gemfibrozil : lopid	Fibrates
gemfibrozil / lopid	Fibrates
gemfibrozil (lopid)	Fibrates
gemfibrozil: lopid	Fibrates
gemfibrozil oral	Fibrates
gemfibrozil product	Fibrates
gemfibrozil (triglycerides)	Fibrates
lopid / gemfibrozil	Fibrates
lopid (gemfibrozil)	Fibrates
nabumetone (gemfibrozil)	Fibrates
lopid	Fibrates
lopid 600mg	Fibrates
lopid 600 mg tablet	Fibrates
lopid oral	Fibrates

Medicine	Type
b3 (niacin)	Niacin
b - complex w/niacin	Niacin
fa-niacinamide-cupric ox-zinc	Niacin
flush free niacin	Niacin
inositol niacinate	Niacin
inositol niacinate (bulk) misc	Niacin
insulin aspart (niacinamide) subq	Niacin
insulin aspart (niacinamide)(u-100) 100 unit/ml(3 ml) subcutaneous pen	Niacin
insulin aspart (niacinamide) (u-100) 100 unit/ml subcutaneous solution	Niacin
iron fumarate;polysac comp 125 mg-vitamin c 40 mg-niacin 3 mg capsule	Niacin
iron fum;pscplx 125 mg-folic acid 1 mg-vit c 40 mg-niacin 3 mg capsule	Niacin
niacin	Niacin
niacin 1000mg	Niacin
niacin 100 mg tablet	Niacin
niacin 2000mg sr	Niacin
niacin 250 mg tablet	Niacin
niacin 400 mg (inositol niacinate 500 mg) capsule	Niacin
niacin 500-1000mg	Niacin
niacin 500mg	Niacin
niacin 500 mg	Niacin
niacin 500 mg tablet	Niacin
niacin 50 mg tablet	Niacin
niacinamide	Niacin
niacinamide 500 mg tablet	Niacin
niacinamide (bulk) misc	Niacin
niacinamide-fa-cupric ox-zinc	Niacin
niacinamide (niacin)	Niacin
niacinamide oral	Niacin
niacin (antihyperlipidemic)	Niacin
niacin (as inositol hexanicotinate)	Niacin
niacin (as niacinamide)	Niacin
niacin (b3)	Niacin
niacin (bulk) misc	Niacin

Medicine	Type
niacin controlled release	Niacin
niacin er	Niacin
niacin er 1;000 mg tablet;extended release	Niacin
niacin er 1;000 mg tablet;extended release 24 hr	Niacin
niacin er 250 mg capsule;extended release	Niacin
niacin er 500 mg capsule;extended release	Niacin
niacin er 500 mg-lovastatin 20 mg tablet;extended release 24h mphase	Niacin
niacin er 500 mg tablet;extended release	Niacin
niacin er 500 mg tablet;extended release 24 hr	Niacin
niacin er 750 mg tablet;extended release	Niacin
niacin er 750 mg tablet;extended release 24 hr	Niacin
niacin er invest 500 mg tablet	Niacin
niacin er (niaspan)	Niacin
niacin extended release	Niacin
niacin flush free	Niacin
niacin flush free 400 mg niacin (500 mg) capsule	Niacin
niacin flush free oral	Niacin
niacin (generic) 500mg	Niacin
niacin (inositol niacinate)	Niacin
niacin (inositol niacinate)	Niacin
niacin la 500 mg	Niacin
niacin (long acting)	Niacin
niacin-lovastatin	Niacin
niacin (niacin)	Niacin
niacin (niacinamide)	Niacin
niacin (niaspan)	Niacin
niacin (nicotinic acid)	Niacin
niacin no flush oral	Niacin
niacin oral	Niacin
niacin powder	Niacin
niacin preparation	Niacin
niacin sa	Niacin
niacin - simvastatin	Niacin
niacin / simvastatin	Niacin
niacin (slo - niacin)	Niacin

Medicine	Type
niacin sr	Niacin
niacin-sr capsule: nicobid sr	Niacin
niacin s.r: niaspan	Niacin
niacin sr (niaspan)	Niacin
niacin sr (niaspan er)	Niacin
niacin sustained-release	Niacin
niacin tablet:	Niacin
niacin tr	Niacin
niaspan / niacin	Niacin
niaspan (niacin)	Niacin
nicotinamide (niacinamide)	Niacin
nicotinic acid (niacin)	Niacin
policosanol-garlic-niacin oral	Niacin
simcor (niacin / simvastatin)	Niacin
slo - niacin	Niacin
slo-niacin	Niacin
slo-niacin oral	Niacin
vitamin b3 (niacin)	Niacin
vitamin b3 (niacinamide)	Niacin
vitamin b complex no.12-niacinamide 50 mg/15 ml oral liquid	Niacin
vitamin b complex no.12-niacin oral	Niacin
niacor	Niacin
niacor 500 mg tablet	Niacin
advicor (lovastatin / niacin)	Statins
altocor (lovastatin)	Statins
altoprev (lovastatin)	Statins
amlodipine 10 mg-atorvastatin 10 mg tablet	Statins
amlodipine 10 mg-atorvastatin 20 mg tablet	Statins
amlodipine 10 mg-atorvastatin 40 mg tablet	Statins
amlodipine 10 mg-atorvastatin 80 mg tablet	Statins
amlodipine 2.5 mg-atorvastatin 10 mg tablet	Statins
amlodipine 2.5 mg-atorvastatin 20 mg tablet	Statins
amlodipine 5 mg-atorvastatin 10 mg tablet	Statins
amlodipine 5 mg-atorvastatin 20 mg tablet	Statins

Medicine	Type
amlodipine 5 mg-atorvastatin 80 mg tablet	Statins
amlodipine - atorvastatin	Statins
amlodipine / atorvastatin	Statins
amlodipine-atorvastatin	Statins
amlodipine - atorvastatin (caduet)	Statins
atorvastatin	Statins
atorvastatin 10 mg	Statins
atorvastatin 10 mg tablet	Statins
atorvastatin 20 mg.	Statins
atorvastatin 20 mg tablet	Statins
atorvastatin 40mg or placebo	Statins
atorvastatin 40 mg tablet	Statins
atorvastatin 80mg	Statins
atorvastatin 80 mg	Statins
atorvastatin 80 mg qday 10	Statins
atorvastatin 80 mg tablet	Statins
atorvastatin and amlodipine	Statins
atorvastatin (atorvastatin)	Statins
atorvastatin (atorvastatin calcium)	Statins
atorvastatin calcium	Statins
atorvastatin calcium (lipitor)	Statins
atorvastatin (crestor)	Statins
atorvastatin : lipitor	Statins
atorvastatin / lipitor	Statins
atorvastatin (lipitor)	Statins
atorvastatin: lipitor	Statins
atorvastatin oral	Statins
atorvastatin or placebo	Statins
atorvastatin (vytorin)	Statins
atorvastatin (zocor)	Statins
caduet (amlodipine - atorvastatin)	Statins
caduet (amlodipine / atorvastatin)	Statins
ezetimibe 10 mg-atorvastatin 10 mg tablet	Statins
ketoconazole w/atorvastatin	Statins
lipitor / atorvastatin	Statins
lipitor (atorvastatin)	Statins
lipitor (atorvastatin calcium)	Statins

Medicine	Type
livalo (atorvastatin)	Statins
simvastatin w/atorvastatin	Statins
statin w/atorvastatin	Statins
baycol (cerivastatin)	Statins
cerivastatin	Statins
cerivastatin (baycol)	Statins
cpm w/simvastatin (zocor)	Statins
crestor (simvastatin)	Statins
elavil (simvastatin)	Statins
ezetimibe 10 mg-simvastatin 10 mg tablet	Statins
ezetimibe 10 mg-simvastatin 20 mg tablet	Statins
ezetimibe 10 mg / simvastatin 40 mg	Statins
ezetimibe 10 mg-simvastatin 40 mg tablet	Statins
ezetimibe 10 mg-simvastatin 80 mg tablet	Statins
ezetimibe - simvastatin	Statins
ezetimibe / simvastatin	Statins
ezetimibe (simvastatin)	Statins
ezetimibe-simvastatin	Statins
ezetimibe-simvastatin oral	Statins
ezetimibe - simvastatin (vytorin)	Statins
ezetimibe / simvastatin (vytorin)	Statins
ezetimibe-simvastatin (vytorin 10/20) combination tablet	Statins
ezetimibe-simvastatin (vytorin 10/40) combination tablet	Statins
ezetimibe - simvastatin (zocor)	Statins
lipitor (simvastatin)	Statins
lovastatin (simvastatin)	Statins
niacin - simvastatin	Statins
niacin / simvastatin	Statins
simcor (niacin / simvastatin)	Statins
simvastatin	Statins
simvastatin 10 mg tablet	Statins
simvastatin 20mg	Statins
simvastatin 20 mg/5 ml (4 mg/ml) oral suspension	Statins

Medicine	Type
simvastatin 20 mg tablet	Statins
simvastatin 20 mg tablet 0.5 (	Statins
simvastatin 40mg	Statins
simvastatin 40 mg tablet	Statins
simvastatin 5 mg tablet	Statins
simvastatin 60mg	Statins
simvastatin 80 mg tablet	Statins
simvastatin and ezetimibe	Statins
simvastatin and ezetimibe (zetia)	Statins
simvastatin and fenofibrate	Statins
simvastatin (crestor)	Statins
simvastatin (lipitor)	Statins
simvastatin oral	Statins
simvastatin (simvastatin)	Statins
simvastatin (vytorin)	Statins
simvastatin w/amlodipine	Statins
simvastatin w/atorvastatin	Statins
simvastatin (zetia)	Statins
simvastatin : zocor	Statins
simvastatin / zocor	Statins
simvastatin (zocor)	Statins
simvastatin: zocor	Statins
statin (simvastatin)	Statins
vytorin (ezetimibe - simvastatin)	Statins
vytorin (ezetimibe / simvastatin)	Statins
vytorin (ezetimibe/simvastatin) 10/40 mg	Statins
vytorin (simvastatin)	Statins
vytorin with simvastatin	Statins
zocor / simvastatin	Statins
zocor (simvastatin)	Statins
crestor / rosuvastatin	Statins
crestor (rosuvastatin)	Statins
crestor (rosuvastatin calcium)	Statins
null rosuvastatin	Statins
rosuvastatin	Statins
rosuvastatin	Statins
rosuvastatin 10mg	Statins
rosuvastatin 10 mg	Statins

Medicine	Type
rosuvastatin 10mg po	Statins
rosuvastatin 10 mg tablet	Statins
rosuvastatin 20mg	Statins
rosuvastatin 20 mg	Statins
rosuvastatin 20mg	Statins
rosuvastatin 20 mg tablet	Statins
rosuvastatin 2.5mg	Statins
rosuvastatin 40mg	Statins
rosuvastatin 40 mg	Statins
rosuvastatin 40mg	Statins
rosuvastatin 40 mg tablet	Statins
rosuvastatin 5mg	Statins
rosuvastatin 5 mg	Statins
rosuvastatin 5mg po	Statins
rosuvastatin 5mg tab	Statins
rosuvastatin 5 mg tablet	Statins
rosuvastatin and ezetimibe	Statins
rosuvastatin calcium	Statins
rosuvastatin calcium (crestor)	Statins
rosuvastatin : crestor	Statins
rosuvastatin (crestor)	Statins
rosuvastatin (crestor)	Statins
rosuvastatin: crestor	Statins
rosuvastatin (crestor) 40mg	Statins
rosuvastatin (crestor) 5mg	Statins
rosuvastatin (crestor) 5 mg	Statins
rosuvastatin (crestor) 5 mg tablet	Statins
rosuvastatin (home med)	Statins
rosuvastatin oral	Statins
rosuvastatin or placebo	Statins
rosuvastatin w/calcium	Statins
rosuvastatin (zetia)	Statins
fluvastatin	Statins
fluvastatin:	Statins
fluvastatin 20 mg capsule	Statins
fluvastatin 40 mg capsule	Statins
fluvastatin 80mg	Statins
fluvastatin e.r.	Statins
fluvastatin er 80 mg tablet;extended release 24 hr	Statins
fluvastatin / lescol	Statins

Medicine	Type
fluvastatin (lescol)	Statins
fluvastatin (lescol xl)	Statins
fluvastatin sodium	Statins
fluvastatin sodium (lescol)	Statins
fluvastatin sr 80mg	Statins
fluvastatin s.r: lescol xl	Statins
lescol / fluvastatin	Statins
lescol (fluvastatin)	Statins
lescol xl (fluvastatin)	Statins
mevacor (fluvastatin)	Statins
null fluvastatin e.r.	Statins
hmg - coa reductase inhibitors (statins)	Statins
hmg (statin)	Statins
inv pitavastatin or placebo (actg 5332 - irb 150075) 4mg	Statins
livalo (pitavastatin)	Statins
livalo (pitavastatin) 1mg	Statins
livalo (pitavastatin calcium)	Statins
pitavastatin	Statins
pitavastatin 1mg	Statins
pitavastatin 2mg	Statins
pitavastatin 2 mg	Statins
pitavastatin 4mg	Statins
pitavastatin 4 mg or placebo	Statins
pitavastatin calcium 1 mg tablet	Statins
pitavastatin calcium 2 mg tablet	Statins
pitavastatin calcium 4 mg tablet	Statins
pitavastatin calcium (livalo)	Statins
pitavastatin / livalo	Statins
pitavastatin (livalo)	Statins
pitavastatin oral	Statins
pitavastatin or placebo	Statins
amlodipine (lipitor)	Statins
atorvastatin calcium (lipitor)	Statins
atorvastatin : lipitor	Statins
atorvastatin / lipitor	Statins
atorvastatin (lipitor)	Statins

Medicine	Type
atorvastatin: lipitor	Statins
calcium (lipitor)	Statins
lipitor	Statins
lipitor 10mg	Statins
lipitor 10 mg	Statins
lipitor 10 mg tablet	Statins
lipitor 20mg	Statins
lipitor 20mg po	Statins
lipitor 20 mg tablet	Statins
lipitor 30mg	Statins
lipitor 40mg	Statins
lipitor 40 mg tablet	Statins
lipitor 5mg	Statins
lipitor 80mg	Statins
lipitor 80 mg	Statins
lipitor 80 mg tablet	Statins
lipitor / atorvastatin	Statins
lipitor (atorvastatin)	Statins
lipitor (atorvastatin calcium)	Statins
lipitor (lovastatin)	Statins
lipitor oral	Statins
lipitor (simvastatin)	Statins
lipitor (statin)	Statins
simvastatin (lipitor)	Statins
livalo	Statins
livalo 1mg	Statins
livalo 1mg	Statins
livalo 1 mg	Statins
livalo 1mg	Statins
livalo 1 mg tablet	Statins
livalo 2mg	Statins
livalo 2 mg	Statins
livalo 2 mg tablet	Statins
livalo 4mg	Statins
livalo 4mg	Statins
livalo 4 mg	Statins
livalo 4 mg tablet	Statins
livalo (atorvastatin)	Statins
livalo oral	Statins
livalo (pitavastatin)	Statins
livalo (pitavastatin) 1mg	Statins

Medicine	Type
livalo (pitavastatin calcium)	Statins
livalo (pravastatin)	Statins
livalo (statin)	Statins
pitavastatin calcium (livalo)	Statins
pitavastatin / livalo	Statins
pitavastatin (livalo)	Statins
pitavastin (livalo) 2mg	Statins
pravastatin (livalo)	Statins
nisvastatin	Statins
livalo (pravastatin)	Statins
pravachol / pravastatin	Statins
pravachol (pravastatin)	Statins
pravachol (pravastatin sodium)	Statins
pravastatin	Statins
pravastatin:	Statins
pravastatin 10mg	Statins
pravastatin 10 mg	Statins
pravastatin 10 mg tablet	Statins
pravastatin 15mg	Statins
pravastatin 20mg	Statins
pravastatin 20mg	Statins
pravastatin 20 mg tablet	Statins
pravastatin 2.5 mg ng	Statins
pravastatin 40mg	Statins
pravastatin 40 mg tablet	Statins
pravastatin 80mg	Statins
pravastatin 80 mg tablet	Statins
pravastatin (livalo)	Statins
pravastatin (lovastatin)	Statins
pravastatin oral	Statins
pravastatin / pravachol	Statins
pravastatin (pravachol)	Statins
pravastatin (pravacol)	Statins
pravastatin sodium	Statins
pravastatin sodium (pravachol)	Statins
pravastatin sodium (pravastatin sodium)	Statins
pravastatin (zocor)	Statins
baycol (cerivastatin)	Statins
cerivastatin	Statins

Medicine	Type
cerivastatin (baycol)	Statins
rivastatin	Statins
statin	Statins
statins	Statins
statins (hmg - coa reductase inhibitors)	Statins
statin (simvastatin)	Statins
statin w/atorvastatin	Statins
ezetimibe 10 mg-atorvastatin 10 mg tablet	Statins/Cholesterol absorption inhibitors
ezetimibe 10 mg-simvastatin 10 mg tablet	Statins/Cholesterol absorption inhibitors
ezetimibe 10 mg-simvastatin 20 mg tablet	Statins/Cholesterol absorption inhibitors
ezetimibe 10 mg / simvastatin 40 mg	Statins/Cholesterol absorption inhibitors
ezetimibe 10 mg-simvastatin 40 mg tablet	Statins/Cholesterol absorption inhibitors
ezetimibe 10 mg-simvastatin 80 mg tablet	Statins/Cholesterol absorption inhibitors
ezetimibe - simvastatin	Statins/Cholesterol absorption inhibitors
ezetimibe / simvastatin	Statins/Cholesterol absorption inhibitors
ezetimibe (simvastatin)	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin oral	Statins/Cholesterol absorption inhibitors
ezetimibe - simvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
ezetimibe / simvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin (vytorin 10/20) combination tablet	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin (vytorin 10/40) combination tablet	Statins/Cholesterol absorption inhibitors
ezetimibe - simvastatin (zocor)	Statins/Cholesterol absorption inhibitors
ezetimibe (vytorin 10 / 40)	Statins/Cholesterol absorption inhibitors
rosuvastatin and ezetimibe	Statins/Cholesterol absorption inhibitors
simvastatin and ezetimibe	Statins/Cholesterol absorption inhibitors
simvastatin and ezetimibe (zetia)	Statins/Cholesterol absorption inhibitors

Medicine	Type
vytorin (ezetimibe)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe - simvastatin)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe / simvastatin)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe/simvastatin) 10/40 mg	Statins/Cholesterol absorption inhibitors
rosuvastatin (zetia)	Statins/Cholesterol absorption inhibitors
simvastatin and ezetimibe (zetia)	Statins/Cholesterol absorption inhibitors
simvastatin (zetia)	Statins/Cholesterol absorption inhibitors
zetia (vytorin)	Statins/Cholesterol absorption inhibitors
atorvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
ezetimibe - simvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
ezetimibe / simvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin (vytorin 10/20) combination tablet	Statins/Cholesterol absorption inhibitors
ezetimibe-simvastatin (vytorin 10/40) combination tablet	Statins/Cholesterol absorption inhibitors
ezetimibe (vytorin 10 / 40)	Statins/Cholesterol absorption inhibitors
simvastatin (vytorin)	Statins/Cholesterol absorption inhibitors
vytorin	Statins/Cholesterol absorption inhibitors
vytorin 10 / 10	Statins/Cholesterol absorption inhibitors
vytorin 10-10	Statins/Cholesterol absorption inhibitors
vytorin 10/10	Statins/Cholesterol absorption inhibitors
vytorin 10-10 oral	Statins/Cholesterol absorption inhibitors
vytorin--10/10 tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 / 20	Statins/Cholesterol absorption inhibitors
vytorin 10-20	Statins/Cholesterol absorption inhibitors
vytorin 10/20	Statins/Cholesterol absorption inhibitors
vytorin 10/20 mg.	Statins/Cholesterol absorption inhibitors

Medicine	Type
vytorin 10-20 oral	Statins/Cholesterol absorption inhibitors
vytorin--10/20 tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 / 40	Statins/Cholesterol absorption inhibitors
vytorin 10-40	Statins/Cholesterol absorption inhibitors
vytorin 10/40	Statins/Cholesterol absorption inhibitors
vytorin 10-40 oral	Statins/Cholesterol absorption inhibitors
vytorin--10/40 tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 / 80	Statins/Cholesterol absorption inhibitors
vytorin 10-80	Statins/Cholesterol absorption inhibitors
vytorin 10/80	Statins/Cholesterol absorption inhibitors
vytorin 10-80 oral	Statins/Cholesterol absorption inhibitors
vytorin--10/80 tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 mg-20 mg tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 mg-40 mg tablet	Statins/Cholesterol absorption inhibitors
vytorin 10 mg-80 mg tablet	Statins/Cholesterol absorption inhibitors
vytorin 40 mg	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe - simvastatin)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe / simvastatin)	Statins/Cholesterol absorption inhibitors
vytorin (ezetimibe/simvastatin) 10/40 mg	Statins/Cholesterol absorption inhibitors
vytorin (simvastatin)	Statins/Cholesterol absorption inhibitors
vytorin with simvastatin	Statins/Cholesterol absorption inhibitors
zetia (vytorin)	Statins/Cholesterol absorption inhibitors
simvastatin and fenofibrate	Statins/Fibrates
advicor (lovastatin / niacin)	Statins/Niacin

Appendix II. Lipid lowering drugs adjustment

Medicine type	HDL-C constant (mg/dL)	LDL-C constant (mg/dL)	TG constant (mg/dL)	TC constant (mg/dL)
Statins	−2.3	49.9	18.4	51.28
Fibrates	−5.9	40.1	57.1	45.62
Bile acid sequestrants	−1.9	40.5	0	38.6
Niacin	−9.9	24.7	89.4	32.68
Cholesterol absorption inhibitors	0	40.5	0	40.5

Appendix III. Metabolic traits used for annotating IBD segments

Blood glucose levels
Blood pressure
Blood pressure (age interaction)
Blood pressure (anthropometric measures interaction)
Blood pressure (smoking interaction)
Blood pressure measurement (cold pressor test)
Blood pressure measurement (high sodium and potassium intervention)
Blood pressure measurement (high sodium intervention)
Blood pressure measurement (low sodium intervention)
Blood pressure traits (multi-trait analysis)
BMI (adjusted for smoking behaviour)
BMI (smoking interaction)
BMI in non-smokers
BMI in smokers
Body fat distribution (arm fat ratio)
Body fat distribution (leg fat ratio)
Body fat distribution (trunk fat ratio)
Body fat mass
Body fat percentage
Body mass (lean)
Body mass in chronic obstructive pulmonary disease
Body mass index
Body mass index (smoking years interaction)
Body mass index (adult)
Body mass index (age <50)
Body mass index (age interaction)
Body mass index (age>50)
Body mass index (alcohol intake interaction)
Body mass index (change over time)
Body mass index (change over time) in cancer
Body mass index (change over time) in cancer or chronic obstructive pulmonary disease
Body mass index (change over time) in chronic obstructive pulmonary disease
Body mass index (change over time) in gastrointestinal cancer
Body mass index (change over time) in gastrointestinal cancer or chronic obstructive pulmonary disease
Body mass index (change over time) in lung cancer
Body mass index (change over time) in lung cancer or chronic obstructive pulmonary disease
Body mass index (dietary energy interaction)
Body mass index (education interaction)
Body mass index (ever vs never smoking interaction)
Body mass index (joint analysis main effects and physical activity interaction)
Body mass index (joint analysis main effects and smoking interaction)
Body mass index (physical activity interaction)
Body mass index (recreational physical activity interaction)
Body mass index (SNP x SNP interaction)
Body mass index and cholesterol (psychopharmacological treatment)
Body mass index and waist-hip ratio (pleiotropy)
Body mass index in asthmatics
Body mass index in non-asthmatics
Body mass index in physically active individuals
Body mass index in physically inactive individuals
Body mass index variance
Body mass index x age interaction
Body mass index x sex x age interaction (4df test)
C-reactive protein levels or HDL-cholesterol levels (pleiotropy)
C-reactive protein levels or LDL-cholesterol levels (pleiotropy)
C-reactive protein levels or total cholesterol levels (pleiotropy)
C-reactive protein levels or triglyceride levels (pleiotropy)
Cholesterol
Cholesterol and Triglycerides
Cholesterol ester levels in large LDL
Cholesterol ester levels in medium HDL
Cholesterol ester levels in medium LDL
Cholesterol ester levels in medium VLDL
Cholesterol ester levels in very large HDL
Cholesterol, total
Chylomicron and largest VLDL particle concentration
Coronary artery disease and HDL cholesterol levels (multivariate analysis)
Coronary artery disease and LDL cholesterol levels (multivariate analysis)
Coronary artery disease and total cholesterol levels (multivariate analysis)
Coronary artery disease and triglyceride levels (multivariate analysis)
Diabetes (gestational)
Diabetes (incident)
Diabetes mellitus
Diabetes related insulin traits
Diabetic retinopathy
Diabetic retinopathy (all NPDR and PDR)
Diabetic retinopathy (moderate NPDR and PDR)
Diabetic retinopathy in type 2 diabetes
Diastolic blood pressure
Diastolic blood pressure (alcohol consumption interaction)
Diastolic blood pressure (cigarette smoking interaction)
Diastolic blood pressure (long-term average)
Diastolic blood pressure in combination therapy (beta blocker and thiazide diuretic)

Diastolic blood pressure night-to-day ratio in hypertension
Diastolic blood pressure response to hydrochlorothiazide in hypertension
Diastolic blood pressure x alcohol consumption (light vs heavy) interaction (2df test)
Diastolic blood pressure x alcohol consumption interaction (1df test)
Diastolic blood pressure x alcohol consumption interaction (2df test)
Diastolic blood pressure x smoking status (current vs non-current) interaction (1df test)
Diastolic blood pressure x smoking status (current vs non-current) interaction (2df test)
Diastolic blood pressure x smoking status (ever vs never) interaction (1df test)
Diastolic blood pressure x smoking status (ever vs never) interaction (2df test)
Diastolic blood pressure x sodium interaction (1df test)
Diastolic blood pressure x sodium interaction (2df test)
Disorders of lipid metabolism
Fasting blood glucose
Fasting blood glucose (BMI interaction)
Fasting blood glucose adjusted for BMI
Fasting glucose in pregnancy (gestational week 14-16)
Fasting plasma glucose
Fasting plasma glucose (childhood)
Free cholesterol levels
Free cholesterol levels in IDL
Free cholesterol levels in large HDL
Free cholesterol levels in large LDL
Free cholesterol levels in medium HDL
Free cholesterol levels in medium VLDL
Free cholesterol levels in small VLDL
Free cholesterol levels in very large HDL
Glucose homeostasis traits
Glycated hemoglobin levels
HDL cholesterol
HDL Cholesterol - Triglycerides (HDLC-TG)
HDL cholesterol and triglyceride levels
HDL cholesterol and triglyceride levels (pleiotropy)
HDL cholesterol change in response to fenofibrate in statin-treated type 2 diabetes
HDL Cholesterol in HIV-infection
HDL cholesterol levels
HDL cholesterol x physical activity interaction (1df test)
HDL cholesterol x physical activity interaction (2df test)
Hemoglobin A1c levels
High density lipoprotein cholesterol levels
Hypertension
Hypertension (SNP x SNP interaction)
Hypertension (young onset)
Hypertension risk in short sleep duration
Hypertriglyceridemia
Insulin levels in response to oral glucose tolerance test (120 minutes)
Insulin levels in response to oral glucose tolerance test (30 minutes)
Insulin levels in response to oral glucose tolerance test (fasting)
Insulin resistance/response
Insulin secretion rate
Insulin sensitivity index
Large HDL particle concentration
Large LDL particle concentration
LDL (oxidized)
LDL cholesterol
LDL cholesterol change in response to fenofibrate in statin-treated type 2 diabetes
LDL cholesterol levels
LDL cholesterol to HDL cholesterol ratio
LDL cholesterol x physical activity interaction (1df test)
LDL cholesterol x physical activity interaction (2df test)
LDL peak particle diameter (total fat intake interaction)
Lipoprotein (a) - cholesterol levels
Low density lipoprotein cholesterol levels
Low high density lipoprotein cholesterol levels
Mean diameter of HDL particles
Mean diameter of LDL particles
Mean diameter of VLDL particles
Medium HDL particle concentration
Medium LDL particle concentration
Medium VLDL particle concentration
Multiple sclerosis and HDL levels (pleiotropy)
Multiple sclerosis and LDL levels (pleiotropy)
Multiple sclerosis and triglyceride levels (pleiotropy)
Multiple sclerosis and waist-to-hip-ratio (pleiotropy)
NHDL cholesterol to HDL cholesterol ratio
Obese vs. thin
Obesity
Obesity (early onset extreme)
Obesity (extreme)
Obesity and osteoporosis
Obesity in adult survivors of childhood cancer exposed to cranial radiation
Obesity in adult survivors of childhood cancer not exposed to cranial radiation
Obesity without metabolic disease
Obesity-related traits
Phospholipid levels in chylomicrons and largest VLDL
Phospholipid levels in large HDL
Phospholipid levels in large VLDL
Phospholipid levels in medium HDL
Phospholipid levels in medium LDL
Phospholipid levels in medium VLDL
Phospholipid levels in small VLDL
Phospholipid levels in very large VLDL
Phospholipid levels in very small VLDL

Postprandial triglyceride response to high fat diet meal
Ratio of the area under the curve for insulin and the area under the curve for glucose
Response to exercise (triglyceride level interaction)
Response to fenofibrate (HDL cholesterol levels)
Response to statins (HDL cholesterol change)
Response to statins (LDL cholesterol change)
Serum total cholesterol levels
Small HDL particle concentration
Small LDL particle concentration
Small VLDL particle concentration
Systolic blood pressure
Systolic blood pressure (alcohol consumption interaction)
Systolic blood pressure (cigarette smoking interaction)
Systolic blood pressure (dietary potassium intake interaction)
Systolic blood pressure (long-term average)
Systolic blood pressure change trajectories
Systolic blood pressure in combination therapy (beta blocker and thiazide diuretic)
Systolic blood pressure in sickle cell anemia
Systolic blood pressure night-to-day ratio in hypertension
Systolic blood pressure response to hydrochlorothiazide in hypertension
Systolic blood pressure x alcohol consumption (light vs heavy) interaction (2df test)
Systolic blood pressure x alcohol consumption interaction (2df test)
Systolic blood pressure x smoking status (current vs non-current) interaction (1df test)
Systolic blood pressure x smoking status (current vs non-current) interaction (2df test)
Systolic blood pressure x smoking status (ever vs never) interaction (2df test)
Systolic blood pressure x sodium interaction (1df test)
Systolic blood pressure x sodium interaction (2df test)
Total cholesterol change in response to fenofibrate in statin-treated type 2 diabetes
Total cholesterol levels
Total cholesterol levels in HDL
Total cholesterol levels in large HDL
Total cholesterol levels in large LDL
Total cholesterol levels in LDL
Total cholesterol levels in medium HDL
Total cholesterol levels in medium LDL
Total cholesterol levels in medium VLDL
Total cholesterol levels in small LDL
Total cholesterol levels in small VLDL
Total triglycerides levels
Triglyceride change in response to fenofibrate in statin-treated type 2 diabetes
Triglyceride levels
Triglyceride levels (parental genotype effect)
Triglyceride levels in chylomicrons and largest VLDL
Response to fenofibrate (LDL cholesterol levels)
Response to fenofibrate (total cholesterol levels)
Response to fenofibrate (triglyceride levels)
Response to long-chain n-3 polyunsaturated fatty acid supplementation (change in triglyceride levels)
Triglyceride levels in IDL
Triglyceride levels in large VLDL
Triglyceride levels in medium VLDL
Triglyceride levels in response to fenofibrate treatment (parental genotype effect)
Triglyceride levels in small HDL
Triglyceride levels in small VLDL
Triglyceride levels in very large HDL
Triglyceride levels in very large VLDL
Triglyceride levels in very small VLDL
Triglyceride to HDL cholesterol ratio
Triglycerides
Triglycerides x physical activity interaction (2df test)
Triglycerides-Blood Pressure (TG-BP)
Two-hour glucose
Two-hour glucose challenge
Type 2 diabetes
Type 2 diabetes (adjusted for BMI)
Type 2 diabetes (age of onset)
Type 2 diabetes (dietary heme iron intake interaction)
Type 2 diabetes (SNP x SNP interaction, 1df)
Type 2 diabetes (SNP x SNP interaction, 2df)
Type 2 diabetes (young onset) and obesity
Type 2 diabetes nephropathy
Type 2 diabetes nephropathy including microalbuminuria
Very large HDL particle concentration
Very large VLDL particle concentration
Very low density lipoprotein cholesterol levels
Very small VLDL particle concentration
Waist circumference
Waist Circumference - Triglycerides (WC-TG)
Waist circumference adjusted for BMI (adjusted for smoking behaviour)
Waist circumference adjusted for BMI (joint analysis main effects and physical activity interaction)
Waist circumference adjusted for BMI (joint analysis main effects and smoking interaction)
Waist circumference adjusted for BMI (smoking interaction)
Waist circumference adjusted for BMI in active individuals
Waist circumference adjusted for BMI in inactive individuals
Waist circumference adjusted for BMI in non-smokers
Waist circumference adjusted for BMI in smokers
Waist circumference adjusted for body mass index
Waist circumference and related phenotypes
Waist-hip ratio

Waist-to-hip circumference ratio (alcohol intake interaction)
Waist-to-hip circumference ratio (dietary energy interaction)
Waist-to-hip circumference ratio (ever vs never smoking interaction)
Waist-to-hip circumference ratio (recreational physical activity interaction)
Waist-to-hip circumference ratio (smoking years interaction)
Waist-to-hip ratio adjusted for BMI
Waist-to-hip ratio adjusted for BMI (additive genetic model)
Waist-to-hip ratio adjusted for BMI (adjusted for smoking behaviour)
Waist-to-hip ratio adjusted for BMI (age <50)
Waist-to-hip ratio adjusted for BMI (age >50)
Waist-to-hip ratio adjusted for BMI (joint analysis for main effect and physical activity interaction)
Waist-to-hip ratio adjusted for BMI (joint analysis main effects and smoking interaction)
Waist-to-hip ratio adjusted for BMI (recessive genetic model)
Waist-to-hip ratio adjusted for BMI (smoking interaction)
Waist-to-hip ratio adjusted for BMI in active individuals
Waist-to-hip ratio adjusted for BMI in inactive individuals
Waist-to-hip ratio adjusted for BMI in non-smokers
Waist-to-hip ratio adjusted for BMI in smokers
Waist-to-hip ratio adjusted for BMI x sex interaction
Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test)
Waist-to-hip ratio adjusted for body mass indexDisorders of lipid metabolism

Appendix IV. SUGEN output of specific IBD segments

Study	CHR	DASH ID	N	N of case	IBD carrier	IBD case carrier	BETA	SE	P-value
BioVU	5	cs1195827	36674	18337	25	21	1.66	0.55	2.36×10^{-3}
BioVU	5	cs1234067	36674	18337	29	23	1.34	0.46	3.36×10^{-3}
BioVU	5	cs1234859	36674	18337	30	23	1.19	0.43	5.83×10^{-3}
BioVU	5	cs1196647	36674	18337	30	23	1.19	0.43	5.86×10^{-3}
BioVU	5	cs1272747	36674	18337	30	23	1.19	0.43	5.86×10^{-3}
BioVU	5	cs1216244	36674	18337	27	21	1.25	0.46	6.78×10^{-3}
BioVU	5	cs1208613	36674	18337	26	20	1.20	0.47	9.67×10^{-3}
BioVU	5	cs1198443	36674	18337	16	2	-1.95	0.76	1.00×10^{-2}
BioVU	5	cs1231637	36674	18337	16	2	-1.95	0.76	1.00×10^{-2}
BioVU	5	cs1225941	36674	18337	31	23	1.06	0.41	1.01×10^{-2}
BioVU	5	cs1197850	36674	18337	15	14	2.64	1.04	1.08×10^{-2}
BioVU	5	cs1222766	36674	18337	15	14	2.64	1.04	1.08×10^{-2}
BioVU	5	cs1208497	36674	18337	15	1	-2.64	1.04	1.08×10^{-2}
BioVU	5	cs1235172	36674	18337	15	1	-2.64	1.04	1.08×10^{-2}
BioVU	5	cs1227108	36674	18337	18	15	1.61	0.63	1.09×10^{-2}
BioVU	5	cs1228109	36674	18337	18	15	1.61	0.63	1.09×10^{-2}
BioVU	5	cs1231949	36674	18337	18	15	1.61	0.63	1.09×10^{-2}
BioVU	5	cs1229425	36674	18337	28	21	1.10	0.44	1.18×10^{-2}
BioVU	5	cs1186046	36674	18337	14	13	2.57	1.04	1.34×10^{-2}
BioVU	5	cs1218521	36674	18337	15	13	1.87	0.76	1.37×10^{-2}
BioVU	5	cs1191984	36674	18337	30	22	1.01	0.41	1.43×10^{-2}
BioVU	5	cs1190087	36674	18337	17	14	1.54	0.64	1.54×10^{-2}
BioVU	5	cs1227107	36674	18337	17	14	1.54	0.64	1.54×10^{-2}
BioVU	5	cs1228110	36674	18337	17	14	1.54	0.64	1.54×10^{-2}
BioVU	5	cs1186738	36674	18337	17	3	-1.54	0.64	1.54×10^{-2}
BioVU	5	cs1216502	36674	18337	17	3	-1.54	0.64	1.54×10^{-2}
BioVU	5	cs1195966	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	5	cs1196228	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	5	cs1212264	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	5	cs1217394	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	5	cs1221558	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	5	cs1221559	36674	18337	16	13	1.47	0.64	2.20×10^{-2}
BioVU	5	cs1192157	36674	18337	16	3	-1.47	0.64	2.20×10^{-2}
BioVU	5	cs1221656	36674	18337	21	16	1.16	0.51	2.32×10^{-2}
BioVU	5	cs1219461	36674	18337	26	7	-1.00	0.44	2.39×10^{-2}
BioVU	5	cs1208537	36674	18337	13	11	1.71	0.77	2.65×10^{-2}
BioVU	5	cs1222003	36674	18337	13	2	-1.71	0.77	2.65×10^{-2}
BioVU	5	cs1205249	36674	18337	15	12	1.39	0.65	3.17×10^{-2}
BioVU	5	cs1216407	36674	18337	20	5	-1.10	0.52	3.33×10^{-2}

Study	CHR	DASH ID	N	N of case	IBD carrier	IBD case carrier	BETA	SE	P-value
BioVU	5	cs1189759	36674	18337	25	7	-0.95	0.45	3.39×10^{-2}
BioVU	5	cs1185491	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	5	cs1190949	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	5	cs1203068	36674	18337	10	1	-2.20	1.05	3.71×10^{-2}
BioVU	5	cs1223538	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	5	cs1225283	36674	18337	10	1	-2.20	1.05	3.71×10^{-2}
BioVU	5	cs1189914	36674	18337	12	2	-1.61	0.77	3.77×10^{-2}
BioVU	5	cs1209432	36674	18337	12	2	-1.61	0.77	3.77×10^{-2}
BioVU	5	cs1211950	36674	18337	12	10	1.61	0.77	3.77×10^{-2}
BioVU	5	cs1211949	36674	18337	12	10	1.61	0.77	3.77×10^{-2}
BioVU	5	cs1222002	36674	18337	12	2	-1.61	0.77	3.77×10^{-2}
BioVU	5	cs1222295	36674	18337	32	22	0.79	0.38	3.95×10^{-2}
BioVU	5	cs1184154	36674	18337	22	6	-0.98	0.48	4.04×10^{-2}
BioVU	5	cs1230497	36674	18337	15	3	-1.39	0.69	4.52×10^{-2}
BioVU	5	cs1203057	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	5	cs1208727	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	5	cs1232637	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	5	cs1222630	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	5	cs1236682	36674	18337	29	20	0.80	0.40	4.66×10^{-2}
BioVU	5	cs1190142	36674	18337	19	14	1.03	0.52	4.81×10^{-2}
BioVU	5	cs1226966	36674	18337	19	5	-1.03	0.52	4.81×10^{-2}
BioVU	5	cs1219459	36674	18337	36	12	-0.69	0.35	4.98×10^{-2}
BioVU	5	cs1229779	36674	18337	15	3	-1.39	0.71	4.99×10^{-2}
BioVU	22	cs365404	36674	18337	22	17	1.22	0.51	1.61×10^{-2}
BioVU	22	cs360219	36674	18337	13	12	2.49	1.04	1.69×10^{-2}
BioVU	22	cs376828	36674	18337	20	16	1.39	0.59	1.87×10^{-2}
BioVU	22	cs380336	36674	18337	20	16	1.39	0.59	1.87×10^{-2}
BioVU	22	cs385414	36674	18337	20	16	1.39	0.59	1.87×10^{-2}
BioVU	22	cs386779	36674	18337	14	12	1.79	0.76	1.90×10^{-2}
BioVU	22	cs357468	36674	18337	24	18	1.10	0.47	1.97×10^{-2}
BioVU	22	cs386381	36674	18337	12	1	-2.40	1.04	2.17×10^{-2}
BioVU	22	cs367355	36674	18337	16	13	1.47	0.64	2.20×10^{-2}
BioVU	22	cs375448	36674	18337	21	16	1.16	0.51	2.32×10^{-2}
BioVU	22	cs358413	36674	18337	39	27	0.81	0.36	2.34×10^{-2}
BioVU	22	cs386781	36674	18337	13	11	1.71	0.77	2.65×10^{-2}
BioVU	22	cs386081	36674	18337	11	10	2.30	1.05	2.81×10^{-2}
BioVU	22	cs380275	36674	18337	11	1	-2.30	1.05	2.81×10^{-2}
BioVU	22	cs386382	36674	18337	11	1	-2.30	1.05	2.81×10^{-2}
BioVU	22	cs358551	36674	18337	15	12	1.39	0.65	3.17×10^{-2}
BioVU	22	cs380016	36674	18337	15	12	1.39	0.65	3.17×10^{-2}
BioVU	22	cs384577	36674	18337	15	12	1.39	0.65	3.17×10^{-2}
BioVU	22	cs380449	36674	18337	20	15	1.10	0.52	3.33×10^{-2}

Study	CHR	DASH ID	N	N of case	IBD carrier	IBD case carrier	BETA	SE	P-value
BioVU	22	cs385862	36674	18337	30	21	0.85	0.40	3.37×10^{-2}
BioVU	22	cs366347	36674	18337	25	18	0.95	0.45	3.39×10^{-2}
BioVU	22	cs390975	36674	18337	25	18	0.95	0.45	3.39×10^{-2}
BioVU	22	cs365597	36674	18337	30	21	0.85	0.40	3.45×10^{-2}
BioVU	22	cs386809	36674	18337	18	14	1.25	0.59	3.50×10^{-2}
BioVU	22	cs369966	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	22	cs380223	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	22	cs386078	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	22	cs389687	36674	18337	10	9	2.20	1.05	3.71×10^{-2}
BioVU	22	cs376157	36674	18337	10	1	-2.20	1.05	3.71×10^{-2}
BioVU	22	cs381778	36674	18337	10	1	-2.20	1.05	3.71×10^{-2}
BioVU	22	cs366770	36674	18337	12	10	1.61	0.77	3.77×10^{-2}
BioVU	22	cs358325	36674	18337	22	16	0.98	0.48	4.04×10^{-2}
BioVU	22	cs366258	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	22	cs380794	36674	18337	14	11	1.30	0.65	4.60×10^{-2}
BioVU	22	cs367329	36674	18337	19	14	1.03	0.52	4.81×10^{-2}
SOL	1	cs109514	8482	4241	19	4	-1.33	0.62	3.33×10^{-2}
SOL	1	cs111986	8482	4241	29	21	0.98	0.42	1.86×10^{-2}
SOL	1	cs112129	8482	4241	29	22	1.14	0.52	2.96×10^{-2}
SOL	1	cs112186	8482	4241	82	32	-0.45	0.23	4.84×10^{-2}
SOL	1	cs113049	8482	4241	17	13	1.19	0.59	4.42×10^{-2}
SOL	1	cs113107	8482	4241	12	10	1.61	0.78	3.77×10^{-2}
SOL	1	cs114327	8482	4241	18	14	1.26	0.57	2.78×10^{-2}
SOL	1	cs115547	8482	4241	14	2	-1.66	0.76	2.79×10^{-2}
SOL	1	cs116897	8482	4241	10	1	-2.19	1.05	3.76×10^{-2}
SOL	1	cs117448	8482	4241	42	28	0.70	0.33	3.37×10^{-2}
SOL	1	cs117754	8482	4241	18	14	1.26	0.57	2.78×10^{-2}
SOL	1	cs117930	8482	4241	14	11	1.30	0.65	4.60×10^{-2}
SOL	1	cs118247	8482	4241	13	11	1.72	0.79	3.03×10^{-2}
SOL	1	cs118248	8482	4241	12	10	1.62	0.79	3.97×10^{-2}
SOL	1	cs119561	8482	4241	10	1	-2.20	1.05	3.72×10^{-2}
SOL	1	cs122280	8482	4241	30	22	1.01	0.48	3.68×10^{-2}

Appendix V. Tissue-specific GReX results of the genes significantly associated with HDL-C in BioVU

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
CETP	Lung	0.05	10	-16.42	0.74	7.4×10^{-110}	1.9×10^{-104}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	Esophagus Mucosa	0.02	7	-29.08	1.33	1.4×10^{-106}	1.9×10^{-101}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	Artery Coronary	0.10	3	-14.16	0.69	5.9×10^{-94}	5.1×10^{-89}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	Small Intestine Terminal Ileum	0.15	19	-9.49	0.47	2.8×10^{-89}	1.8×10^{-84}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
NLRC5	Cells Transformed fibroblasts	0.38	33	-3.87	0.20	2.4×10^{-82}	1.2×10^{-77}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
NLRC5	Adrenal Gland	0.10	17	-9.20	0.49	6.9×10^{-80}	3.0×10^{-75}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	Cells Transformed fibroblasts	0.09	10	-10.49	0.56	7.0×10^{-79}	2.6×10^{-74}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	Colon Transverse	0.08	31	-7.66	0.41	4.5×10^{-78}	1.5×10^{-73}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
SLC12A3	DGN-WB	0.01	42	-10.24	0.73	5.0×10^{-45}	1.4×10^{-40}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CETP	DGN-WB	0.02	30	-9.20	0.72	1.5×10^{-37}	3.9×10^{-33}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LPL	Nerve Tibial	0.14	33	5.05	0.43	2.3×10^{-31}	5.5×10^{-27}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
LPL	Whole Blood	0.05	11	7.11	0.64	2.4×10^{-28}	5.1×10^{-24}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
CPNE2	Cells Transformed fibroblasts	0.02	22	-6.71	0.62	4.2×10^{-27}	8.4×10^{-23}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LIPC	Liver	0.27	60	-2.33	0.22	8.4×10^{-26}	1.6×10^{-21}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
LPL	Adipose Subcutaneous	0.07	24	5.17	0.51	5.8×10^{-24}	1.0×10^{-19}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
MT1DP	Lung	0.06	21	5.27	0.52	8.7×10^{-24}	1.4×10^{-19}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
RSPRY1	Heart Atrial Appendage	0.03	19	6.90	0.78	1.4×10^{-18}	2.2×10^{-14}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LPL	DGN-WB	0.30	66	2.04	0.24	5.9×10^{-18}	8.5×10^{-14}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
LZTS1	Uterus	0.09	49	-2.47	0.30	4.1×10^{-16}	5.6×10^{-12}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
BBS2	Brain Frontal Cortex BA9	0.06	10	-4.91	0.62	2.0×10^{-15}	2.7×10^{-11}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
MT1A	Uterus	0.08	122	-1.24	0.16	2.2×10^{-14}	2.7×10^{-10}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
DOK4	Brain Cerebellar Hemisphere	0.04	6	-12.15	1.61	4.3×10^{-14}	5.1×10^{-10}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
GPR56	Breast Mammary Tissue	0.02	33	-4.89	0.65	5.9×10^{-14}	6.6×10^{-10}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LPL	Skin Not Sun Exposed Suprapubic	0.04	11	6.67	0.93	6.7×10^{-13}	7.2×10^{-9}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
MT2A	Spleen	0.13	68	1.73	0.25	2.5×10^{-12}	2.6×10^{-8}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LIPC	Pancreas	0.16	28	-2.19	0.32	6.6×10^{-12}	6.6×10^{-8}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
ALDH1A2	Liver	0.13	17	-4.08	0.60	9.2×10^{-12}	8.9×10^{-8}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
DNAH10OS	Prostate	0.17	19	4.81	0.72	2.0×10^{-11}	1.9×10^{-7}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
NLRC5	Thyroid	0.06	30	-3.12	0.49	1.6×10^{-10}	1.4×10^{-6}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HERPUD1	DGN-WB	0.09	15	-3.20	0.51	2.6×10^{-10}	2.3×10^{-6}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
APOC1	Lung	0.03	2	7.52	1.19	3.0×10^{-10}	2.5×10^{-6}	rs429358 (pval=6.31×10^{-12})	APOE region
INTS10	DGN-WB	0.11	30	4.05	0.65	4.8×10^{-10}	3.9×10^{-6}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
APOE	Lung	0.08	11	3.68	0.60	8.9×10^{-10}	7.0×10^{-6}	rs429358 (pval=6.31×10^{-12})	APOE region
MT3	Small Intestine Terminal Ileum	0.05	26	-1.92	0.32	1.8×10^{-9}	1.4×10^{-5}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
ABCB9	Liver	0.23	24	1.62	0.27	1.9×10^{-9}	1.4×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SETD8	Nerve Tibial	0.04	29	-2.95	0.49	2.0×10^{-9}	1.4×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
APOC2	Brain Putamen basal ganglia	0.06	7	3.09	0.52	2.0×10^{-9}	1.4×10^{-5}	rs429358 (pval=6.31×10^{-12})	APOE region
NUDT21	Esophagus Muscularis	0.06	15	-3.63	0.61	2.1×10^{-9}	1.4×10^{-5}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10OS	Lung	0.13	8	2.89	0.48	2.4×10^{-9}	1.6×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Nerve Tibial	0.13	21	2.59	0.44	3.2×10^{-9}	2.0×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Brain Cortex	0.10	27	2.52	0.43	4.2×10^{-9}	2.7×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
SETD8	Esophagus Gastroesophageal Junction	0.04	6	4.33	0.74	6.2×10^{-9}	3.8×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Colon Sigmoid	0.22	31	1.72	0.30	6.4×10^{-9}	3.9×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Breast Mammary Tissue	0.10	34	2.81	0.48	6.7×10^{-9}	3.9×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Adipose Subcutaneous	0.12	22	2.48	0.43	6.8×10^{-9}	3.9×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
PITPNM2	Brain Cerebellum	0.14	12	-2.46	0.43	7.9×10^{-9}	4.4×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Heart Atrial Appendage	0.10	16	3.66	0.63	7.9×10^{-9}	4.4×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ZNF259	Skin Sun Exposed Lower leg	0.02	21	4.51	0.79	9.7×10^{-9}	5.1×10^{-5}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
DNAH10OS	Muscle Skeletal	0.13	33	2.22	0.39	9.8×10^{-9}	5.1×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
PITPNM2	Brain Cerebellar Hemisphere	0.14	15	-2.38	0.41	9.8×10^{-9}	5.1×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Artery Aorta	0.12	25	2.21	0.39	1.1×10^{-8}	5.8×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
HERPUD1	Artery Tibial	0.03	5	-5.86	1.03	1.2×10^{-8}	5.9×10^{-5}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
DNAH10	DGN-WB	0.01	7	12.34	2.17	1.2×10^{-8}	6.0×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Esophagus Mucosa	0.08	14	3.18	0.56	1.4×10^{-8}	6.6×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
APOC4	Lung	0.08	8	3.58	0.63	1.4×10^{-8}	6.6×10^{-5}	rs429358 (pval=6.31×10^{-12})	APOE region
APOC4	Liver	0.06	21	2.83	0.50	1.9×10^{-8}	8.6×10^{-5}	rs429358 (pval=6.31×10^{-12})	APOE region
SETD8	DGN-WB	0.33	47	1.08	0.19	2.1×10^{-8}	9.4×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Skin Sun Exposed Lower leg	0.17	28	1.97	0.35	2.1×10^{-8}	9.6×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ZNF664	DGN-WB	0.04	19	-3.78	0.68	2.2×10^{-8}	9.7×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
OGFOD2	Cells Transformed fibroblasts	0.15	13	1.92	0.34	2.3×10^{-8}	9.8×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Heart Left Ventricle	0.14	28	1.79	0.32	2.4×10^{-8}	1.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Adipose Visceral Omentum	0.10	19	2.96	0.53	2.4×10^{-8}	1.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ZNF664	Thyroid	0.14	21	-2.00	0.36	2.5×10^{-8}	1.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ARL6IP4	Whole Blood	0.06	13	-4.95	0.89	2.7×10^{-8}	1.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CCDC92	Pancreas	0.03	12	4.77	0.86	2.8×10^{-8}	1.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ARL6IP4	Lung	0.04	6	-4.49	0.81	2.8×10^{-8}	1.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ARL6IP4	Heart Atrial Appendage	0.08	21	-3.22	0.58	2.9×10^{-8}	1.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	DGN-WB	0.23	19	1.40	0.25	2.9×10^{-8}	1.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Small Intestine Terminal Ileum	0.21	23	2.00	0.36	3.5×10^{-8}	1.3×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ZNF664	Cells Transformed fibroblasts	0.13	15	-2.75	0.50	3.7×10^{-8}	1.4×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
DNAH10OS	Esophagus Gastroesophageal Junction	0.27	45	1.13	0.21	3.7×10^{-8}	1.4×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ATP6V1B2	Spleen	0.11	58	1.50	0.27	4.0×10^{-8}	1.4×10^{-4}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
DNAH10OS	Colon Transverse	0.08	30	2.99	0.54	4.1×10^{-8}	1.5×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10OS	Skin Not Sun Exposed Suprapubic	0.02	14	4.68	0.85	4.2×10^{-8}	1.5×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
CCDC92	Thyroid	0.09	15	2.34	0.43	4.6×10^{-8}	1.6×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
NLRC5	Esophagus Mucosa	0.02	4	-6.48	1.19	4.8×10^{-8}	1.6×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ARL6IP4	Pancreas	0.08	33	-1.92	0.35	5.4×10^{-8}	1.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Thyroid	0.08	24	2.31	0.43	7.2×10^{-8}	2.4×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
DNAH10	Brain Anterior cingulate cortex BA24	0.04	9	4.14	0.77	7.5×10^{-8}	2.5×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ABCB9	Heart Left Ventricle	0.12	20	2.19	0.41	8.1×10^{-8}	2.6×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
HERPUD1	Esophagus Mucosa	0.10	25	-2.75	0.51	8.3×10^{-8}	2.6×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ABCB9	Colon Transverse	0.14	29	2.09	0.39	8.6×10^{-8}	2.7×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CDK2AP1	Prostate	0.05	7	-5.50	1.03	8.7×10^{-8}	2.7×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CCDC92	Adrenal Gland	0.19	13	2.05	0.38	8.7×10^{-8}	2.7×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
CDK2AP1	Testis	0.13	10	-3.21	0.60	9.2×10^{-8}	2.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Lung	0.05	19	3.60	0.68	9.6×10^{-8}	2.9×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ARL6IP4	Esophagus Mucosa	0.04	9	-4.16	0.78	1.1×10^{-7}	3.4×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
OGFOD2	DGN-WB	0.04	12	3.71	0.70	1.2×10^{-7}	3.6×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RILPL2	Cells Transformed fibroblasts	0.05	13	4.24	0.81	1.4×10^{-7}	4.2×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Cells Transformed fibroblasts	0.09	19	2.43	0.46	1.5×10^{-7}	4.2×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SETD8	Brain Cerebellum	0.23	18	-1.64	0.31	1.5×10^{-7}	4.3×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CCDC92	Breast Mammary Tissue	0.19	34	1.65	0.32	1.7×10^{-7}	4.7×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
CCDC92	Skin Not Sun Exposed Suprapubic	0.05	6	4.81	0.92	1.8×10^{-7}	5.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
MPHOSPH9	Testis	0.32	23	1.22	0.23	1.8×10^{-7}	5.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Skin Not Sun Exposed Suprapubic	0.20	22	1.48	0.28	1.9×10^{-7}	5.2×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Esophagus Muscularis	0.37	25	1.04	0.20	2.0×10^{-7}	5.3×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
HERPUD1	Adipose Subcutaneous	0.05	30	-2.54	0.49	2.0×10^{-7}	5.4×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ABCB9	Artery Tibial	0.04	28	2.86	0.55	2.2×10^{-7}	5.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ZNF664	Whole Blood	0.04	51	-1.93	0.37	2.2×10^{-7}	5.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ARL6IP4	Adipose Visceral Omentum	0.09	38	-2.42	0.47	2.3×10^{-7}	6.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Testis	0.06	6	-3.40	0.66	2.4×10^{-7}	6.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10	Artery Tibial	0.08	18	2.49	0.48	2.4×10^{-7}	6.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ARL6IP4	Cells Transformed fibroblasts	0.09	20	-1.96	0.38	2.4×10^{-7}	6.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
OGFOD2	Colon Transverse	0.06	10	3.91	0.76	2.5×10^{-7}	6.2×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
GFOD2	Esophagus Mucosa	0.12	13	-1.99	0.39	2.6×10^{-7}	6.5×10^{-4}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
ABCB9	Skin Sun Exposed Lower leg	0.12	44	1.61	0.31	2.8×10^{-7}	6.9×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SETD8	Thyroid	0.05	58	-1.58	0.31	3.2×10^{-7}	7.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10OS	Artery Tibial	0.26	47	1.16	0.23	3.3×10^{-7}	8.0×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
RP11-813F20.2	Thyroid	0.09	28	-2.05	0.40	3.4×10^{-7}	8.0×10^{-4}	rs10438978 (pval=6.39×10^{-11})	rs2156552 pval=2×10^{-74} (Spracklen, 28334899)
CPNE2	Skin Sun Exposed Lower leg	0.06	107	1.36	0.27	3.9×10^{-7}	9.1×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ACP2	Brain Cerebellum	0.11	29	-1.65	0.33	4.3×10^{-7}	9.9×10^{-4}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
ACP2	Skin Sun Exposed Lower leg	0.24	26	-1.13	0.23	4.7×10^{-7}	1.1×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
MPHOSPH9	Thyroid	0.07	41	1.68	0.34	5.2×10^{-7}	1.2×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CLPTM1	Skin Sun Exposed Lower leg	0.15	39	-1.55	0.31	5.9×10^{-7}	1.3×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
ARL6IP4	DGN-WB	0.07	17	-2.68	0.54	6.4×10^{-7}	1.5×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	Artery Aorta	0.03	8	3.92	0.80	8.6×10^{-7}	1.9×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CD3EAP	Brain Substantia nigra	0.08	6	-3.14	0.64	9.2×10^{-7}	2.0×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
ARL6IP4	Testis	0.11	32	-1.44	0.29	9.9×10^{-7}	2.2×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SETD8	Esophagus Mucosa	0.03	7	4.97	1.02	1.0×10^{-6}	2.3×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DNAH10	Whole Blood	0.10	15	2.51	0.51	1.0×10^{-6}	2.3×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ZNF664	Heart Atrial Appendage	0.09	29	1.99	0.41	1.1×10^{-6}	2.4×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
APOC2	Lung	0.13	11	-2.28	0.47	1.2×10^{-6}	2.5×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
ACP2	Adipose Subcutaneous	0.07	32	-1.92	0.40	1.3×10^{-6}	2.7×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
C12orf65	Colon Sigmoid	0.12	60	-1.66	0.34	1.3×10^{-6}	2.7×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
HERPUD1	Lung	0.02	3	-4.98	1.04	1.6×10^{-6}	3.2×10^{-3}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CKAP5	Brain Cortex	0.04	17	-1.99	0.41	1.6×10^{-6}	3.2×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
DNAH10OS	Brain Anterior cingulate cortex BA24	0.15	24	1.66	0.35	1.6×10^{-6}	3.2×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ETV5	DGN-WB	0.03	18	-3.35	0.70	1.7×10^{-6}	3.5×10^{-3}	NA	rs112545201 pval=3×10^{-19} (Hoffmann, 29507422)
ENKD1	Brain Cerebellum	0.10	17	2.31	0.48	1.8×10^{-6}	3.6×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
ACP2	Lung	0.10	22	-2.04	0.43	1.8×10^{-6}	3.6×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
AP006216.11	Adipose Subcutaneous	0.03	12	3.65	0.77	1.9×10^{-6}	3.8×10^{-3}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
SETD8	Muscle Skeletal	0.07	14	2.82	0.59	2.0×10^{-6}	3.8×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
MPHOSPH9	DGN-WB	0.10	27	1.83	0.39	2.0×10^{-6}	3.8×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PPP1R18	Prostate	0.11	70	-1.93	0.41	2.0×10^{-6}	3.8×10^{-3}	NA	NA
NR1H3	Brain Hypothalamus	0.15	9	2.17	0.46	2.0×10^{-6}	3.8×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
MYBPC3	Heart Atrial Appendage	0.04	13	-3.37	0.71	2.0×10^{-6}	3.9×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
MT1G	Nerve Tibial	0.22	46	1.21	0.25	2.1×10^{-6}	4.0×10^{-3}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ACP2	Whole Blood	0.17	16	-1.61	0.34	2.1×10^{-6}	4.0×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
LCAT	Adipose Subcutaneous	0.06	19	2.33	0.49	2.1×10^{-6}	4.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
SETD8	Esophagus Muscularis	0.06	18	3.17	0.67	2.2×10^{-6}	4.1×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ARFGAP2	Skin Not Sun Exposed Suprapubic	0.03	8	4.60	0.97	2.4×10^{-6}	4.4×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
ACP2	Adipose Visceral Omentum	0.07	10	-2.69	0.57	2.5×10^{-6}	4.6×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
ARL6IP4	Thyroid	0.01	18	-3.82	0.81	2.6×10^{-6}	4.8×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LCAT	Whole Blood	0.04	11	3.28	0.70	2.7×10^{-6}	4.8×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
SIDT2	Adrenal Gland	0.14	38	-1.49	0.32	2.9×10^{-6}	5.3×10^{-3}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
NRN1L	Esophagus Muscularis	0.02	19	-2.33	0.50	3.0×10^{-6}	5.3×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
LILRA3	Whole Blood	0.46	13	-0.89	0.19	3.1×10^{-6}	5.4×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
LILRA3	Adipose Subcutaneous	0.26	7	-1.25	0.27	3.1×10^{-6}	5.4×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
PITPNM2	DGN-WB	0.02	20	3.46	0.74	3.1×10^{-6}	5.4×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PIWIL2	Ovary	0.17	13	-2.02	0.43	3.1×10^{-6}	5.4×10^{-3}	rs15285 (pval=3.45×10^{-31})	NA
ACP2	Muscle Skeletal	0.06	11	-2.32	0.50	3.1×10^{-6}	5.4×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
ACP2	DGN-WB	0.40	30	-0.98	0.21	3.3×10^{-6}	5.7×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
SLC12A4	Cells Transformed fibroblasts	0.03	13	2.87	0.62	3.4×10^{-6}	5.8×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
CCDC92	Heart Left Ventricle	0.30	36	1.11	0.24	3.6×10^{-6}	6.0×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
SLC12A4	Skin Sun Exposed Lower leg	0.04	3	4.01	0.87	3.6×10^{-6}	6.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
DNAH10OS	Testis	0.07	35	1.61	0.35	3.8×10^{-6}	6.2×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
CCDC92	Prostate	0.17	13	2.14	0.46	3.8×10^{-6}	6.2×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
RBM6	Stomach	0.37	50	0.90	0.20	3.8×10^{-6}	6.2×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Heart Left Ventricle	0.18	20	-1.62	0.35	3.9×10^{-6}	6.4×10^{-3}	rs15285 (pval=3.45×10^{-31})	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
ACP2	Testis	0.06	13	-2.12	0.46	4.0×10^{-6}	6.5×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
MPHOSPH9	Esophagus Muscularis	0.15	23	1.49	0.32	4.0×10^{-6}	6.5×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SBNO1	Brain Substantia nigra	0.11	12	-3.43	0.74	4.1×10^{-6}	6.5×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LILRA3	DGN-WB	0.60	32	-0.64	0.14	4.4×10^{-6}	7.1×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
SETD8	Cells Transformed fibroblasts	0.11	16	2.07	0.45	4.5×10^{-6}	7.1×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LINC00161	Brain Spinal cord cervical c-1	0.07	34	1.82	0.40	4.9×10^{-6}	7.7×10^{-3}	NA	NA
AP006216.11	Nerve Tibial	0.07	9	3.10	0.68	5.0×10^{-6}	7.8×10^{-3}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
GFOD2	DGN-WB	0.00	1	8.90	1.95	5.2×10^{-6}	8.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
LILRA3	Artery Tibial	0.04	13	-2.88	0.63	5.2×10^{-6}	8.0×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
MPHOSPH9	Heart Atrial Appendage	0.03	15	3.33	0.73	5.2×10^{-6}	8.0×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SPRYD4	Lung	0.09	18	1.89	0.42	5.4×10^{-6}	8.2×10^{-3}	NA	rs61352607 pval=4×10^{-17} (Hoffmann, 29507422)
LILRA3	Spleen	0.30	9	-1.13	0.25	5.5×10^{-6}	8.3×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
PABPC1P4	Thyroid	0.11	13	2.70	0.59	5.6×10^{-6}	8.4×10^{-3}	NA	NA
DNAH10	Testis	0.08	40	2.11	0.46	5.9×10^{-6}	8.8×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
GMPPB	Artery Aorta	0.07	11	-2.84	0.63	5.9×10^{-6}	8.8×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
CLPTM1	Testis	0.26	22	1.19	0.26	6.2×10^{-6}	9.2×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
CCDC92	Adipose Visceral Omentum	0.25	46	1.05	0.23	6.3×10^{-6}	9.4×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
PSKH1	Cells Transformed fibroblasts	0.04	11	-4.80	1.06	6.4×10^{-6}	9.4×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
LILRA3	Adipose Visceral Omentum	0.40	30	-0.92	0.20	6.5×10^{-6}	9.4×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
C12orf65	Breast Mammary Tissue	0.03	36	-1.59	0.35	6.5×10^{-6}	9.4×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Adrenal Gland	0.20	53	1.31	0.29	6.5×10^{-6}	9.4×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
DNAH10	Adipose Visceral Omentum	0.13	18	1.66	0.37	6.6×10^{-6}	9.5×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
MPHOSPH9	Skin Not Sun Exposed Suprapubic	0.06	13	3.57	0.79	6.9×10^{-6}	9.9×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Brain Anterior cingulate cortex BA24	0.38	31	0.86	0.19	7.0×10^{-6}	9.9×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
MT1X	Esophagus Muscularis	0.03	56	-1.81	0.40	7.2×10^{-6}	1.0×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
RBM6	Heart Left Ventricle	0.41	61	0.79	0.18	7.5×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
LILRA3	Artery Aorta	0.29	9	-1.18	0.26	7.5×10^{-6}	1.1×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Breast Mammary Tissue	0.38	50	0.75	0.17	7.8×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
LILRA3	Nerve Tibial	0.13	7	-1.87	0.42	8.0×10^{-6}	1.1×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
LIPG	Skin Sun Exposed Lower leg	0.04	17	2.99	0.67	8.2×10^{-6}	1.1×10^{-2}	rs10438978 (pval=6.39×10^{-11})	rs2156552 pval=2×10^{-74} (Spracklen, 28334899)
RBM6	Esophagus Muscularis	0.48	24	0.74	0.17	8.2×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ACYP2	Brain Cerebellum	0.21	19	-1.43	0.32	8.4×10^{-6}	1.1×10^{-2}	NA	NA
LILRA3	Testis	0.14	6	-1.71	0.38	8.6×10^{-6}	1.1×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
IRS1	Adipose Subcutaneous	0.11	34	1.50	0.34	8.6×10^{-6}	1.1×10^{-2}	NA	rs2203452 pval=9×10^{-52} (Klarin, 30275531)
RBM6	Nerve Tibial	0.47	44	0.86	0.19	8.6×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
SETD8	Pancreas	0.18	12	-1.50	0.34	8.6×10^{-6}	1.1×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
FRMD1	Esophagus Gastroesophageal Junction	0.02	25	-2.28	0.51	8.7×10^{-6}	1.1×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
CDK2AP1	Esophagus Mucosa	0.46	43	-0.78	0.18	8.7×10^{-6}	1.1×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Whole Blood	0.48	41	0.73	0.16	8.8×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Testis	0.32	52	0.83	0.19	8.8×10^{-6}	1.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Artery Tibial	0.49	38	0.80	0.18	8.9×10^{-6}	1.2×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Prostate	0.34	57	0.96	0.22	9.0×10^{-6}	1.2×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
AP006216.11	Cells Transformed fibroblasts	0.04	14	3.76	0.85	9.3×10^{-6}	1.2×10^{-2}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
PIWIL2	Artery Coronary	0.22	12	-1.43	0.32	9.8×10^{-6}	1.3×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
TSNAXIP1	Brain Cerebellar Hemisphere	0.08	19	1.80	0.41	9.9×10^{-6}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
MST1R	Brain Anterior cingulate cortex BA24	0.10	46	-1.89	0.43	1.0×10^{-5}	1.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
LILRA3	Esophagus Gastroesophageal Junction	0.18	24	-1.43	0.32	1.0×10^{-5}	1.3×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Colon Sigmoid	0.40	52	0.80	0.18	1.0×10^{-5}	1.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
SIK3	Esophagus Mucosa	0.04	9	3.29	0.75	1.0×10^{-5}	1.3×10^{-2}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
DPEP3	Whole Blood	0.04	4	-3.78	0.86	1.0×10^{-5}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
TSNAXIP1	DGN-WB	0.02	14	4.39	1.00	1.0×10^{-5}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
RBM6	Pancreas	0.47	36	0.80	0.18	1.1×10^{-5}	1.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
DEF6	Pituitary	0.14	17	-2.26	0.51	1.1×10^{-5}	1.3×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
P2RX7	DGN-WB	0.09	24	-1.78	0.40	1.1×10^{-5}	1.3×10^{-2}	rs7133378 (pval=7.55×10^{-10})	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
RBM6	Cells Transformed fibroblasts	0.39	36	0.83	0.19	1.1×10^{-5}	1.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
TSNAXIP1	Nerve Tibial	0.04	15	4.14	0.94	1.1×10^{-5}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
TSNAXIP1	Brain Cerebellum	0.05	9	3.23	0.74	1.1×10^{-5}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
RBM6	Spleen	0.43	25	0.92	0.21	1.1×10^{-5}	1.4×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PSMC3	Brain Caudate basal ganglia	0.15	16	-1.68	0.38	1.2×10^{-5}	1.4×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
CLPTM1	Skin Not Sun Exposed Suprapubic	0.04	35	-2.38	0.54	1.2×10^{-5}	1.4×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Brain Cerebellum	0.59	40	0.73	0.17	1.2×10^{-5}	1.4×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PSMC3	Adipose Subcutaneous	0.11	32	-1.68	0.38	1.3×10^{-5}	1.5×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
PIWIL2	Adipose Visceral Omentum	0.26	23	-1.11	0.26	1.3×10^{-5}	1.5×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
CDK2AP1	Breast Mammary Tissue	0.15	22	-1.89	0.43	1.3×10^{-5}	1.5×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Lung	0.44	52	0.78	0.18	1.3×10^{-5}	1.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Brain Hippocampus	0.25	32	1.39	0.32	1.3×10^{-5}	1.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Brain Cortex	0.48	35	0.91	0.21	1.3×10^{-5}	1.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Heart Atrial Appendage	0.49	69	0.71	0.16	1.3×10^{-5}	1.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Artery Coronary	0.33	38	1.03	0.24	1.4×10^{-5}	1.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RP11-395N3.2	Adipose Subcutaneous	0.07	9	3.11	0.71	1.4×10^{-5}	1.6×10^{-2}	NA	rs2203452 pval=9×10^{-52} (Klarin, 30275531)
RBM6	Muscle Skeletal	0.26	36	1.10	0.25	1.4×10^{-5}	1.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RAPSN	Skin Not Sun Exposed Suprapubic	0.07	26	2.79	0.64	1.4×10^{-5}	1.6×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
LILRA3	Thyroid	0.17	43	-1.14	0.26	1.4×10^{-5}	1.6×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Colon Transverse	0.53	48	0.65	0.15	1.4×10^{-5}	1.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
COQ9	Vagina	0.20	18	1.83	0.42	1.4×10^{-5}	1.6×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LILRA3	Lung	0.36	41	-0.88	0.20	1.5×10^{-5}	1.6×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
LCAT	Adipose Visceral Omentum	0.04	20	2.95	0.68	1.5×10^{-5}	1.6×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
DUS2	Artery Aorta	0.07	20	2.20	0.51	1.5×10^{-5}	1.6×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
APOA1	Heart Atrial Appendage	0.15	54	1.19	0.27	1.5×10^{-5}	1.6×10^{-2}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
RBM6	Adipose Visceral Omentum	0.45	42	0.78	0.18	1.5×10^{-5}	1.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
CDK2AP1	Spleen	0.09	12	-2.33	0.54	1.5×10^{-5}	1.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	DGN-WB	0.50	51	0.68	0.16	1.5×10^{-5}	1.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
SETD8	Whole Blood	0.04	14	2.92	0.68	1.5×10^{-5}	1.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CDK2AP1	Adipose Visceral Omentum	0.21	22	-1.30	0.30	1.5×10^{-5}	1.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DDB2	Esophagus Mucosa	0.04	14	3.77	0.87	1.5×10^{-5}	1.6×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
CCDC92	Heart Atrial Appendage	0.14	16	1.70	0.39	1.6×10^{-5}	1.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
RBM6	Liver	0.29	43	1.18	0.27	1.6×10^{-5}	1.7×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Thyroid	0.50	48	0.72	0.17	1.6×10^{-5}	1.7×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Adipose Subcutaneous	0.31	8	-1.10	0.25	1.6×10^{-5}	1.7×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
ZNF76	DGN-WB	0.12	23	-1.90	0.44	1.6×10^{-5}	1.7×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
PARP15	Muscle Skeletal	0.21	40	-1.15	0.27	1.6×10^{-5}	1.7×10^{-2}	NA	rs7614016 pval=1×10^{-09} (Hoffmann, 29507422)
CDK2AP1	Small Intestine Terminal Ileum	0.05	9	-2.52	0.59	1.7×10^{-5}	1.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
XXbac-BPG248L24.12	Brain Cerebellum	0.41	45	1.42	0.33	1.7×10^{-5}	1.7×10^{-2}	NA	NA
CDK2AP1	Colon Transverse	0.32	25	-1.07	0.25	1.7×10^{-5}	1.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
AP006216.11	Skin Not Sun Exposed Suprapubic	0.11	9	2.04	0.48	1.7×10^{-5}	1.8×10^{-2}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
LILRA3	Adrenal Gland	0.27	6	-1.72	0.40	1.7×10^{-5}	1.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Brain Putamen basal ganglia	0.44	135	0.73	0.17	1.8×10^{-5}	1.8×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ACD	DGN-WB	0.04	17	-2.05	0.48	1.8×10^{-5}	1.8×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
CDK2AP1	Esophagus Muscularis	0.10	25	-1.82	0.42	1.8×10^{-5}	1.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CETP	Colon Sigmoid	0.07	13	-2.83	0.66	1.8×10^{-5}	1.8×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LILRA3	Brain Anterior cingulate cortex BA24	0.14	14	-1.58	0.37	1.8×10^{-5}	1.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
SNRPC	Pancreas	0.02	59	3.78	0.88	1.9×10^{-5}	1.8×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
C12orf65	Esophagus Mucosa	0.11	15	-2.19	0.51	1.9×10^{-5}	1.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
SEMA3F	Brain Anterior cingulate cortex BA24	0.05	6	2.41	0.56	1.9×10^{-5}	1.8×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RBM6	Artery Aorta	0.41	47	0.80	0.19	1.9×10^{-5}	1.8×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Artery Tibial	0.40	25	-0.82	0.19	1.9×10^{-5}	1.8×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
N6AMT1	Muscle Skeletal	0.15	32	-1.49	0.35	1.9×10^{-5}	1.8×10^{-2}	NA	NA
ZNF572	Colon Transverse	0.02	1	-5.32	1.24	1.9×10^{-5}	1.8×10^{-2}	rs2980880 (pval=1.17×10^{-09})	rs2954038 pval=1×10^{-41} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
C12orf65	Esophagus Muscularis	0.07	11	-2.67	0.62	1.9×10^{-5}	1.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PGBD3	Skin Sun Exposed Lower leg	0.06	52	-2.19	0.51	1.9×10^{-5}	1.8×10^{-2}	NA	NA
DEF6	Artery Tibial	0.02	14	-6.01	1.41	1.9×10^{-5}	1.8×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
SLC39A13	Muscle Skeletal	0.06	11	-2.35	0.55	1.9×10^{-5}	1.9×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
CCDC92	Artery Coronary	0.11	57	1.41	0.33	1.9×10^{-5}	1.9×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
CTRL	Skin Sun Exposed Lower leg	0.07	8	2.68	0.63	2.0×10^{-5}	1.9×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
PIWIL2	Brain Caudate basal ganglia	0.36	25	-1.07	0.25	2.0×10^{-5}	1.9×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
CCDC92	Nerve Tibial	0.19	18	1.36	0.32	2.0×10^{-5}	1.9×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
PIWIL2	Nerve Tibial	0.39	17	-0.90	0.21	2.0×10^{-5}	1.9×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
LILRA3	Esophagus Muscularis	0.21	43	-1.11	0.26	2.0×10^{-5}	1.9×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
PGS1	Artery Aorta	0.05	16	-2.99	0.70	2.0×10^{-5}	1.9×10^{-2}	NA	rs12601079 pval=8×10^{-35} (Klarin, 30275531)
ARL6IP4	Stomach	0.04	23	-2.61	0.61	2.0×10^{-5}	1.9×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DGKG	Brain Amygdala	0.13	15	-1.95	0.46	2.1×10^{-5}	1.9×10^{-2}	NA	rs112545201 pval=3×10^{-19} (Hoffmann, 29507422)
ACP2	Esophagus Mucosa	0.23	30	-1.10	0.26	2.1×10^{-5}	1.9×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
N6AMT1	Brain Caudate basal ganglia	0.07	24	-1.84	0.43	2.1×10^{-5}	1.9×10^{-2}	NA	NA
LILRA3	Small Intestine Terminal Ileum	0.22	10	-1.41	0.33	2.1×10^{-5}	1.9×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Skin Not Sun Exposed Suprapubic	0.36	48	0.86	0.20	2.1×10^{-5}	2.0×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ORC3	Brain Frontal Cortex BA9	0.06	17	1.68	0.40	2.2×10^{-5}	2.0×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
SLC12A4	Whole Blood	0.07	5	4.20	0.99	2.3×10^{-5}	2.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
NUP93	Brain Spinal cord cervical c-1	0.24	30	-1.20	0.28	2.3×10^{-5}	2.1×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
B3GNT9	DGN-WB	0.03	25	2.50	0.59	2.3×10^{-5}	2.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
TSNAXIP1	Artery Aorta	0.08	8	2.40	0.57	2.3×10^{-5}	2.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
PIWIL2	Skin Sun Exposed Lower leg	0.27	25	-1.07	0.25	2.3×10^{-5}	2.1×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
TSNAXIP1	Adrenal Gland	0.12	13	2.45	0.58	2.3×10^{-5}	2.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
DOK4	Brain Cortex	0.03	12	2.57	0.61	2.3×10^{-5}	2.1×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ACP2	Skin Not Sun Exposed Suprapubic	0.15	33	-1.40	0.33	2.3×10^{-5}	2.1×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
DPEP3	DGN-WB	0.07	14	-2.05	0.48	2.4×10^{-5}	2.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
RBM6	Adipose Subcutaneous	0.52	47	0.68	0.16	2.4×10^{-5}	2.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
MST1R	DGN-WB	0.02	6	3.69	0.87	2.5×10^{-5}	2.2×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
FGFR1OP	Skin Sun Exposed Lower leg	0.04	17	-2.87	0.68	2.5×10^{-5}	2.2×10^{-2}	NA	NA
RP11-166B2.1	Uterus	0.61	89	-0.63	0.15	2.5×10^{-5}	2.2×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
RBM6	Minor Salivary Gland	0.37	27	0.99	0.24	2.6×10^{-5}	2.2×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
LILRA3	Muscle Skeletal	0.11	22	-1.96	0.47	2.6×10^{-5}	2.3×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
SETD8	Brain Cerebellar Hemisphere	0.06	12	-2.06	0.49	2.6×10^{-5}	2.3×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Brain Nucleus accumbens basal ganglia	0.45	34	0.84	0.20	2.6×10^{-5}	2.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PGS1	Skin Not Sun Exposed Suprapubic	0.03	11	-3.78	0.90	2.7×10^{-5}	2.3×10^{-2}	NA	rs12601079 pval=8×10^{-35} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
SPDYE6	Testis	0.07	19	-1.72	0.41	2.7×10^{-5}	2.3×10^{-2}	NA	NA
IFITM4P	Small Intestine Terminal Ileum	0.18	59	1.61	0.38	2.9×10^{-5}	2.4×10^{-2}	NA	NA
HCG27	Adipose Subcutaneous	0.39	46	-0.91	0.22	2.9×10^{-5}	2.5×10^{-2}	NA	NA
FGFR1OP	Esophagus Muscularis	0.06	18	-2.37	0.57	3.0×10^{-5}	2.5×10^{-2}	NA	NA
RBM6	Esophagus Gastroesophageal Junction	0.33	65	0.80	0.19	3.0×10^{-5}	2.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
POLR2J	Adipose Visceral Omentum	0.03	28	-2.16	0.52	3.0×10^{-5}	2.5×10^{-2}	NA	NA
LCAT	DGN-WB	0.11	8	1.78	0.43	3.0×10^{-5}	2.5×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
SEMA3F	Adipose Subcutaneous	0.03	21	2.19	0.53	3.0×10^{-5}	2.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
LILRA3	Esophagus Mucosa	0.09	8	-2.15	0.51	3.0×10^{-5}	2.5×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RBM6	Esophagus Mucosa	0.51	34	0.65	0.16	3.0×10^{-5}	2.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PHF14	DGN-WB	0.03	12	-3.54	0.85	3.0×10^{-5}	2.5×10^{-2}	NA	NA
AL133458.1	Stomach	0.07	7	2.98	0.71	3.1×10^{-5}	2.5×10^{-2}	NA	NA
MPHOSPH9	Heart Left Ventricle	0.13	27	1.86	0.45	3.1×10^{-5}	2.5×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CTD-2330K9.3	Breast Mammary Tissue	0.07	6	-3.23	0.78	3.1×10^{-5}	2.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
FGFR1OP	Esophagus Mucosa	0.04	10	-5.23	1.26	3.1×10^{-5}	2.6×10^{-2}	NA	NA
FAM103A2P	Pancreas	0.07	15	3.36	0.81	3.2×10^{-5}	2.6×10^{-2}	NA	NA
CTD-2330K9.3	Artery Coronary	0.04	17	-3.02	0.73	3.2×10^{-5}	2.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ACTBP13	Stomach	0.06	8	3.17	0.76	3.2×10^{-5}	2.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
OGFOD2	Esophagus Muscularis	0.03	16	5.07	1.22	3.2×10^{-5}	2.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
RBM6	Brain Cerebellar Hemisphere	0.35	52	0.99	0.24	3.2×10^{-5}	2.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Thyroid	0.33	15	-0.94	0.23	3.3×10^{-5}	2.6×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
CAMKV	Testis	0.06	13	-2.14	0.52	3.3×10^{-5}	2.7×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RPS17P1	Esophagus Mucosa	0.03	8	3.67	0.88	3.4×10^{-5}	2.7×10^{-2}	NA	NA
SEMA3F	Adipose Visceral Omentum	0.04	20	2.53	0.61	3.4×10^{-5}	2.7×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Muscle Skeletal	0.54	12	-0.69	0.17	3.4×10^{-5}	2.7×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
RXRG	Liver	0.04	28	-2.24	0.54	3.5×10^{-5}	2.7×10^{-2}	NA	NA
VIMP1	Nerve Tibial	0.02	31	-2.82	0.68	3.5×10^{-5}	2.7×10^{-2}	NA	rs72961007 pval=8×10^{-12} (Hoffmann, 29507422)
NUDT21	DGN-WB	0.01	25	3.89	0.94	3.6×10^{-5}	2.8×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
RBM6	Skin Sun Exposed Lower leg	0.45	54	0.69	0.17	3.6×10^{-5}	2.8×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
CX3CL1	Adrenal Gland	0.10	16	1.91	0.46	3.6×10^{-5}	2.8×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
PIWIL2	Colon Transverse	0.03	13	-2.97	0.72	3.6×10^{-5}	2.8×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
OGFOD2	Cells EBV-transformed lymphocytes	0.21	23	1.32	0.32	3.6×10^{-5}	2.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LILRA3	Liver	0.23	22	-1.01	0.24	3.6×10^{-5}	2.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
LILRA3	Colon Sigmoid	0.19	15	-1.41	0.34	3.6×10^{-5}	2.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
RP11-166B2.1	Brain Spinal cord cervical c-1	0.49	60	-0.73	0.18	3.7×10^{-5}	2.8×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
RNASET2	Esophagus Gastroesophageal Junction	0.12	58	1.32	0.32	3.7×10^{-5}	2.8×10^{-2}	NA	NA
LCAT	Skin Sun Exposed Lower leg	0.05	14	2.89	0.70	3.7×10^{-5}	2.8×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
PLCD3	Nerve Tibial	0.05	26	1.82	0.44	3.8×10^{-5}	2.9×10^{-2}	rs72836561 (pval=3.63×10^{-09})	NA
MPHOSPH9	Esophagus Gastroesophageal Junction	0.13	17	1.65	0.40	3.8×10^{-5}	2.9×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RBM6	Brain Caudate basal ganglia	0.22	65	0.86	0.21	3.9×10^{-5}	3.0×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
MST1R	Heart Atrial Appendage	0.09	35	-2.00	0.49	4.1×10^{-5}	3.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
DEF6	Brain Cerebellar Hemisphere	0.06	25	-2.39	0.58	4.2×10^{-5}	3.2×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
ATP6V1B2	DGN-WB	0.00	12	10.06	2.46	4.3×10^{-5}	3.2×10^{-2}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
PGS1	Heart Atrial Appendage	0.18	9	-1.70	0.41	4.3×10^{-5}	3.2×10^{-2}	NA	rs12601079 pval=8×10^{-35} (Klarin, 30275531)
MT1G	Lung	0.03	32	2.37	0.58	4.5×10^{-5}	3.3×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ELMSAN1	Skin Sun Exposed Lower leg	0.03	12	-3.25	0.80	4.5×10^{-5}	3.3×10^{-2}	NA	rs13379043 pval=1×10^{-08} (Klarin, 30275531)
RP11-425L10.1	Uterus	0.16	26	-1.45	0.35	4.5×10^{-5}	3.3×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
RNF123	Brain Caudate basal ganglia	0.09	33	-2.56	0.63	4.5×10^{-5}	3.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PARD6A	Skin Not Sun Exposed Suprapubic	0.02	4	-4.95	1.21	4.5×10^{-5}	3.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
LCAT	Cells Transformed fibroblasts	0.05	10	2.41	0.59	4.5×10^{-5}	3.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
NLRC5	DGN-WB	0.26	23	-1.12	0.27	4.5×10^{-5}	3.3×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CAMKV	Stomach	0.18	14	-1.25	0.31	4.6×10^{-5}	3.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
CEP120	Skin Sun Exposed Lower leg	0.04	35	2.36	0.58	4.6×10^{-5}	3.3×10^{-2}	NA	NA
CCDC92	Esophagus Mucosa	0.08	22	1.97	0.48	4.6×10^{-5}	3.3×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
RNASEH2C	Pancreas	0.21	45	1.00	0.25	4.6×10^{-5}	3.4×10^{-2}	NA	rs12801636 pval=4×10^{-10} (Spracklen, 28334899)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
PSMC3	Brain Frontal Cortex BA9	0.11	7	-3.13	0.77	4.7×10^{-5}	3.4×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
FAM101A	Muscle Skeletal	0.03	4	-5.45	1.34	4.8×10^{-5}	3.4×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
MST1R	Brain Cerebellar Hemisphere	0.15	19	-1.15	0.28	4.9×10^{-5}	3.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PIWIL2	Heart Atrial Appendage	0.26	12	-1.17	0.29	4.9×10^{-5}	3.5×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
HLA-B	Skin Sun Exposed Lower leg	0.11	29	-1.56	0.38	4.9×10^{-5}	3.5×10^{-2}	NA	NA
RP11-166B2.1	Skin Sun Exposed Lower leg	0.64	42	-0.61	0.15	5.0×10^{-5}	3.5×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
BBS2	Brain Cerebellar Hemisphere	0.34	38	-1.08	0.27	5.0×10^{-5}	3.6×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
RBM6	Pituitary	0.41	51	0.83	0.20	5.1×10^{-5}	3.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
N6AMT1	Adrenal Gland	0.04	37	-2.18	0.54	5.1×10^{-5}	3.6×10^{-2}	NA	NA
PGS1	Cells Transformed fibroblasts	0.11	11	-2.28	0.56	5.1×10^{-5}	3.6×10^{-2}	NA	rs12601079 pval=8×10^{-35} (Klarin, 30275531)
GPR75	Colon Transverse	0.02	4	-9.03	2.23	5.2×10^{-5}	3.7×10^{-2}	NA	NA
LILRA3	Artery Coronary	0.21	22	-1.04	0.26	5.3×10^{-5}	3.7×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
P2RX7	Brain Cerebellum	0.15	38	-1.29	0.32	5.3×10^{-5}	3.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	NA
RP11-166B2.1	Pancreas	0.67	37	-0.66	0.16	5.3×10^{-5}	3.7×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
CDK2AP1	Skin Not Sun Exposed Suprapubic	0.24	41	-1.02	0.25	5.4×10^{-5}	3.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PLIN3	DGN-WB	0.01	15	-5.06	1.25	5.5×10^{-5}	3.8×10^{-2}	rs116843064 (pval=1.17×10^{-09})	NA
CDK2AP1	Cells Transformed fibroblasts	0.43	27	-0.74	0.18	5.5×10^{-5}	3.8×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
CTD-2330K9.3	Artery Aorta	0.03	24	-2.97	0.74	5.5×10^{-5}	3.8×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
HLA-B	Skin Not Sun Exposed Suprapubic	0.06	13	-2.18	0.54	5.6×10^{-5}	3.8×10^{-2}	NA	NA
FGFR1OP	Thyroid	0.10	28	-1.54	0.38	5.6×10^{-5}	3.8×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
MST1R	Liver	0.08	10	-1.64	0.41	5.6×10^{-5}	3.9×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RNASEH2C	Skin Not Sun Exposed Suprapubic	0.24	43	0.85	0.21	5.7×10^{-5}	3.9×10^{-2}	NA	rs12801636 pval=4×10^{-10} (Spracklen, 28334899)
HCG27	Brain Hypothalamus	0.11	37	-1.79	0.44	5.7×10^{-5}	3.9×10^{-2}	NA	NA
LCAT	Artery Tibial	0.03	17	3.63	0.90	5.8×10^{-5}	3.9×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
PSMC3	Skin Sun Exposed Lower leg	0.13	28	-1.30	0.32	5.8×10^{-5}	3.9×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
LILRA3	Heart Atrial Appendage	0.21	20	-1.26	0.31	5.8×10^{-5}	3.9×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
CDK2AP1	Liver	0.07	28	-2.17	0.54	5.8×10^{-5}	3.9×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RNASET2	Heart Atrial Appendage	0.03	46	2.31	0.58	5.9×10^{-5}	3.9×10^{-2}	NA	NA
PIWIL2	Cells Transformed fibroblasts	0.35	57	-0.70	0.18	5.9×10^{-5}	4.0×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
F2	Artery Tibial	0.08	15	-2.23	0.56	6.0×10^{-5}	4.0×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
RBM6	Vagina	0.26	59	1.12	0.28	6.2×10^{-5}	4.1×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
RP11-166B2.1	Colon Transverse	0.59	27	-0.65	0.16	6.5×10^{-5}	4.3×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
FGFR1OP	Whole Blood	0.04	10	-4.12	1.03	6.5×10^{-5}	4.3×10^{-2}	NA	NA
PARP15	DGN-WB	0.18	31	-1.21	0.30	6.6×10^{-5}	4.4×10^{-2}	NA	rs7614016 pval=1×10^{-09} (Hoffmann, 29507422)
OGFOD1	Nerve Tibial	0.06	26	1.58	0.40	6.6×10^{-5}	4.4×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
RNASET2	Thyroid	0.14	44	1.38	0.35	6.7×10^{-5}	4.4×10^{-2}	NA	NA
GFOD2	Skin Not Sun Exposed Suprapubic	0.05	8	-2.31	0.58	6.8×10^{-5}	4.4×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
C12orf65	Artery Aorta	0.15	12	-1.89	0.47	6.8×10^{-5}	4.4×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PINLYP	Pancreas	0.20	37	-1.19	0.30	6.9×10^{-5}	4.5×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
XXbac-BPG248L24.12	Brain Cerebellar Hemisphere	0.47	58	1.05	0.26	7.0×10^{-5}	4.6×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS SNPs	NHGRI-EBI catalog
ELMSAN1	Esophagus Muscularis	0.05	20	-2.15	0.54	7.1×10^{-5}	4.6×10^{-2}	NA	rs13379043 pval=1×10^{-08} (Klarin, 30275531)
LRP4	Pancreas	0.42	49	-0.76	0.19	7.1×10^{-5}	4.6×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
CDK2AP1	Heart Atrial Appendage	0.04	2	-4.57	1.15	7.1×10^{-5}	4.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LILRA3	Breast Mammary Tissue	0.23	17	-1.30	0.33	7.2×10^{-5}	4.6×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
COQ10A	Artery Tibial	0.03	6	-5.77	1.45	7.2×10^{-5}	4.7×10^{-2}	NA	NA
RWDD2B	Ovary	0.10	34	1.97	0.50	7.2×10^{-5}	4.7×10^{-2}	NA	NA
FGFR1OP	Colon Sigmoid	0.04	9	-3.12	0.79	7.3×10^{-5}	4.7×10^{-2}	NA	NA
YWHAZP4	Adipose Subcutaneous	0.04	30	4.29	1.08	7.5×10^{-5}	4.8×10^{-2}	NA	rs72961007 pval=8×10^{-12} (Hoffmann, 29507422)
ZNF76	Whole Blood	0.13	28	-1.50	0.38	7.6×10^{-5}	4.9×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
PARD6A	Pancreas	0.17	8	-1.50	0.38	7.8×10^{-5}	5.0×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Appendix VI. Tissue-specific GReX results of the genes significantly associated with LDL-C in BioVU

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
CELSR2	Pancreas	0.02	5	-48.92	3.07	4.3×10^{-57}	1.1×10^{-51}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	DGN-WB	0.25	11	-8.01	0.51	2.7×10^{-56}	2.8×10^{-51}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SORT1	Liver	0.58	25	-5.91	0.37	3.2×10^{-56}	2.8×10^{-51}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Liver	0.45	15	-6.95	0.44	1.1×10^{-55}	7.1×10^{-51}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Muscle Skeletal	0.39	13	-6.42	0.41	2.3×10^{-54}	1.2×10^{-49}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Liver	0.48	50	-5.97	0.39	1.1×10^{-53}	4.8×10^{-49}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Esophagus Mucosa	0.17	17	-9.78	0.64	2.0×10^{-52}	7.0×10^{-48}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Heart Left Ventricle	0.04	7	-32.54	2.14	2.2×10^{-52}	7.0×10^{-48}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SORT1	Minor Salivary Gland	0.07	13	-18.40	1.28	8.7×10^{-47}	2.5×10^{-42}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Brain Cerebellum	0.08	11	-20.14	1.45	9.7×10^{-44}	2.5×10^{-39}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Nerve Tibial	0.02	7	-26.80	1.99	1.8×10^{-41}	4.3×10^{-37}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSMA5	Liver	0.09	33	-10.58	0.82	8.8×10^{-38}	1.9×10^{-33}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Esophagus Mucosa	0.15	17	-10.17	0.79	1.4×10^{-37}	2.8×10^{-33}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Brain Cortex	0.13	17	-13.07	1.02	1.5×10^{-37}	2.8×10^{-33}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Testis	0.18	14	-8.46	0.72	3.8×10^{-32}	6.5×10^{-28}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Muscle Skeletal	0.08	45	-11.03	0.94	8.7×10^{-32}	1.4×10^{-27}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
PSRC1	Whole Blood	0.04	12	-14.42	1.40	9.1×10^{-25}	1.4×10^{-20}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
APOB	Colon Sigmoid	0.05	15	-17.73	1.77	1.0×10^{-23}	1.5×10^{-19}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
PSRC1	Pancreas	0.16	26	-6.50	0.65	1.3×10^{-23}	1.7×10^{-19}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Adipose Visceral Omentum	0.04	22	-14.13	1.46	3.7×10^{-22}	4.8×10^{-18}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
APOB	Esophagus Gastroesophageal Junction	0.03	10	-15.33	1.59	6.0×10^{-22}	7.5×10^{-18}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
PSRC1	Colon Transverse	0.14	9	-9.05	0.96	5.3×10^{-21}	6.2×10^{-17}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Skin Not Sun Exposed Suprapubic	0.20	63	-5.43	0.58	5.5×10^{-21}	6.3×10^{-17}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CD3EAP	Brain Substantia nigra	0.08	6	12.54	1.35	1.4×10^{-20}	1.5×10^{-16}	rs7412 (pval=3.55×10^{-178})	APOE region
SARS	Adrenal Gland	0.09	25	6.57	0.72	5.8×10^{-20}	6.0×10^{-16}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SARS	Skin Sun Exposed Lower leg	0.02	21	-11.50	1.28	2.8×10^{-19}	2.8×10^{-15}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Skin Sun Exposed Lower leg	0.01	27	-10.61	1.20	7.8×10^{-19}	7.5×10^{-15}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Brain Frontal Cortex BA9	0.10	51	-5.32	0.60	1.4×10^{-18}	1.3×10^{-14}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
BCAM	Lung	0.06	3	-14.49	1.71	3.0×10^{-17}	2.6×10^{-13}	rs7412 (pval=3.55×10^{-178})	APOE region
PSRC1	Minor Salivary Gland	0.27	20	-5.59	0.67	8.8×10^{-17}	7.6×10^{-13}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
APOB	Adipose Subcutaneous	0.19	18	5.32	0.66	5.9×10^{-16}	4.9×10^{-12}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
GEMIN7	Ovary	0.10	37	6.79	0.87	6.0×10^{-15}	4.9×10^{-11}	rs7412 (pval=3.55×10^{-178})	APOE region
DOCK6	Nerve Tibial	0.08	25	6.87	0.89	9.6×10^{-15}	7.6×10^{-11}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
APOB	Thyroid	0.02	13	-16.26	2.12	1.8×10^{-14}	1.3×10^{-10}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
APOB	Skin Sun Exposed Lower leg	0.29	10	-4.56	0.61	5.3×10^{-14}	4.0×10^{-10}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
CLCC1	Heart Left Ventricle	0.09	36	6.25	0.84	1.1×10^{-13}	8.1×10^{-10}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
APOB	Skin Not Sun Exposed Suprapubic	0.19	12	-5.79	0.78	1.2×10^{-13}	8.1×10^{-10}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
DMPK	Stomach	0.06	23	-11.40	1.57	4.2×10^{-13}	2.9×10^{-9}	rs7412 (pval=3.55×10^{-178})	APOE region
APOB	Uterus	0.14	28	-5.03	0.70	4.8×10^{-13}	3.2×10^{-9}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
ABCG8	Colon Transverse	0.15	8	-6.76	0.95	8.6×10^{-13}	5.6×10^{-9}	rs4299376 (pval=7.87×10^{-13})	rs4245791 pval=6×10^{-94} (Klarin, 30275531)
BCAM	Skin Not Sun Exposed Suprapubic	0.02	10	-11.28	1.58	9.4×10^{-13}	6.0×10^{-9}	rs7412 (pval=3.55×10^{-178})	APOE region
ATXN7L2	Liver	0.29	60	-3.07	0.43	1.3×10^{-12}	8.3×10^{-9}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Pituitary	0.15	35	-4.10	0.61	1.5×10^{-11}	8.9×10^{-8}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SMARCA4	Esophagus Mucosa	0.09	35	4.55	0.67	1.6×10^{-11}	9.6×10^{-8}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ZNF221	Ovary	0.11	25	-7.11	1.06	1.9×10^{-11}	1.1×10^{-7}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF69	Pituitary	0.08	27	7.02	1.05	2.0×10^{-11}	1.1×10^{-7}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PVRL2	Artery Aorta	0.08	11	-8.01	1.19	2.0×10^{-11}	1.1×10^{-7}	rs7412 (pval=3.55×10^{-178})	APOE region
GSTM1	Muscle Skeletal	0.25	72	4.24	0.63	2.3×10^{-11}	1.2×10^{-7}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Adipose Visceral Omentum	0.20	15	4.87	0.73	3.1×10^{-11}	1.7×10^{-7}	rs7412 (pval=3.55×10^{-178})	APOE region
HMGCR	Muscle Skeletal	0.03	12	12.32	1.86	3.7×10^{-11}	1.9×10^{-7}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
APOC2	Skin Not Sun Exposed Suprapubic	0.04	47	6.03	0.92	5.3×10^{-11}	2.7×10^{-7}	rs7412 (pval=3.55×10^{-178})	APOE region
RELB	Lung	0.01	24	10.23	1.58	9.6×10^{-11}	4.8×10^{-7}	rs7412 (pval=3.55×10^{-178})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
AC012065.7	Pituitary	0.08	21	6.89	1.07	1.3×10^{-10}	6.5×10^{-7}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
PSMA5	Uterus	0.06	31	6.41	1.00	1.7×10^{-10}	8.3×10^{-7}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
FDX1L	DGN-WB	0.00	7	33.62	5.35	3.3×10^{-10}	1.6×10^{-6}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
P2RY11	Heart Atrial Appendage	0.18	48	3.38	0.55	5.8×10^{-10}	2.7×10^{-6}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Brain Hippocampus	0.04	14	-7.12	1.15	7.0×10^{-10}	3.2×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Lung	0.08	23	-6.72	1.09	8.0×10^{-10}	3.5×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PVRL2	Muscle Skeletal	0.12	23	-4.23	0.69	8.0×10^{-10}	3.5×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	Colon Sigmoid	0.25	71	2.76	0.45	8.4×10^{-10}	3.6×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
PVRL2	Esophagus Muscularis	0.05	3	-9.18	1.50	8.8×10^{-10}	3.7×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
CELSR2	Lung	0.03	5	12.96	2.12	9.7×10^{-10}	4.1×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SYPL2	Liver	0.45	44	-2.33	0.38	1.0×10^{-9}	4.2×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SYPL2	Brain Cerebellar Hemisphere	0.23	50	-3.97	0.66	2.2×10^{-9}	8.9×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PCSK9	Nerve Tibial	0.36	14	2.82	0.47	2.2×10^{-9}	8.9×10^{-6}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
PCSK9	Adipose Subcutaneous	0.02	1	34.55	5.84	3.3×10^{-9}	1.3×10^{-5}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
ERCC1	Ovary	0.17	53	-3.03	0.51	3.3×10^{-9}	1.3×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	Brain Anterior cingulate cortex BA24	0.20	55	3.35	0.57	4.0×10^{-9}	1.5×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF285B	Brain Cerebellar Hemisphere	0.06	59	3.74	0.64	4.2×10^{-9}	1.6×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
ATXN7L2	Stomach	0.05	31	-6.41	1.09	4.3×10^{-9}	1.6×10^{-5}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
YIPF2	Skin Sun Exposed Lower leg	0.01	15	12.17	2.07	4.3×10^{-9}	1.6×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ST3GAL4	Cells EBV-transformed lymphocytes	0.22	4	4.55	0.78	5.0×10^{-9}	1.8×10^{-5}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
AC067959.1	Colon Sigmoid	0.08	73	-4.11	0.70	5.3×10^{-9}	1.9×10^{-5}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
ANKDD1B	Nerve Tibial	0.19	14	-3.65	0.63	5.7×10^{-9}	2.0×10^{-5}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
SMARCA4	Esophagus Gastroesophageal Junction	0.04	6	15.40	2.66	7.0×10^{-9}	2.4×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
SMARCA4	Skin Not Sun Exposed Suprapubic	0.11	21	5.59	0.97	7.7×10^{-9}	2.6×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
GSTM1	Thyroid	0.22	105	3.31	0.58	1.1×10^{-8}	3.7×10^{-5}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Stomach	0.29	27	3.49	0.61	1.1×10^{-8}	3.7×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM258	Artery Tibial	0.04	24	-7.64	1.34	1.3×10^{-8}	4.4×10^{-5}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
LPA	Liver	0.18	120	2.50	0.44	1.4×10^{-8}	4.5×10^{-5}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
HPR	Brain Cortex	0.55	11	1.86	0.33	1.7×10^{-8}	5.2×10^{-5}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
C19orf52	Pancreas	0.05	23	4.94	0.88	1.7×10^{-8}	5.2×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
HPR	Brain Cerebellum	0.48	34	1.93	0.34	1.7×10^{-8}	5.2×10^{-5}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
KANK2	Brain Cerebellar Hemisphere	0.05	3	16.88	3.00	1.8×10^{-8}	5.4×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
CBLC	Stomach	0.03	30	4.77	0.85	1.8×10^{-8}	5.4×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF225	DGN-WB	0.01	38	9.35	1.66	1.8×10^{-8}	5.5×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	Nerve Tibial	0.27	34	3.21	0.57	2.0×10^{-8}	5.8×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
ZNF625	Lung	0.03	2	13.78	2.46	2.1×10^{-8}	6.3×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs2278426 pval=2×10^{-09} (Kanai, 29403010)
KANK2	Brain Nucleus accumbens basal ganglia	0.19	3	5.83	1.04	2.3×10^{-8}	6.7×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
GEMIN7	Heart Atrial Appendage	0.10	21	3.96	0.71	2.9×10^{-8}	8.5×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
TXNL4B	Brain Anterior cingulate cortex BA24	0.09	16	3.83	0.70	3.6×10^{-8}	1.0×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SMARCA4	Colon Transverse	0.03	4	16.05	2.92	3.7×10^{-8}	1.0×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ST3GAL4	Stomach	0.06	48	4.50	0.82	4.6×10^{-8}	1.3×10^{-4}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
GDF7	Esophagus Muscularis	0.08	16	6.54	1.20	4.7×10^{-8}	1.3×10^{-4}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
HPR	Heart Left Ventricle	0.18	18	4.17	0.76	4.7×10^{-8}	1.3×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SMARCA4	Adipose Subcutaneous	0.05	28	6.18	1.13	4.9×10^{-8}	1.3×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
GDF7	Adrenal Gland	0.10	8	5.94	1.09	5.0×10^{-8}	1.3×10^{-4}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
SYPL2	Thyroid	0.12	7	4.81	0.88	5.4×10^{-8}	1.4×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Artery Aorta	0.17	23	4.34	0.80	5.6×10^{-8}	1.5×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
HPR	Brain Hippocampus	0.36	24	2.02	0.37	6.2×10^{-8}	1.6×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SPC24	Skin Not Sun Exposed Suprapubic	0.04	25	7.08	1.31	6.2×10^{-8}	1.6×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
APOB	Prostate	0.06	67	-3.22	0.60	7.7×10^{-8}	2.0×10^{-4}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
AC069278.4	Thyroid	0.02	24	-7.87	1.47	8.0×10^{-8}	2.0×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS1	Brain Cerebellum	0.44	19	2.18	0.41	8.3×10^{-8}	2.1×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ST3GAL4	Pancreas	0.26	16	3.27	0.61	9.7×10^{-8}	2.4×10^{-4}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
FADS2	Testis	0.04	7	-6.11	1.15	9.9×10^{-8}	2.4×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ST3GAL4	Muscle Skeletal	0.20	27	3.35	0.63	1.0×10^{-7}	2.5×10^{-4}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
GEMIN7	Brain Caudate basal ganglia	0.13	21	5.66	1.07	1.3×10^{-7}	3.1×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM258	Cells Transformed fibroblasts	0.07	24	-4.62	0.88	1.3×10^{-7}	3.1×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
RP11-288H12.3	Skin Sun Exposed Lower leg	0.05	20	7.50	1.42	1.4×10^{-7}	3.2×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
HPR	Brain Nucleus accumbens basal ganglia	0.59	14	1.72	0.33	1.4×10^{-7}	3.3×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SMARCA4	Adipose Visceral Omentum	0.08	17	5.54	1.05	1.5×10^{-7}	3.5×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
METTL12	Brain Cerebellum	0.06	3	-12.38	2.36	1.5×10^{-7}	3.5×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GSTM2	Lung	0.15	52	4.19	0.80	1.5×10^{-7}	3.5×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
TMEM258	Artery Aorta	0.03	9	-5.29	1.01	1.6×10^{-7}	3.6×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
PCSK9	Testis	0.06	2	8.33	1.59	1.7×10^{-7}	3.8×10^{-4}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
SORT1	Esophagus Mucosa	0.06	15	-6.42	1.23	1.7×10^{-7}	3.8×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Lung	0.02	2	-20.56	3.94	1.8×10^{-7}	4.0×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
TMED1	Esophagus Mucosa	0.03	18	7.01	1.35	1.9×10^{-7}	4.2×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Esophagus Mucosa	0.08	27	-6.49	1.25	1.9×10^{-7}	4.2×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
COL4A3BP	Esophagus Mucosa	0.05	16	-5.37	1.03	2.0×10^{-7}	4.2×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
TMED1	Brain Amygdala	0.10	2	9.10	1.75	2.0×10^{-7}	4.2×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ANKDD1B	Thyroid	0.05	29	-5.36	1.03	2.0×10^{-7}	4.2×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
HPR	Brain Frontal Cortex BA9	0.42	13	1.99	0.38	2.0×10^{-7}	4.2×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
GEMIN7	Uterus	0.08	54	-1.92	0.37	2.2×10^{-7}	4.6×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
C19orf52	Stomach	0.08	40	4.43	0.86	2.3×10^{-7}	4.8×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
HPR	Brain Cerebellar Hemisphere	0.60	14	1.62	0.31	2.4×10^{-7}	4.9×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
C19orf52	DGN-WB	0.06	6	8.85	1.72	2.5×10^{-7}	5.1×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
SMARCA4	Nerve Tibial	0.01	25	6.33	1.23	2.7×10^{-7}	5.4×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PCSK9	Lung	0.06	20	6.47	1.26	2.8×10^{-7}	5.7×10^{-4}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
ANKDD1B	Brain Cerebellar Hemisphere	0.05	11	-6.82	1.33	2.9×10^{-7}	5.8×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
HPR	Brain Putamen basal ganglia	0.33	12	2.24	0.44	2.9×10^{-7}	5.8×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
WTAP	Minor Salivary Gland	0.06	138	1.51	0.29	3.0×10^{-7}	5.8×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
HPR	Heart Atrial Appendage	0.16	27	2.95	0.58	3.1×10^{-7}	6.1×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
HPR	Brain Caudate basal ganglia	0.43	37	1.65	0.32	3.4×10^{-7}	6.5×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
TMEM258	Ovary	0.10	31	-2.64	0.52	3.4×10^{-7}	6.5×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS1	Brain Frontal Cortex BA9	0.11	5	4.85	0.95	3.4×10^{-7}	6.5×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ZNF653	Brain Amygdala	0.10	70	2.81	0.55	3.5×10^{-7}	6.5×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
FADS1	Brain Anterior cingulate cortex BA24	0.04	7	6.97	1.37	3.6×10^{-7}	6.7×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GEMIN7	Brain Nucleus accumbens basal ganglia	0.19	32	3.82	0.75	3.7×10^{-7}	6.8×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
ATG4D	Muscle Skeletal	0.01	17	11.83	2.33	3.7×10^{-7}	6.8×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
CEACAM19	Adrenal Gland	0.13	75	2.94	0.58	3.7×10^{-7}	6.8×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
CKM	DGN-WB	0.40	61	-1.91	0.38	3.9×10^{-7}	7.1×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
CEACAM19	Brain Hippocampus	0.25	7	4.49	0.89	4.1×10^{-7}	7.3×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
SYPL2	Testis	0.65	37	1.57	0.31	4.1×10^{-7}	7.4×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
HMGCR	Small Intestine Terminal Ileum	0.06	21	4.23	0.84	4.2×10^{-7}	7.4×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
ZNF20	Skin Not Sun Exposed Suprapubic	0.02	37	5.40	1.07	4.3×10^{-7}	7.5×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs2738464 pval=4×10^{-40} (Kanai, 29403010)
HPR	Brain Anterior cingulate cortex BA24	0.60	38	1.52	0.30	4.6×10^{-7}	8.1×10^{-4}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
ANKDD1B	Skin Not Sun Exposed Suprapubic	0.14	13	-3.86	0.77	4.8×10^{-7}	8.4×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
TIRAP	Thyroid	0.01	15	9.69	1.94	5.6×10^{-7}	9.8×10^{-4}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
FADS1	Brain Cerebellar Hemisphere	0.27	7	3.24	0.65	5.7×10^{-7}	9.8×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS1	Esophagus Mucosa	0.19	7	3.26	0.65	5.9×10^{-7}	1.0×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
PVRL2	Whole Blood	0.57	7	1.85	0.37	6.1×10^{-7}	1.0×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
GSTM1	Esophagus Muscularis	0.24	35	3.78	0.76	6.7×10^{-7}	1.1×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
TMEM258	Skin Sun Exposed Lower leg	0.05	7	-8.60	1.73	6.9×10^{-7}	1.1×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
HP	Brain Anterior cingulate cortex BA24	0.06	11	4.93	0.99	7.2×10^{-7}	1.2×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
CCDC159	Spleen	0.03	5	-8.84	1.78	7.3×10^{-7}	1.2×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PVR	Spleen	0.08	25	-4.91	0.99	7.8×10^{-7}	1.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Heart Atrial Appendage	0.19	16	-3.13	0.63	7.9×10^{-7}	1.3×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
C11orf10	DGN-WB	0.08	18	-4.72	0.96	8.0×10^{-7}	1.3×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS1	Brain Putamen basal ganglia	0.22	6	4.85	0.99	8.5×10^{-7}	1.4×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GEMIN7	Muscle Skeletal	0.22	20	2.94	0.60	9.0×10^{-7}	1.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
MARK4	Muscle Skeletal	0.19	7	-3.25	0.66	9.2×10^{-7}	1.5×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CEACAM19	Small Intestine Terminal Ileum	0.27	18	3.18	0.65	9.7×10^{-7}	1.5×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM258	Muscle Skeletal	0.02	15	-6.09	1.25	1.0×10^{-6}	1.6×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS1	Thyroid	0.15	11	4.06	0.83	1.1×10^{-6}	1.6×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GEMIN7	Testis	0.18	44	3.33	0.68	1.1×10^{-6}	1.7×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CEP85	Brain Cortex	0.26	33	2.62	0.54	1.2×10^{-6}	1.8×10^{-3}	NA	rs11802413 pval=2×10^{-18} (Spracklen, 28334899)
FADS1	Pancreas	0.42	46	1.97	0.41	1.3×10^{-6}	1.9×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FUT2	Esophagus Mucosa	0.64	37	-1.51	0.31	1.4×10^{-6}	2.1×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FUT2	Colon Transverse	0.17	24	-2.87	0.60	1.4×10^{-6}	2.2×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Artery Coronary	0.31	29	2.26	0.47	1.5×10^{-6}	2.3×10^{-3}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
RP11-295M18.2	Heart Left Ventricle	0.13	46	2.89	0.60	1.6×10^{-6}	2.3×10^{-3}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
TXNL4B	Brain Caudate basal ganglia	0.14	6	6.51	1.36	1.7×10^{-6}	2.5×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
QPCTL	Cells Transformed fibroblasts	0.03	46	-4.43	0.93	1.8×10^{-6}	2.6×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS1	DGN-WB	0.23	12	-2.50	0.52	1.9×10^{-6}	2.7×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GSTM2	Brain Frontal Cortex BA9	0.10	57	3.03	0.64	1.9×10^{-6}	2.7×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
NTN5	Brain Cerebellar Hemisphere	0.08	9	7.16	1.50	1.9×10^{-6}	2.7×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
KANK2	Brain Cerebellum	0.14	22	3.65	0.77	1.9×10^{-6}	2.7×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Spleen	0.14	6	-6.69	1.41	1.9×10^{-6}	2.8×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
FUT2	Pancreas	0.53	16	-1.74	0.37	2.0×10^{-6}	2.8×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HPR	Brain Amygdala	0.53	17	1.83	0.39	2.0×10^{-6}	2.8×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
GEMIN7	Adipose Visceral Omentum	0.07	19	5.38	1.13	2.1×10^{-6}	2.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM258	Colon Transverse	0.04	7	-10.31	2.18	2.1×10^{-6}	3.0×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ST3GAL4	Cells Transformed fibroblasts	0.07	14	5.41	1.14	2.2×10^{-6}	3.0×10^{-3}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
AMIGO1	Brain Substantia nigra	0.10	16	-5.24	1.11	2.2×10^{-6}	3.1×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
TMEM258	Esophagus Muscularis	0.06	15	-6.05	1.28	2.2×10^{-6}	3.1×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
AC011242.5	Skin Sun Exposed Lower leg	0.01	10	-9.78	2.07	2.2×10^{-6}	3.1×10^{-3}	rs4299376 (pval=7.87×10^{-13})	rs4245791 pval=6×10^{-94} (Klarin, 30275531)
FADS1	Testis	0.12	26	3.62	0.77	2.3×10^{-6}	3.1×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CELSR2	Artery Tibial	0.07	5	6.74	1.43	2.3×10^{-6}	3.2×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CETP	Artery Coronary	0.10	3	7.01	1.48	2.3×10^{-6}	3.2×10^{-3}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)
SORT1	Skin Sun Exposed Lower leg	0.03	14	-6.67	1.41	2.3×10^{-6}	3.2×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SYPL2	Ovary	0.60	23	1.92	0.41	2.4×10^{-6}	3.2×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Artery Tibial	0.08	11	-6.47	1.37	2.4×10^{-6}	3.2×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
FADS1	Adipose Visceral Omentum	0.04	6	10.36	2.20	2.4×10^{-6}	3.2×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
ZNF112	Esophagus Gastroesophageal Junction	0.06	26	5.67	1.20	2.5×10^{-6}	3.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
MAU2	DGN-WB	0.13	25	3.25	0.69	2.5×10^{-6}	3.3×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
GEMIN7	Artery Aorta	0.12	72	2.56	0.54	2.5×10^{-6}	3.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CEACAM19	Colon Sigmoid	0.13	14	5.06	1.07	2.5×10^{-6}	3.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF283	Whole Blood	0.01	22	7.34	1.56	2.6×10^{-6}	3.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
DMPK	Brain Spinal cord cervical c-1	0.08	48	-2.19	0.47	2.6×10^{-6}	3.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS1	Artery Tibial	0.02	20	5.09	1.09	2.7×10^{-6}	3.5×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
PSRC1	Artery Aorta	0.15	26	-3.53	0.75	2.8×10^{-6}	3.6×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
NTN5	Cells Transformed fibroblasts	0.03	8	11.80	2.52	2.8×10^{-6}	3.6×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HPR	Brain Spinal cord cervical c-1	0.27	27	2.39	0.51	2.9×10^{-6}	3.6×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SYPL2	Uterus	0.29	51	2.67	0.57	2.9×10^{-6}	3.6×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PCSK9	Adipose Visceral Omentum	0.18	12	4.05	0.87	2.9×10^{-6}	3.7×10^{-3}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
DMPK	Esophagus Gastroesophageal Junction	0.03	62	-3.10	0.66	3.0×10^{-6}	3.8×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FTH1	Brain Amygdala	0.11	41	3.06	0.66	3.1×10^{-6}	3.8×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
TXNL4B	Brain Amygdala	0.13	11	4.38	0.94	3.1×10^{-6}	3.8×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
FUT2	Brain Anterior cingulate cortex BA24	0.10	36	3.74	0.80	3.2×10^{-6}	3.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HOMER3	DGN-WB	0.00	2	40.56	8.70	3.2×10^{-6}	3.9×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
ATP13A1	Artery Coronary	0.14	11	-6.80	1.46	3.4×10^{-6}	4.1×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
FADS1	Muscle Skeletal	0.14	30	3.30	0.71	3.4×10^{-6}	4.1×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ATP13A1	Skin Sun Exposed Lower leg	0.02	5	-12.80	2.76	3.4×10^{-6}	4.1×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
FUT2	Small Intestine Terminal Ileum	0.20	13	-3.34	0.72	3.6×10^{-6}	4.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Skin Sun Exposed Lower leg	0.03	13	-6.04	1.31	3.7×10^{-6}	4.4×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ATP13A1	Nerve Tibial	0.15	9	-3.97	0.86	3.7×10^{-6}	4.4×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
HP	Brain Caudate basal ganglia	0.06	18	4.32	0.93	3.8×10^{-6}	4.5×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
CETP	Lung	0.05	10	7.29	1.58	3.9×10^{-6}	4.6×10^{-3}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)
GEMIN7	Esophagus Mucosa	0.21	26	3.01	0.65	4.0×10^{-6}	4.7×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS1	Nerve Tibial	0.13	4	4.31	0.93	4.0×10^{-6}	4.7×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS1	Colon Sigmoid	0.05	17	5.39	1.17	4.1×10^{-6}	4.8×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ST3GAL4	Esophagus Muscularis	0.03	6	7.82	1.70	4.3×10^{-6}	4.9×10^{-3}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
RP11-295M18.2	Esophagus Mucosa	0.14	27	3.88	0.84	4.3×10^{-6}	4.9×10^{-3}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
NTN5	Skin Not Sun Exposed Suprapubic	0.16	37	3.25	0.71	4.3×10^{-6}	4.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HAVCR1	Thyroid	0.09	13	5.67	1.24	4.6×10^{-6}	5.3×10^{-3}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
ZNF593	Brain Hypothalamus	0.06	25	-3.78	0.83	4.6×10^{-6}	5.3×10^{-3}	NA	rs11802413 pval=2×10^{-18} (Spracklen, 28334899)
POLK	Nerve Tibial	0.11	14	4.87	1.07	5.1×10^{-6}	5.8×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
GSTM2	Adrenal Gland	0.20	43	3.31	0.73	5.1×10^{-6}	5.8×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
GEMIN7	Brain Spinal cord cervical c-1	0.35	32	3.51	0.77	5.1×10^{-6}	5.8×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Esophagus Gastroesophageal Junction	0.29	17	-2.31	0.51	5.2×10^{-6}	5.8×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
ST3GAL4	Pituitary	0.03	7	8.01	1.76	5.3×10^{-6}	5.9×10^{-3}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
ZNF235	Prostate	0.07	19	-6.75	1.48	5.3×10^{-6}	5.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CEACAM19	Brain Putamen basal ganglia	0.16	17	5.33	1.17	5.4×10^{-6}	6.0×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
USP1	Nerve Tibial	0.03	5	10.28	2.26	5.4×10^{-6}	6.0×10^{-3}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
ATP13A1	Artery Aorta	0.14	18	-3.90	0.86	5.5×10^{-6}	6.0×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
CETP	Esophagus Mucosa	0.02	7	12.91	2.84	5.6×10^{-6}	6.1×10^{-3}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)
GEMIN7	Cells Transformed fibroblasts	0.30	35	2.28	0.50	5.8×10^{-6}	6.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
PVRL2	DGN-WB	0.90	58	1.04	0.23	5.8×10^{-6}	6.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
ATP13A1	Esophagus Muscularis	0.10	5	-6.58	1.45	5.9×10^{-6}	6.3×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
ATP13A1	Adipose Subcutaneous	0.12	11	-4.52	1.00	5.9×10^{-6}	6.3×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
PVRL2	Artery Coronary	0.03	19	-4.21	0.93	6.0×10^{-6}	6.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CEACAM19	Brain Frontal Cortex BA9	0.24	11	3.79	0.84	6.1×10^{-6}	6.5×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HAVCR1	Lung	0.18	8	3.71	0.82	6.3×10^{-6}	6.6×10^{-3}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
HAVCR1	Artery Coronary	0.11	14	7.29	1.61	6.3×10^{-6}	6.6×10^{-3}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
FUT2	Skin Sun Exposed Lower leg	0.30	27	-2.37	0.52	6.3×10^{-6}	6.6×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Whole Blood	0.53	25	-1.52	0.34	6.3×10^{-6}	6.6×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
NTN5	Thyroid	0.16	24	2.80	0.62	6.4×10^{-6}	6.7×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Skin Not Sun Exposed Suprapubic	0.03	4	-12.27	2.72	6.5×10^{-6}	6.8×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GSTM1	DGN-WB	0.43	133	1.94	0.43	6.5×10^{-6}	6.8×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
FUT2	Brain Nucleus accumbens basal ganglia	0.05	9	7.39	1.64	6.7×10^{-6}	6.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
SLC22A3	Brain Caudate basal ganglia	0.11	98	1.73	0.38	6.7×10^{-6}	6.9×10^{-3}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
FUT2	Skin Not Sun Exposed Suprapubic	0.35	40	-1.97	0.44	6.8×10^{-6}	6.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CELSR2	Colon Transverse	0.06	25	5.47	1.21	6.8×10^{-6}	6.9×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM22P	Liver	0.07	29	-3.58	0.80	7.0×10^{-6}	7.1×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
POLK	Pancreas	0.10	50	5.91	1.32	7.1×10^{-6}	7.2×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
FOSB	Thyroid	0.02	78	-3.38	0.75	7.3×10^{-6}	7.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Uterus	0.08	33	-3.13	0.70	7.3×10^{-6}	7.3×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CEACAM19	Prostate	0.32	12	3.36	0.75	7.4×10^{-6}	7.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-288H12.3	Muscle Skeletal	0.07	55	3.84	0.86	7.6×10^{-6}	7.5×10^{-3}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
KEAP1	Heart Left Ventricle	0.02	28	4.24	0.95	7.7×10^{-6}	7.6×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
DOCK7	Whole Blood	0.07	19	4.76	1.06	7.7×10^{-6}	7.6×10^{-3}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
SLC22A1	Thyroid	0.15	96	-2.38	0.53	7.9×10^{-6}	7.8×10^{-3}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
HAVCR1	Adipose Subcutaneous	0.18	14	3.66	0.82	8.0×10^{-6}	7.8×10^{-3}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
PSMA5	Esophagus Mucosa	0.06	16	6.29	1.41	8.1×10^{-6}	7.8×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
SYPL2	Breast Mammary Tissue	0.08	16	-8.05	1.80	8.1×10^{-6}	7.8×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Artery Coronary	0.23	25	2.99	0.67	8.1×10^{-6}	7.8×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
DKFZP761J1410	Pituitary	0.07	20	3.83	0.86	8.4×10^{-6}	8.1×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
KLC3	Brain Anterior cingulate cortex BA24	0.07	24	-4.53	1.02	8.6×10^{-6}	8.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
IRF2BP1	Muscle Skeletal	0.04	6	10.57	2.38	8.8×10^{-6}	8.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Esophagus Muscularis	0.36	5	-2.01	0.45	8.8×10^{-6}	8.4×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
POLK	Brain Cerebellar Hemisphere	0.17	11	3.73	0.84	9.1×10^{-6}	8.7×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
CTD-2235C13.3	Esophagus Mucosa	0.01	55	-4.48	1.01	9.3×10^{-6}	8.8×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
CEACAM19	Artery Tibial	0.17	64	2.77	0.63	9.5×10^{-6}	9.0×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Pancreas	0.23	32	2.83	0.64	9.6×10^{-6}	9.0×10^{-3}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
FADS1	Heart Left Ventricle	0.05	13	5.95	1.35	9.6×10^{-6}	9.0×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CEACAM19	Brain Cortex	0.11	2	5.15	1.17	1.0×10^{-5}	9.4×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
PLEC	Artery Coronary	0.20	23	-2.79	0.63	1.0×10^{-5}	9.4×10^{-3}	NA	rs7832643 pval=2×10^{-17} (Spracklen, 28334899)
CEACAM19	Cells Transformed fibroblasts	0.34	6	2.51	0.57	1.0×10^{-5}	9.5×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
CDKN2D	Brain Caudate basal ganglia	0.07	28	4.01	0.91	1.0×10^{-5}	9.6×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
DCPS	Cells Transformed fibroblasts	0.09	5	-4.59	1.04	1.1×10^{-5}	9.7×10^{-3}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
SMARCA4	Cells Transformed fibroblasts	0.02	27	5.70	1.29	1.1×10^{-5}	9.8×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Artery Tibial	0.03	9	-6.55	1.49	1.1×10^{-5}	9.8×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
POLK	Thyroid	0.06	25	6.63	1.51	1.1×10^{-5}	9.8×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
CARM1	Cells Transformed fibroblasts	0.05	10	-6.35	1.44	1.1×10^{-5}	9.9×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
FADS2	Artery Aorta	0.13	17	-4.30	0.98	1.1×10^{-5}	1.0×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
DOCK7	Skin Sun Exposed Lower leg	0.10	5	4.35	0.99	1.1×10^{-5}	1.0×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
CEACAM19	Esophagus Muscularis	0.22	50	2.48	0.57	1.2×10^{-5}	1.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
APOB	Nerve Tibial	0.11	43	3.03	0.69	1.2×10^{-5}	1.0×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
ST3GAL4	Nerve Tibial	0.04	10	5.64	1.29	1.2×10^{-5}	1.1×10^{-2}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
TBKBP1	Prostate	0.21	33	-2.82	0.64	1.2×10^{-5}	1.1×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
CEACAM19	Ovary	0.16	1	6.11	1.39	1.2×10^{-5}	1.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	DGN-WB	0.17	44	2.58	0.59	1.2×10^{-5}	1.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
MRPL14	Spleen	0.06	13	-5.84	1.33	1.2×10^{-5}	1.1×10^{-2}	NA	NA
POLK	Brain Cerebellum	0.13	27	5.15	1.18	1.2×10^{-5}	1.1×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
TMEM258	Heart Atrial Appendage	0.02	15	-6.29	1.44	1.2×10^{-5}	1.1×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
NTN5	Skin Sun Exposed Lower leg	0.12	15	3.43	0.79	1.3×10^{-5}	1.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
MAMSTR	Esophagus Muscularis	0.05	9	7.20	1.65	1.3×10^{-5}	1.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
FUT2	Stomach	0.34	21	-2.03	0.47	1.3×10^{-5}	1.2×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
CELSR2	Whole Blood	0.04	56	5.62	1.29	1.4×10^{-5}	1.2×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	DGN-WB	0.12	83	2.62	0.60	1.5×10^{-5}	1.2×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
SORT1	DGN-WB	0.02	11	-11.36	2.63	1.5×10^{-5}	1.3×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
RP11-295M18.6	Esophagus Gastroesophageal Junction	0.42	42	1.46	0.34	1.5×10^{-5}	1.3×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
CCDC151	Brain Cortex	0.06	38	2.80	0.65	1.6×10^{-5}	1.3×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
KANK2	Artery Aorta	0.08	42	3.40	0.79	1.6×10^{-5}	1.3×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	Adipose Subcutaneous	0.17	16	3.51	0.81	1.6×10^{-5}	1.3×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
DOCK7	DGN-WB	0.20	36	2.84	0.66	1.6×10^{-5}	1.4×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
TMEM258	Uterus	0.15	17	-3.60	0.83	1.6×10^{-5}	1.4×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
RP11-295M18.2	Prostate	0.06	8	5.41	1.25	1.6×10^{-5}	1.4×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
MYBPHL	Nerve Tibial	0.04	18	-6.06	1.41	1.6×10^{-5}	1.4×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ZNF235	Adipose Subcutaneous	0.02	51	4.22	0.98	1.6×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
HAVCR1	Skin Not Sun Exposed Suprapubic	0.08	19	6.38	1.48	1.7×10^{-5}	1.4×10^{-2}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
DOCK7	Lung	0.02	2	14.47	3.36	1.7×10^{-5}	1.4×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
RP11-288H12.3	Breast Mammary Tissue	0.03	25	5.34	1.24	1.7×10^{-5}	1.4×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RP11-295M18.6	Esophagus Mucosa	0.19	52	2.53	0.59	1.7×10^{-5}	1.4×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
FADS1	Brain Cortex	0.11	11	4.06	0.95	1.7×10^{-5}	1.4×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
NTN5	DGN-WB	0.35	25	1.94	0.45	1.7×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-15A1.3	Whole Blood	0.03	20	6.94	1.61	1.7×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
NTN5	Spleen	0.15	46	2.33	0.54	1.8×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
FUT2	Minor Salivary Gland	0.50	19	-1.72	0.40	1.8×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
GEMIN7	Esophagus Muscularis	0.19	24	2.70	0.63	1.8×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
HPR	Brain Substantia nigra	0.47	44	1.55	0.36	1.8×10^{-5}	1.4×10^{-2}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
ZNF284	Artery Aorta	0.09	52	2.87	0.67	1.8×10^{-5}	1.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
MRPL45P2	Heart Left Ventricle	0.04	28	5.97	1.39	1.8×10^{-5}	1.5×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
CELSR2	DGN-WB	0.16	30	3.31	0.77	1.9×10^{-5}	1.5×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
AP1G1	Testis	0.05	58	2.61	0.61	1.9×10^{-5}	1.5×10^{-2}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
TMEM59	Esophagus Muscularis	0.06	4	52.19	12.21	1.9×10^{-5}	1.5×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
RP11-777F6.3	Artery Aorta	0.05	7	-7.04	1.65	2.0×10^{-5}	1.5×10^{-2}	NA	NA
CTD-2235C13.3	Skin Not Sun Exposed Suprapubic	0.10	37	-3.77	0.88	2.0×10^{-5}	1.5×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
ZNF513	Brain Anterior cingulate cortex BA24	0.10	31	3.17	0.74	2.0×10^{-5}	1.5×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs780094 pval=3×10^{-21} (Klarin, 30275531)
SYPL2	Esophagus Mucosa	0.06	11	-6.90	1.62	2.0×10^{-5}	1.5×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Adipose Subcutaneous	0.08	5	-5.97	1.40	2.0×10^{-5}	1.5×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
NTN5	Brain Hypothalamus	0.07	5	4.20	0.99	2.0×10^{-5}	1.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
AC006126.4	Testis	0.12	22	-3.42	0.80	2.1×10^{-5}	1.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	Skin Sun Exposed Lower leg	0.25	47	2.34	0.55	2.1×10^{-5}	1.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ANKDD1B	Brain Cortex	0.10	12	-4.18	0.98	2.1×10^{-5}	1.6×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
SLC44A2	Muscle Skeletal	0.26	19	-2.23	0.53	2.1×10^{-5}	1.6×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
FADS2	Lung	0.09	6	-4.64	1.09	2.2×10^{-5}	1.7×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CETP	Small Intestine Terminal Ileum	0.15	19	4.30	1.01	2.2×10^{-5}	1.7×10^{-2}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
ATXN7L2	Ovary	0.20	15	4.22	1.00	2.2×10^{-5}	1.7×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.2	Heart Atrial Appendage	0.36	31	1.99	0.47	2.2×10^{-5}	1.7×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
SLC22A3	DGN-WB	0.06	18	4.82	1.14	2.2×10^{-5}	1.7×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
HPR	Brain Hypothalamus	0.40	70	1.08	0.25	2.3×10^{-5}	1.7×10^{-2}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
SLC22A3	Ovary	0.17	27	2.97	0.70	2.3×10^{-5}	1.7×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
CLPTM1	Artery Aorta	0.02	29	5.24	1.24	2.4×10^{-5}	1.8×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF404	Prostate	0.12	98	-1.78	0.42	2.4×10^{-5}	1.8×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
DNAI2	Brain Substantia nigra	0.26	43	2.51	0.60	2.6×10^{-5}	1.9×10^{-2}	rs740516 (pval=3.11×10^{-10})	NA
EFCAB13	Brain Spinal cord cervical c-1	0.19	27	3.00	0.71	2.6×10^{-5}	2.0×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
CEACAM19	Lung	0.09	27	3.71	0.88	2.6×10^{-5}	2.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
MRPL45P2	Skin Not Sun Exposed Suprapubic	0.21	30	2.34	0.56	2.7×10^{-5}	2.0×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
RP11-295M18.6	Adipose Subcutaneous	0.45	26	1.60	0.38	2.7×10^{-5}	2.0×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
ILF3-AS1	Whole Blood	0.04	13	10.51	2.50	2.7×10^{-5}	2.0×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
HAVCR1	DGN-WB	0.01	13	9.76	2.33	2.7×10^{-5}	2.0×10^{-2}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
SYPL2	Minor Salivary Gland	0.12	16	-4.35	1.04	2.8×10^{-5}	2.1×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
VASP	Testis	0.03	53	-2.81	0.67	2.8×10^{-5}	2.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
MRPL45P2	Minor Salivary Gland	0.08	33	2.76	0.66	2.8×10^{-5}	2.1×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
CETP	Colon Transverse	0.08	31	3.67	0.88	2.8×10^{-5}	2.1×10^{-2}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
CYB561A3	Skin Not Sun Exposed Suprapubic	0.01	10	-10.12	2.42	2.9×10^{-5}	2.1×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
DOCK7	Cells Transformed fibroblasts	0.27	54	2.18	0.52	2.9×10^{-5}	2.1×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
SH3D19	Pancreas	0.02	22	-6.57	1.58	3.0×10^{-5}	2.2×10^{-2}	NA	NA
FADS2	Stomach	0.08	8	-5.20	1.25	3.0×10^{-5}	2.2×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
TOMM40	Adipose Subcutaneous	0.03	1	-11.68	2.81	3.2×10^{-5}	2.3×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
TBKBP1	Colon Transverse	0.12	14	-3.92	0.94	3.2×10^{-5}	2.3×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
SYT7	Lung	0.02	14	-7.83	1.89	3.3×10^{-5}	2.4×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
EPOR	Heart Left Ventricle	0.03	18	5.01	1.21	3.5×10^{-5}	2.5×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
OSBPL3	Artery Coronary	0.14	102	-1.31	0.32	3.5×10^{-5}	2.5×10^{-2}	NA	rs4722551 pval=9×10^{-18} (Klarin, 30275531)
TYK2	Brain Cerebellar Hemisphere	0.21	100	1.84	0.45	3.5×10^{-5}	2.5×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
TBKBP1	Minor Salivary Gland	0.17	33	-2.67	0.65	3.6×10^{-5}	2.5×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
TMEM258	Colon Sigmoid	0.05	36	-2.98	0.72	3.6×10^{-5}	2.5×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
RP11-288H12.3	Adipose Subcutaneous	0.11	66	2.65	0.64	3.6×10^{-5}	2.5×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
DOCK7	Skin Not Sun Exposed Suprapubic	0.03	6	8.19	1.98	3.7×10^{-5}	2.6×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
ZNF625	Esophagus Muscularis	0.04	15	-6.64	1.61	3.7×10^{-5}	2.6×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs2278426 pval=2×10^{-09} (Kanai, 29403010)
RP11-295M18.2	Esophagus Gastroesophageal Junction	0.33	50	1.67	0.40	3.7×10^{-5}	2.6×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
EFCAB13	Testis	0.31	20	2.16	0.53	3.8×10^{-5}	2.6×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
RPL39P36	Breast Mammary Tissue	0.04	13	7.34	1.78	3.8×10^{-5}	2.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
FADS2	Heart Left Ventricle	0.26	18	-2.35	0.57	3.8×10^{-5}	2.6×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
DCPS	Artery Tibial	0.08	24	-4.82	1.17	3.8×10^{-5}	2.6×10^{-2}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
FADS2	Nerve Tibial	0.24	15	-2.37	0.57	3.8×10^{-5}	2.6×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CYB561D1	Muscle Skeletal	0.01	8	7.86	1.91	3.9×10^{-5}	2.6×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
NTN5	Brain Cerebellum	0.09	18	3.93	0.96	3.9×10^{-5}	2.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
C1orf106	Minor Salivary Gland	0.24	35	2.25	0.55	3.9×10^{-5}	2.6×10^{-2}	NA	NA
ZNF235	Brain Cerebellum	0.07	17	4.57	1.11	3.9×10^{-5}	2.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.6	Adipose Visceral Omentum	0.33	39	1.96	0.48	4.0×10^{-5}	2.7×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
ZNF233	Lung	0.02	10	-10.98	2.67	4.0×10^{-5}	2.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Lung	0.33	15	1.89	0.46	4.0×10^{-5}	2.7×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
ERCC2	Esophagus Gastroesophageal Junction	0.04	10	-7.64	1.86	4.1×10^{-5}	2.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
GSTM2	Muscle Skeletal	0.14	57	3.02	0.74	4.1×10^{-5}	2.7×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RAB3D	DGN-WB	0.06	41	-4.74	1.16	4.1×10^{-5}	2.7×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PKN3	DGN-WB	0.58	77	-1.34	0.33	4.1×10^{-5}	2.7×10^{-2}	rs532436 (pval=2.31×10^{-11})	NA
CEACAM19	Esophagus Gastroesophageal Junction	0.17	13	4.31	1.05	4.1×10^{-5}	2.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Stomach	0.12	20	2.93	0.72	4.1×10^{-5}	2.7×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
LPAL2	Testis	0.04	17	6.59	1.61	4.2×10^{-5}	2.8×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
FADS2	DGN-WB	0.88	35	-0.98	0.24	4.3×10^{-5}	2.8×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
AP1M2	Stomach	0.03	37	3.90	0.95	4.3×10^{-5}	2.8×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.6	Artery Coronary	0.41	8	1.95	0.48	4.4×10^{-5}	2.9×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
TTC21B	Breast Mammary Tissue	0.07	9	-8.06	1.97	4.4×10^{-5}	2.9×10^{-2}	NA	NA
CARM1	Thyroid	0.03	24	-5.35	1.31	4.4×10^{-5}	2.9×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
BLOC1S3	Esophagus Muscularis	0.04	9	-8.32	2.04	4.5×10^{-5}	2.9×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
AP1M2	Adipose Visceral Omentum	0.08	32	-3.62	0.89	4.5×10^{-5}	2.9×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.2	Adipose Subcutaneous	0.48	31	1.47	0.36	4.6×10^{-5}	3.0×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
YIPF2	Adipose Subcutaneous	0.01	17	6.54	1.61	4.6×10^{-5}	3.0×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
IGFLR1	Cells EBV-transformed lymphocytes	0.13	20	2.73	0.67	4.7×10^{-5}	3.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	Stomach	0.02	8	6.20	1.52	4.7×10^{-5}	3.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
WTAP	Small Intestine Terminal Ileum	0.16	123	1.45	0.36	4.8×10^{-5}	3.1×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
PCSK9	Whole Blood	0.03	1	12.31	3.03	4.9×10^{-5}	3.1×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
RP11-295M18.2	Breast Mammary Tissue	0.35	16	1.93	0.48	4.9×10^{-5}	3.1×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
NPAS4	Pancreas	0.04	3	9.32	2.29	4.9×10^{-5}	3.1×10^{-2}	rs174601 (pval=2.14×10^{-08})	NA
WDFY2	Adipose Subcutaneous	0.07	61	2.95	0.73	4.9×10^{-5}	3.1×10^{-2}	NA	NA
EFCAB13	Artery Coronary	0.15	16	3.59	0.88	4.9×10^{-5}	3.1×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
TMEM258	Nerve Tibial	0.04	8	-6.57	1.62	5.0×10^{-5}	3.1×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
DOCK7	Artery Tibial	0.07	14	5.84	1.44	5.0×10^{-5}	3.1×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
EFCAB13	Pituitary	0.30	63	2.01	0.50	5.0×10^{-5}	3.2×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
TBKBP1	Small Intestine Terminal Ileum	0.27	34	-1.92	0.47	5.1×10^{-5}	3.2×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
ANKDD1B	Brain Cerebellum	0.06	27	-3.18	0.79	5.2×10^{-5}	3.3×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
GNB1L	Brain Caudate basal ganglia	0.08	73	2.29	0.57	5.2×10^{-5}	3.3×10^{-2}	NA	NA
IGF2R	Muscle Skeletal	0.37	23	1.78	0.44	5.2×10^{-5}	3.3×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
CPEB1	Brain Cerebellar Hemisphere	0.05	10	4.97	1.23	5.3×10^{-5}	3.3×10^{-2}	NA	NA
ARL5B	Whole Blood	0.02	33	7.08	1.75	5.4×10^{-5}	3.4×10^{-2}	NA	NA
ZNF283	Brain Cerebellum	0.14	81	-1.91	0.47	5.5×10^{-5}	3.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
IGF2R	Adipose Subcutaneous	0.09	72	3.11	0.77	5.5×10^{-5}	3.4×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
FADS1	Stomach	0.16	15	3.16	0.78	5.5×10^{-5}	3.4×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
GEMIN7	Esophagus Gastroesophageal Junction	0.07	6	5.40	1.34	5.6×10^{-5}	3.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM59	Artery Tibial	0.01	6	8.22	2.04	5.6×10^{-5}	3.4×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
EFCAB13	Artery Tibial	0.32	45	1.94	0.48	5.7×10^{-5}	3.5×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
TBKBP1	Artery Tibial	0.39	42	-1.65	0.41	5.7×10^{-5}	3.5×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
MRPL45P2	Adipose Subcutaneous	0.16	72	2.54	0.63	5.8×10^{-5}	3.5×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
HAVCR1	Adipose Visceral Omentum	0.13	13	4.28	1.06	5.8×10^{-5}	3.5×10^{-2}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
RAB3IL1	Cells Transformed fibroblasts	0.05	14	-6.03	1.50	5.9×10^{-5}	3.6×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
AC144652.1	Brain Nucleus accumbens basal ganglia	0.08	32	2.62	0.65	6.0×10^{-5}	3.6×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
FADS2	Spleen	0.52	26	-1.55	0.39	6.0×10^{-5}	3.6×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
RP11-295M18.2	Adipose Visceral Omentum	0.33	40	1.84	0.46	6.0×10^{-5}	3.6×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
MRPL45P2	Pancreas	0.17	21	2.92	0.73	6.1×10^{-5}	3.6×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
USP1	DGN-WB	0.00	1	37.24	9.29	6.1×10^{-5}	3.7×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
ARL5B	Cells EBV-transformed lymphocytes	0.22	42	3.30	0.82	6.2×10^{-5}	3.7×10^{-2}	NA	NA
CHMP4A	Muscle Skeletal	0.06	61	-3.44	0.86	6.2×10^{-5}	3.7×10^{-2}	NA	rs8017377 pval=3×10^{-15} (Willer, 24097068)
RASIP1	DGN-WB	0.00	3	35.82	8.95	6.3×10^{-5}	3.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Uterus	0.13	32	2.39	0.60	6.4×10^{-5}	3.8×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
SEC1P	Lung	0.05	29	3.74	0.94	6.5×10^{-5}	3.8×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
FREM1	Lung	0.28	18	2.07	0.52	6.5×10^{-5}	3.8×10^{-2}	NA	NA
TM4SF4	Breast Mammary Tissue	0.04	25	4.70	1.18	6.5×10^{-5}	3.8×10^{-2}	NA	NA
EFCAB13	Brain Anterior cingulate cortex BA24	0.15	23	2.90	0.73	6.6×10^{-5}	3.9×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
KPNB1	Skin Sun Exposed Lower leg	0.02	3	-11.49	2.88	6.6×10^{-5}	3.9×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
USP1	Adrenal Gland	0.06	27	3.72	0.93	6.6×10^{-5}	3.9×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
MUS81	Brain Cortex	0.05	8	7.71	1.93	6.7×10^{-5}	3.9×10^{-2}	rs174601 (pval=2.14×10^{-08})	NA
RP11-295M18.6	Lung	0.36	20	1.74	0.44	6.7×10^{-5}	3.9×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
IGFLR1	Adipose Visceral Omentum	0.02	21	4.62	1.16	6.8×10^{-5}	4.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
CLPTM1	Skin Sun Exposed Lower leg	0.15	39	2.65	0.67	6.8×10^{-5}	4.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
NTN5	Colon Transverse	0.09	38	2.82	0.71	6.9×10^{-5}	4.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
PSRC1	Uterus	0.07	24	-4.78	1.20	6.9×10^{-5}	4.0×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.2	Skin Sun Exposed Lower leg	0.26	40	1.80	0.45	7.0×10^{-5}	4.0×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
ITPR2	Brain Cerebellar Hemisphere	0.47	74	1.43	0.36	7.1×10^{-5}	4.1×10^{-2}	NA	NA
CELSR2	Esophagus Gastroesophageal Junction	0.07	5	6.96	1.75	7.1×10^{-5}	4.1×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ACAT1	Thyroid	0.32	28	-1.69	0.43	7.2×10^{-5}	4.1×10^{-2}	NA	NA
H3F3C	Ovary	0.05	36	2.46	0.62	7.2×10^{-5}	4.1×10^{-2}	NA	NA
RASIP1	Cells Transformed fibroblasts	0.30	13	2.06	0.52	7.3×10^{-5}	4.1×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
POLK	Spleen	0.18	73	2.39	0.60	7.4×10^{-5}	4.2×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
MROH2A	Colon Transverse	0.12	34	3.35	0.84	7.4×10^{-5}	4.2×10^{-2}	NA	rs7567229 pval=4×10^{-11} (Klarin, 30275531)
EXOC3L2	Brain Substantia nigra	0.06	49	-2.78	0.70	7.6×10^{-5}	4.3×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
KIAA1324	Pancreas	0.10	29	-3.02	0.76	7.6×10^{-5}	4.3×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.6	Prostate	0.27	41	2.22	0.56	7.7×10^{-5}	4.3×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
CEACAM19	Brain Cerebellar Hemisphere	0.14	20	2.94	0.74	7.7×10^{-5}	4.3×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-295M18.2	Brain Caudate basal ganglia	0.26	26	2.37	0.60	7.8×10^{-5}	4.3×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
ZNF285	Colon Sigmoid	0.10	30	-2.94	0.74	7.8×10^{-5}	4.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
SMOC1	Artery Coronary	0.22	50	1.77	0.45	7.8×10^{-5}	4.4×10^{-2}	NA	rs11620731 pval=1×10^{-11} (Hoffmann, 29507422)
RP11-295M18.6	Stomach	0.09	15	4.22	1.07	7.8×10^{-5}	4.4×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
TMEM59	Adipose Subcutaneous	0.06	7	16.88	4.28	7.8×10^{-5}	4.4×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
GEMIN7	Brain Frontal Cortex BA9	0.16	33	2.93	0.74	7.9×10^{-5}	4.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS2	Adipose Visceral Omentum	0.08	8	-4.92	1.25	8.0×10^{-5}	4.4×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
MRPL45P2	Artery Tibial	0.19	21	2.46	0.62	8.0×10^{-5}	4.4×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
RP11-295M18.6	Pancreas	0.20	16	2.69	0.68	8.1×10^{-5}	4.4×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
CARM1	Muscle Skeletal	0.01	12	-7.47	1.90	8.1×10^{-5}	4.5×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PKN3	Spleen	0.07	4	-5.31	1.35	8.4×10^{-5}	4.6×10^{-2}	rs532436 (pval=2.31×10^{-11})	NA
AC067959.1	Artery Coronary	0.17	32	3.79	0.96	8.4×10^{-5}	4.6×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
TGDS	Liver	0.25	13	-2.46	0.63	8.4×10^{-5}	4.6×10^{-2}	NA	NA
LCN2	DGN-WB	0.03	2	-8.73	2.22	8.5×10^{-5}	4.6×10^{-2}	rs532436 (pval=2.31×10^{-11})	NA
MRPL45P2	Cells Transformed fibroblasts	0.28	24	2.25	0.57	8.6×10^{-5}	4.7×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
ZNF491	Adrenal Gland	0.04	19	3.93	1.00	8.7×10^{-5}	4.7×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
RP11-373D23.3	Pituitary	0.06	7	7.42	1.89	8.9×10^{-5}	4.8×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs780094 pval=3×10^{-21} (Klarin, 30275531)
TBKBP1	Cells EBV-transformed lymphocytes	0.17	14	-2.88	0.74	9.0×10^{-5}	4.8×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
FADS2	Colon Transverse	0.32	14	-2.18	0.56	9.0×10^{-5}	4.8×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
FADS2	Muscle Skeletal	0.06	10	-4.87	1.24	9.0×10^{-5}	4.8×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
MRPL45P2	Adrenal Gland	0.26	12	2.79	0.71	9.0×10^{-5}	4.8×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
PKN3	Whole Blood	0.27	4	-2.21	0.56	9.2×10^{-5}	4.9×10^{-2}	rs532436 (pval=2.31×10^{-11})	NA
RP11-295M18.6	Muscle Skeletal	0.29	25	1.89	0.48	9.2×10^{-5}	4.9×10^{-2}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	Beta	SE	P-value	FDR	GWAS	NHGRI-EBI catalog
MRPL45P2	Muscle Skeletal	0.16	19	2.92	0.75	9.2×10^{-5}	4.9×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
TTC21B	Adipose Subcutaneous	0.08	33	-4.43	1.14	9.3×10^{-5}	5.0×10^{-2}	NA	NA

Appendix VII. Tissue-specific GReX results of the genes significantly associated with TC in BioVU

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
SORT1	Liver	0.58	25	-5.71	0.42	2.8×10^{-42}	4.3×10^{-37}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Pancreas	0.02	5	-46.93	3.45	3.3×10^{-42}	4.3×10^{-37}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Muscle Skeletal	0.39	13	-6.27	0.46	1.5×10^{-41}	1.3×10^{-36}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Liver	0.45	15	-6.68	0.50	2.0×10^{-41}	1.3×10^{-36}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	DGN-WB	0.25	11	-7.65	0.57	2.9×10^{-41}	1.5×10^{-36}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Esophagus Mucosa	0.17	17	-9.54	0.72	3.7×10^{-40}	1.6×10^{-35}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Heart Left Ventricle	0.04	7	-31.47	2.40	2.5×10^{-39}	9.3×10^{-35}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Liver	0.48	50	-5.68	0.43	3.3×10^{-39}	1.1×10^{-34}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SORT1	Minor Salivary Gland	0.07	13	-17.71	1.43	4.4×10^{-35}	1.3×10^{-30}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Brain Cerebellum	0.08	11	-19.28	1.63	3.7×10^{-32}	9.6×10^{-28}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Nerve Tibial	0.02	7	-25.07	2.24	3.7×10^{-29}	8.7×10^{-25}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Brain Cortex	0.13	17	-12.78	1.14	4.8×10^{-29}	1.0×10^{-24}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Muscle Skeletal	0.08	45	-11.12	1.06	5.9×10^{-26}	1.2×10^{-21}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Esophagus Mucosa	0.15	17	-9.35	0.89	7.8×10^{-26}	1.5×10^{-21}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Testis	0.18	14	-8.36	0.80	2.3×10^{-25}	3.9×10^{-21}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSMA5	Liver	0.09	33	-9.43	0.93	2.5×10^{-24}	4.1×10^{-20}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
APOB	Colon Sigmoid	0.05	15	-18.55	1.98	9.0×10^{-21}	1.4×10^{-16}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
PSRC1	Pancreas	0.16	26	-6.57	0.73	2.3×10^{-19}	3.4×10^{-15}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Whole Blood	0.04	12	-13.95	1.58	9.3×10^{-19}	1.3×10^{-14}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Colon Transverse	0.14	9	-9.54	1.08	1.1×10^{-18}	1.5×10^{-14}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Adipose Visceral Omentum	0.04	22	-14.40	1.64	1.4×10^{-18}	1.8×10^{-14}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
APOB	Esophagus Gastroesophageal Junction	0.03	10	-15.62	1.79	2.6×10^{-18}	3.0×10^{-14}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
PSRC1	Brain Frontal Cortex BA9	0.10	51	-5.65	0.68	7.9×10^{-17}	9.0×10^{-13}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	Skin Not Sun Exposed Suprapubic	0.20	63	-5.30	0.65	3.2×10^{-16}	3.5×10^{-12}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SARS	Skin Sun Exposed Lower leg	0.02	21	-11.60	1.44	7.7×10^{-16}	8.0×10^{-12}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
APOB	Skin Sun Exposed Lower leg	0.29	10	-5.30	0.68	8.8×10^{-15}	8.8×10^{-11}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
APOB	Skin Not Sun Exposed Suprapubic	0.19	12	-6.62	0.88	4.9×10^{-14}	4.7×10^{-10}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
APOB	Adipose Subcutaneous	0.19	18	5.49	0.74	1.1×10^{-13}	1.0×10^{-9}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
APOB	Uterus	0.14	28	-5.79	0.78	1.3×10^{-13}	1.2×10^{-9}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
USP1	Nerve Tibial	0.03	5	18.78	2.54	1.5×10^{-13}	1.3×10^{-9}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
SARS	Adrenal Gland	0.09	25	5.94	0.81	1.7×10^{-13}	1.4×10^{-9}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	Skin Sun Exposed Lower leg	0.01	27	-9.88	1.34	1.8×10^{-13}	1.5×10^{-9}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
DOCK6	Nerve Tibial	0.08	25	7.29	1.00	2.4×10^{-13}	1.9×10^{-9}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
DOCK7	Skin Sun Exposed Lower leg	0.10	5	8.10	1.11	3.2×10^{-13}	2.5×10^{-9}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DOCK7	Lung	0.02	2	27.13	3.78	7.4×10^{-13}	5.5×10^{-9}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
DOCK7	DGN-WB	0.20	36	5.26	0.74	1.2×10^{-12}	8.6×10^{-9}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
DOCK7	Whole Blood	0.07	19	8.49	1.19	1.2×10^{-12}	8.6×10^{-9}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
APOB	Thyroid	0.02	13	-16.92	2.38	1.3×10^{-12}	9.0×10^{-9}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
DOCK7	Skin Not Sun Exposed Suprapubic	0.03	6	15.50	2.23	3.5×10^{-12}	2.3×10^{-8}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
ATP13A1	Lung	0.02	2	-30.61	4.42	4.1×10^{-12}	2.7×10^{-8}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
DOCK7	Cells Transformed fibroblasts	0.27	54	4.06	0.59	4.8×10^{-12}	3.0×10^{-8}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
BCAM	Lung	0.06	3	-13.30	1.93	5.5×10^{-12}	3.4×10^{-8}	rs7412 (pval=1.55×10^{-90})	APOE region
USP1	Adrenal Gland	0.06	27	7.15	1.04	7.6×10^{-12}	4.6×10^{-8}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
DOCK7	Artery Tibial	0.07	14	11.07	1.62	7.9×10^{-12}	4.7×10^{-8}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
HMGCR	Muscle Skeletal	0.03	12	14.26	2.09	8.2×10^{-12}	4.7×10^{-8}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
PSRC1	Minor Salivary Gland	0.27	20	-5.10	0.75	1.3×10^{-11}	7.1×10^{-8}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CD3EAP	Brain Substantia nigra	0.08	6	10.25	1.52	1.3×10^{-11}	7.2×10^{-8}	rs7412 (pval=1.55×10^{-90})	APOE region
ATP13A1	Artery Coronary	0.14	11	-11.02	1.64	1.9×10^{-11}	1.1×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ATP13A1	Artery Aorta	0.14	18	-6.45	0.96	2.0×10^{-11}	1.1×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
USP1	DGN-WB	0.00	1	69.07	10.45	3.8×10^{-11}	2.0×10^{-7}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
LIPC	Liver	0.27	60	-3.50	0.53	5.6×10^{-11}	2.9×10^{-7}	rs10468017 (pval=6.54×10^{-13})	rs7350789 pval=4×10^{-78} (Klarin, 30275531)
PSRC1	Pituitary	0.15	35	-4.44	0.68	6.0×10^{-11}	3.0×10^{-7}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
ATP13A1	Skin Sun Exposed Lower leg	0.02	5	-20.24	3.09	6.0×10^{-11}	3.0×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ZNF513	Brain Anterior cingulate cortex BA24	0.10	31	5.40	0.83	8.9×10^{-11}	4.3×10^{-7}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ATP13A1	Spleen	0.14	6	-10.23	1.58	9.4×10^{-11}	4.4×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
USP1	Esophagus Muscularis	0.04	41	9.65	1.49	1.0×10^{-10}	4.7×10^{-7}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
PSRC1	Lung	0.08	23	-7.88	1.23	1.3×10^{-10}	6.1×10^{-7}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ABCG8	Colon Transverse	0.15	8	-6.80	1.06	1.5×10^{-10}	6.9×10^{-7}	rs4953026 (pval=3.79×10^{-11})	rs4299376 pval=3×10^{-73} (Willer, 24097068)
ANKDD1B	Nerve Tibial	0.19	14	-4.46	0.70	2.5×10^{-10}	1.1×10^{-6}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
DMPK	Stomach	0.06	23	-11.15	1.77	2.8×10^{-10}	1.2×10^{-6}	rs7412 (pval=1.55×10^{-90})	APOE region
HOMER3	DGN-WB	0.00	2	61.66	9.78	2.9×10^{-10}	1.2×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ATP13A1	Artery Tibial	0.08	11	-9.66	1.54	3.3×10^{-10}	1.4×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ATP13A1	Nerve Tibial	0.15	9	-6.02	0.96	4.2×10^{-10}	1.7×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
AC012065.7	Pituitary	0.08	21	7.54	1.21	4.8×10^{-10}	1.9×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
GCKR	Thyroid	0.15	16	-5.56	0.90	5.5×10^{-10}	2.2×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
RP11-373D23.3	Pituitary	0.06	7	12.91	2.12	1.1×10^{-9}	4.4×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ANKDD1B	Thyroid	0.05	29	-7.03	1.16	1.4×10^{-9}	5.4×10^{-6}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
HPR	Brain Cerebellum	0.48	34	2.32	0.38	1.4×10^{-9}	5.5×10^{-6}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
DOCK7	Artery Aorta	0.03	13	12.51	2.07	1.5×10^{-9}	5.7×10^{-6}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
HPR	Brain Hippocampus	0.36	24	2.52	0.42	1.6×10^{-9}	6.0×10^{-6}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HPR	Brain Cortex	0.55	11	2.22	0.37	2.1×10^{-9}	7.8×10^{-6}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
SMARCA4	Esophagus Mucosa	0.09	35	4.55	0.76	2.2×10^{-9}	7.8×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATP13A1	Adipose Subcutaneous	0.12	11	-6.67	1.12	2.7×10^{-9}	9.6×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
P2RY11	Heart Atrial Appendage	0.18	48	3.62	0.61	3.0×10^{-9}	1.0×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATP13A1	Esophagus Muscularis	0.10	5	-9.65	1.63	3.0×10^{-9}	1.0×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
MAU2	DGN-WB	0.13	25	4.59	0.78	3.4×10^{-9}	1.2×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
PSRC1	Brain Hippocampus	0.04	14	-7.61	1.30	4.8×10^{-9}	1.6×10^{-5}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
GDF7	Esophagus Muscularis	0.08	16	7.78	1.34	6.8×10^{-9}	2.3×10^{-5}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
HPR	Brain Nucleus accumbens basal ganglia	0.59	14	2.13	0.37	7.5×10^{-9}	2.5×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HPR	Brain Putamen basal ganglia	0.33	12	2.83	0.49	7.8×10^{-9}	2.5×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
MPV17	Ovary	0.15	34	-6.83	1.19	1.0×10^{-8}	3.2×10^{-5}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
HPR	Brain Caudate basal ganglia	0.43	37	2.08	0.36	1.1×10^{-8}	3.4×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HPR	Brain Frontal Cortex BA9	0.42	13	2.44	0.43	1.2×10^{-8}	3.8×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HPR	Heart Atrial Appendage	0.16	27	3.69	0.65	1.2×10^{-8}	3.8×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
FNDC4	Thyroid	0.27	55	-2.89	0.51	1.3×10^{-8}	3.9×10^{-5}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
SPC24	Skin Not Sun Exposed Suprapubic	0.04	25	8.34	1.47	1.3×10^{-8}	4.1×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
CLCC1	Heart Left Ventricle	0.09	36	5.33	0.94	1.6×10^{-8}	4.7×10^{-5}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
YIPF2	Skin Sun Exposed Lower leg	0.01	15	13.15	2.33	1.6×10^{-8}	4.8×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HPR	Brain Anterior cingulate cortex BA24	0.60	38	1.91	0.34	1.7×10^{-8}	4.9×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
ANKDD1B	Skin Not Sun Exposed Suprapubic	0.14	13	-4.84	0.86	1.9×10^{-8}	5.5×10^{-5}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
AC067959.1	Colon Sigmoid	0.08	73	-4.43	0.79	2.0×10^{-8}	5.6×10^{-5}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
HPR	Brain Cerebellar Hemisphere	0.60	14	1.97	0.35	2.1×10^{-8}	6.1×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HP	Brain Anterior cingulate cortex BA24	0.06	11	6.23	1.12	2.4×10^{-8}	6.6×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
RELB	Lung	0.01	24	9.88	1.77	2.6×10^{-8}	7.1×10^{-5}	rs7412 (pval=1.55×10^{-90})	APOE region
TXNL4B	Brain Caudate basal ganglia	0.14	6	8.43	1.53	3.6×10^{-8}	9.8×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
GEMIN7	Ovary	0.10	37	5.37	0.98	4.1×10^{-8}	1.1×10^{-4}	rs7412 (pval=1.55×10^{-90})	APOE region
HPR	Heart Left Ventricle	0.18	18	4.68	0.86	4.7×10^{-8}	1.3×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
ZNF69	Pituitary	0.08	27	6.41	1.18	5.5×10^{-8}	1.4×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
SORT1	Esophagus Mucosa	0.06	15	-7.47	1.38	6.0×10^{-8}	1.6×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ANKDD1B	Brain Cerebellar Hemisphere	0.05	11	-8.08	1.50	6.4×10^{-8}	1.7×10^{-4}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
HPR	Brain Spinal cord cervical c-1	0.27	27	3.09	0.57	7.6×10^{-8}	2.0×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
PSMA5	Uterus	0.06	31	6.04	1.13	9.2×10^{-8}	2.3×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ATG4C	Brain Cerebellum	0.17	43	-4.50	0.85	1.1×10^{-7}	2.7×10^{-4}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
HMGCR	Small Intestine Terminal Ileum	0.06	21	4.99	0.94	1.1×10^{-7}	2.7×10^{-4}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
EMILIN1	Uterus	0.07	12	-8.67	1.63	1.1×10^{-7}	2.8×10^{-4}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
DOCK7	Ovary	0.06	33	3.63	0.69	1.3×10^{-7}	3.1×10^{-4}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
CEACAM19	Adipose Visceral Omentum	0.20	15	4.37	0.83	1.3×10^{-7}	3.2×10^{-4}	rs7412 (pval=1.55×10^{-90})	APOE region
HPR	Brain Amygdala	0.53	17	2.28	0.43	1.4×10^{-7}	3.2×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
ATG4D	Muscle Skeletal	0.01	17	13.70	2.60	1.4×10^{-7}	3.4×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
FDX1L	DGN-WB	0.00	7	31.32	6.02	1.9×10^{-7}	4.6×10^{-4}	rs17248727 (pval=7.18×10^{-41})	pval=2×10^{-281} (Klarin, 30275531)
HP	Brain Caudate basal ganglia	0.06	18	5.46	1.05	2.0×10^{-7}	4.7×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
ABCA1	Liver	0.04	5	11.59	2.23	2.1×10^{-7}	4.9×10^{-4}	rs62568182 (pval=4.62×10^{-10})	rs1883025 pval=4×10^{-64} (Spracklen, 28334899)
C19orf52	Pancreas	0.05	23	5.08	0.98	2.2×10^{-7}	5.0×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
GATAD2A	Esophagus Mucosa	0.04	17	-9.41	1.82	2.3×10^{-7}	5.3×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
RP11-288H12.3	Skin Sun Exposed Lower leg	0.05	20	8.21	1.59	2.4×10^{-7}	5.4×10^{-4}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
ALDH1A2	Liver	0.13	17	-7.42	1.44	2.5×10^{-7}	5.6×10^{-4}	rs10468017 (pval=6.54×10^{-13})	rs7350789 pval=4×10^{-78} (Klarin, 30275531)
TMED1	Brain Amygdala	0.10	2	10.06	1.96	2.8×10^{-7}	6.2×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
TXNL4B	Brain Anterior cingulate cortex BA24	0.09	16	4.00	0.78	2.9×10^{-7}	6.4×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
SORT1	Skin Sun Exposed Lower leg	0.03	14	-8.12	1.59	3.0×10^{-7}	6.6×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ZNF513	Muscle Skeletal	0.01	1	49.24	9.62	3.0×10^{-7}	6.6×10^{-4}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
SMARCA4	Skin Not Sun Exposed Suprapubic	0.11	21	5.54	1.09	3.2×10^{-7}	6.9×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATXN7L2	Liver	0.29	60	-2.49	0.49	3.3×10^{-7}	7.0×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SUGP1	DGN-WB	0.02	22	9.81	1.93	3.9×10^{-7}	8.1×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
TXNL4B	Brain Putamen basal ganglia	0.05	12	5.67	1.12	4.1×10^{-7}	8.7×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
TXNL4B	Brain Amygdala	0.13	11	5.34	1.05	4.2×10^{-7}	8.7×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HPR	Brain Hypothalamus	0.40	70	1.45	0.29	4.3×10^{-7}	8.9×10^{-4}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
BRE	Thyroid	0.04	8	9.56	1.90	4.7×10^{-7}	9.5×10^{-4}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
KANK2	Brain Cerebellar Hemisphere	0.05	3	16.94	3.37	4.9×10^{-7}	9.8×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
GSTM1	Muscle Skeletal	0.25	72	3.59	0.71	4.9×10^{-7}	9.9×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SMARCA4	Esophagus Gastroesophageal Junction	0.04	6	15.02	3.00	5.5×10^{-7}	1.1×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATXN7L2	Stomach	0.05	31	-6.11	1.22	6.1×10^{-7}	1.2×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ST3GAL4	Stomach	0.06	48	4.61	0.93	6.2×10^{-7}	1.2×10^{-3}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
ZNF625	Lung	0.03	2	13.73	2.76	6.6×10^{-7}	1.3×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs2278426 pval=8×10^{-32} (Kanai, 29403010)
KANK2	Brain Nucleus accumbens basal ganglia	0.19	3	5.81	1.17	7.0×10^{-7}	1.3×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ANKDD1B	Brain Cortex	0.10	12	-5.51	1.11	7.0×10^{-7}	1.3×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
AC069278.4	Thyroid	0.02	24	-8.10	1.64	7.8×10^{-7}	1.5×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
LPA	Liver	0.18	120	2.42	0.49	9.2×10^{-7}	1.7×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
CCDC159	Spleen	0.03	5	-9.72	1.99	1.1×10^{-6}	2.0×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
MAU2	Whole Blood	0.05	25	5.54	1.14	1.1×10^{-6}	2.0×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
SMARCA4	Colon Transverse	0.03	4	15.98	3.28	1.1×10^{-6}	2.0×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
HPR	Brain Substantia nigra	0.47	44	1.97	0.41	1.2×10^{-6}	2.3×10^{-3}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
PVRL2	Muscle Skeletal	0.12	23	-3.75	0.77	1.2×10^{-6}	2.3×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
TMED1	Esophagus Mucosa	0.03	18	7.35	1.52	1.3×10^{-6}	2.3×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
PSRC1	Artery Aorta	0.15	26	-4.11	0.85	1.3×10^{-6}	2.3×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
HAVCR1	DGN-WB	0.01	13	12.58	2.61	1.4×10^{-6}	2.5×10^{-3}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
RP11-288H12.3	Breast Mammary Tissue	0.03	25	6.68	1.39	1.5×10^{-6}	2.7×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
GATAD2A	Skin Not Sun Exposed Suprapubic	0.04	5	-11.34	2.36	1.6×10^{-6}	2.8×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
C18orf32	Skin Sun Exposed Lower leg	0.01	35	7.17	1.50	1.6×10^{-6}	2.9×10^{-3}	NA	rs77960347 pval=1×10^{-39} (Klarin, 30275531)
C19orf52	DGN-WB	0.06	6	9.21	1.93	1.7×10^{-6}	3.0×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
COL4A3BP	Esophagus Mucosa	0.05	16	-5.48	1.16	2.2×10^{-6}	3.7×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
PSRC1	Artery Tibial	0.03	9	-7.87	1.67	2.6×10^{-6}	4.5×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
AP1G1	Testis	0.05	58	3.23	0.69	2.7×10^{-6}	4.5×10^{-3}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
CEACAM19	Adrenal Gland	0.13	75	3.05	0.65	2.8×10^{-6}	4.7×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
GEMIN7	Uterus	0.08	54	-1.94	0.42	2.9×10^{-6}	4.9×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
GALNT6	Whole Blood	0.19	11	-3.73	0.80	2.9×10^{-6}	4.9×10^{-3}	NA	NA
ZNF20	Skin Not Sun Exposed Suprapubic	0.02	37	5.59	1.20	3.1×10^{-6}	5.1×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs2738464 pval=8×10^{-49} (Kanai, 29403010)
AP1M2	Adipose Visceral Omentum	0.08	32	-4.67	1.01	3.4×10^{-6}	5.6×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ZNF259	Skin Sun Exposed Lower leg	0.02	21	-8.75	1.88	3.4×10^{-6}	5.6×10^{-3}	rs964184 (pval=2.84×10^{-13})	rs3135506 pval=2×10^{-93} (Klarin, 30275531)
BCAM	Skin Not Sun Exposed Suprapubic	0.02	10	-8.29	1.79	3.7×10^{-6}	6.0×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
SMARCA4	Nerve Tibial	0.01	25	6.34	1.38	4.1×10^{-6}	6.6×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
CEACAM19	Stomach	0.29	27	3.17	0.69	4.1×10^{-6}	6.6×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
TRIM54	Brain Anterior cingulate cortex BA24	0.10	24	-4.14	0.90	4.3×10^{-6}	6.9×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
SMARCA4	Adipose Subcutaneous	0.05	28	5.84	1.27	4.4×10^{-6}	7.0×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
POLK	Brain Cerebellar Hemisphere	0.17	11	4.32	0.94	4.7×10^{-6}	7.5×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
C19orf52	Stomach	0.08	40	4.39	0.96	5.2×10^{-6}	8.2×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
TXNL4B	Brain Cortex	0.17	15	3.65	0.80	5.4×10^{-6}	8.4×10^{-3}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
SMARCA4	Adipose Visceral Omentum	0.08	17	5.36	1.18	5.5×10^{-6}	8.6×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
CTC-366B18.4	Brain Hypothalamus	0.06	53	-3.53	0.78	5.7×10^{-6}	8.8×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
ZNF285B	Brain Cerebellar Hemisphere	0.06	59	3.24	0.71	5.8×10^{-6}	8.9×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
CTD-2235C13.3	Esophagus Mucosa	0.01	55	-5.15	1.14	5.8×10^{-6}	8.9×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
KRTCAP3	Brain Caudate basal ganglia	0.08	25	-4.12	0.91	5.9×10^{-6}	8.9×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
TBKBP1	Prostate	0.21	33	-3.28	0.72	6.0×10^{-6}	9.0×10^{-3}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
APOC1	Skin Sun Exposed Lower leg	0.03	12	-6.68	1.48	6.3×10^{-6}	9.5×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
ZNF653	Brain Amygdala	0.10	70	2.79	0.62	6.4×10^{-6}	9.6×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
TMEM258	Artery Tibial	0.04	24	-6.83	1.51	6.5×10^{-6}	9.6×10^{-3}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
CKM	DGN-WB	0.40	61	-1.90	0.42	6.7×10^{-6}	9.9×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
CEACAM19	Artery Aorta	0.17	23	4.05	0.90	6.8×10^{-6}	1.0×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
DMPK	Esophagus Gastroesophageal Junction	0.03	62	-3.36	0.75	6.9×10^{-6}	1.0×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
HAVCR1	Thyroid	0.09	13	6.22	1.38	7.0×10^{-6}	1.0×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
ST3GAL4	Esophagus Muscularis	0.03	6	8.62	1.92	7.1×10^{-6}	1.0×10^{-2}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
APOC2	Skin Not Sun Exposed Suprapubic	0.04	47	4.61	1.03	8.0×10^{-6}	1.2×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
MRPL45P2	Adipose Subcutaneous	0.16	72	3.15	0.71	8.1×10^{-6}	1.2×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
POP5	Pituitary	0.03	63	3.17	0.71	8.3×10^{-6}	1.2×10^{-2}	NA	rs1169288 pval=2×10^{-30} (Klarin, 30275531)
ITPR2	Brain Cerebellar Hemisphere	0.47	74	1.78	0.40	9.4×10^{-6}	1.3×10^{-2}	NA	NA
UGT2B29P	Cells EBV-transformed lymphocytes	0.17	46	-2.83	0.64	9.4×10^{-6}	1.3×10^{-2}	NA	rs969114 pval=1×10^{-26} (Klarin, 30275531)
MAU2	Esophagus Mucosa	0.03	34	6.09	1.38	9.6×10^{-6}	1.3×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
CYP2W1	Colon Transverse	0.11	17	-4.65	1.05	9.7×10^{-6}	1.3×10^{-2}	NA	rs2362529 pval=8×10^{-19} (Klarin, 30275531)
CHMP4A	Muscle Skeletal	0.06	61	-4.27	0.97	1.0×10^{-5}	1.4×10^{-2}	NA	rs11621792 pval=3×10^{-12} (Hoffmann, 29507422)
AC144652.1	Brain Nucleus accumbens basal ganglia	0.08	32	3.23	0.73	1.0×10^{-5}	1.4×10^{-2}	NA	NA
PVRL2	Artery Aorta	0.08	11	-5.93	1.34	1.0×10^{-5}	1.4×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
ANKDD1B	Colon Sigmoid	0.03	24	-5.30	1.20	1.0×10^{-5}	1.4×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
RP11-288H12.3	Lung	0.02	6	14.73	3.34	1.0×10^{-5}	1.4×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
ST3GAL4	Cells EBV-transformed lymphocytes	0.22	4	3.86	0.88	1.1×10^{-5}	1.4×10^{-2}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
GCNT4	Artery Coronary	0.11	28	-4.10	0.93	1.1×10^{-5}	1.4×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
GPN1	Testis	0.07	35	-4.15	0.94	1.1×10^{-5}	1.5×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ZNF593	Brain Hypothalamus	0.06	25	-4.05	0.92	1.1×10^{-5}	1.5×10^{-2}	NA	rs10903129 pval=3×10^{-16} (Spracklen, 28334899)
ST3GAL4	Muscle Skeletal	0.20	27	3.11	0.71	1.2×10^{-5}	1.5×10^{-2}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
ATP13A1	Adrenal Gland	0.05	54	-2.58	0.59	1.2×10^{-5}	1.5×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
TMEM258	Artery Aorta	0.03	9	-4.97	1.13	1.2×10^{-5}	1.6×10^{-2}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
GPN1	Muscle Skeletal	0.06	27	4.61	1.06	1.3×10^{-5}	1.7×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
NRBP1	Esophagus Gastroesophageal Junction	0.05	22	6.15	1.41	1.4×10^{-5}	1.8×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
POLK	Nerve Tibial	0.11	14	5.21	1.20	1.4×10^{-5}	1.9×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
NLRC5	Cells Transformed fibroblasts	0.38	33	-2.10	0.49	1.5×10^{-5}	1.9×10^{-2}	NA	rs183130 pval=1×10^{-84} (Klarin, 30275531)
GATAD2A	Skin Sun Exposed Lower leg	0.05	19	-6.59	1.52	1.5×10^{-5}	2.0×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ST3GAL4	Pancreas	0.26	16	2.99	0.69	1.5×10^{-5}	2.0×10^{-2}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
APOC1	Adrenal Gland	0.09	3	-7.86	1.82	1.6×10^{-5}	2.0×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
TBKBP1	Small Intestine Terminal Ileum	0.27	34	-2.29	0.53	1.6×10^{-5}	2.0×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
POLK	Pancreas	0.10	50	6.38	1.48	1.6×10^{-5}	2.0×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
MRPL45P2	Skin Not Sun Exposed Suprapubic	0.21	30	2.69	0.63	1.7×10^{-5}	2.1×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
SYPL2	Brain Cerebellar Hemisphere	0.23	50	-3.18	0.74	1.8×10^{-5}	2.2×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
GALNT6	DGN-WB	0.30	23	-2.34	0.54	1.8×10^{-5}	2.2×10^{-2}	NA	NA
CDPF1	Brain Anterior cingulate cortex BA24	0.06	58	3.17	0.74	1.8×10^{-5}	2.2×10^{-2}	NA	rs4253772 pval=1×10^{-08} (Willer, 24097068)
PRDM2	Stomach	0.03	18	10.99	2.56	1.8×10^{-5}	2.2×10^{-2}	NA	NA
EFCAB13	Brain Spinal cord cervical c-1	0.19	27	3.43	0.80	1.9×10^{-5}	2.2×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
POLK	Thyroid	0.06	25	7.25	1.69	1.9×10^{-5}	2.2×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
MVP	Nerve Tibial	0.10	16	-3.79	0.89	1.9×10^{-5}	2.3×10^{-2}	NA	NA
HAVCR1	Adipose Subcutaneous	0.18	14	3.92	0.92	1.9×10^{-5}	2.3×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
NPEPPS	Whole Blood	0.02	19	-7.89	1.85	2.0×10^{-5}	2.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HAVCR1	Lung	0.18	8	3.92	0.92	2.1×10^{-5}	2.4×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
MTCH2	Artery Tibial	0.01	6	-10.90	2.56	2.1×10^{-5}	2.5×10^{-2}	NA	rs555328608 pval=1×10^{-09} (Klarin, 30275531)
MRPL33	Brain Caudate basal ganglia	0.04	7	19.88	4.67	2.1×10^{-5}	2.5×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
PSRC1	Thyroid	0.32	29	-2.40	0.56	2.1×10^{-5}	2.5×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
POLK	Brain Cerebellum	0.13	27	5.62	1.32	2.2×10^{-5}	2.5×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
APOB	Prostate	0.06	67	-2.86	0.67	2.2×10^{-5}	2.6×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
SLC22A1	Thyroid	0.15	96	-2.53	0.60	2.3×10^{-5}	2.6×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
ERCC1	Ovary	0.17	53	-2.43	0.58	2.4×10^{-5}	2.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
MRPL45P2	Cells Transformed fibroblasts	0.28	24	2.72	0.64	2.4×10^{-5}	2.7×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
GDF7	Adrenal Gland	0.10	8	5.16	1.22	2.4×10^{-5}	2.7×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
NRBP1	Artery Tibial	0.06	57	3.52	0.83	2.4×10^{-5}	2.7×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
CETP	Esophagus Mucosa	0.02	7	-13.46	3.19	2.4×10^{-5}	2.7×10^{-2}	NA	rs183130 pval=1×10^{-84} (Klarin, 30275531)
GSTM1	Thyroid	0.22	105	2.75	0.65	2.5×10^{-5}	2.8×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
MRPL45P2	Minor Salivary Gland	0.08	33	3.12	0.74	2.5×10^{-5}	2.8×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
ANGPTL3	Liver	0.18	46	3.25	0.77	2.5×10^{-5}	2.8×10^{-2}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
APOE	Skin Sun Exposed Lower leg	0.13	10	-4.00	0.95	2.6×10^{-5}	2.8×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
HMGN2P19	Colon Sigmoid	0.24	95	1.77	0.42	2.6×10^{-5}	2.9×10^{-2}	NA	NA
CELSR2	Lung	0.03	5	9.99	2.38	2.6×10^{-5}	2.9×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
DNAH11	Liver	0.27	12	2.98	0.71	2.7×10^{-5}	2.9×10^{-2}	NA	rs66476925 pval=9×10^{-19} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DOK7	Adipose Visceral Omentum	0.04	10	-6.54	1.56	2.7×10^{-5}	2.9×10^{-2}	NA	rs59950280 pval=4×10^{-12} (Klarin, 30275531)
ZNF513	Brain Amygdala	0.06	48	3.26	0.78	2.7×10^{-5}	2.9×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
MKRN2	Heart Left Ventricle	0.29	22	-2.52	0.60	2.7×10^{-5}	2.9×10^{-2}	NA	rs7616006 pval=1×10^{-18} (Spracklen, 28334899)
EFCAB13	Artery Coronary	0.15	16	4.15	0.99	2.8×10^{-5}	3.0×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
RP11-288H12.3	Muscle Skeletal	0.07	55	4.03	0.96	2.8×10^{-5}	3.0×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
PSRC1	Adipose Subcutaneous	0.08	5	-6.59	1.57	2.8×10^{-5}	3.0×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
MRPL45P2	Artery Tibial	0.19	21	2.93	0.70	2.8×10^{-5}	3.0×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
ANKDD1B	Brain Cerebellum	0.06	27	-3.70	0.89	2.9×10^{-5}	3.1×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
WTAP	Minor Salivary Gland	0.06	138	1.38	0.33	2.9×10^{-5}	3.1×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
MRPL45P2	Colon Sigmoid	0.12	36	3.42	0.82	2.9×10^{-5}	3.1×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
HAVCR1	Artery Coronary	0.11	14	7.55	1.81	3.0×10^{-5}	3.1×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
MRPL45P2	Adrenal Gland	0.26	12	3.34	0.80	3.0×10^{-5}	3.2×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
PPM1G	Muscle Skeletal	0.02	24	5.58	1.34	3.1×10^{-5}	3.3×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
LOC100421166	Brain Spinal cord cervical c-1	0.17	23	3.17	0.76	3.2×10^{-5}	3.3×10^{-2}	rs740516 (pval=2.95×10^{-09})	rs77542162 pval=2×10^{-33} (Klarin, 30275531)
MRPL45P2	Skin Sun Exposed Lower leg	0.33	14	2.35	0.56	3.3×10^{-5}	3.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
MRPL45P2	Breast Mammary Tissue	0.10	13	6.35	1.53	3.3×10^{-5}	3.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
TBKBP1	Colon Transverse	0.12	14	-4.41	1.06	3.3×10^{-5}	3.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
CTD-2235C13.3	Skin Not Sun Exposed Suprapubic	0.10	37	-4.12	0.99	3.3×10^{-5}	3.4×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MRPL45P2	Muscle Skeletal	0.16	19	3.47	0.84	3.4×10^{-5}	3.5×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
KPNA3	Testis	0.03	19	6.58	1.59	3.6×10^{-5}	3.7×10^{-2}	NA	rs4942859 pval=3×10^{-08} (Klarin, 30275531)
ZNF259	DGN-WB	0.02	24	-8.43	2.04	3.7×10^{-5}	3.7×10^{-2}	rs964184 (pval=2.84×10^{-13})	rs3135506 pval=2×10^{-93} (Klarin, 30275531)
SMARCA4	Cells Transformed fibroblasts	0.02	27	5.98	1.45	3.7×10^{-5}	3.8×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
MRPL45P2	Pancreas	0.17	21	3.36	0.82	3.8×10^{-5}	3.8×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
MRPL45P2	Esophagus Mucosa	0.25	10	2.91	0.71	3.8×10^{-5}	3.8×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
TBKBP1	Cells EBV-transformed lymphocytes	0.17	14	-3.39	0.83	4.0×10^{-5}	4.0×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
UGT2B15	Cells EBV-transformed lymphocytes	0.31	31	-2.42	0.59	4.0×10^{-5}	4.0×10^{-2}	NA	rs969114 pval=1×10^{-26} (Klarin, 30275531)
FUT2	Brain Anterior cingulate cortex BA24	0.10	36	3.70	0.90	4.1×10^{-5}	4.0×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
POLK	Brain Nucleus accumbens basal ganglia	0.06	13	6.59	1.61	4.1×10^{-5}	4.0×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
MRPL45P2	Brain Anterior cingulate cortex BA24	0.11	37	2.55	0.62	4.1×10^{-5}	4.0×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
ADPRHL2	Artery Aorta	0.08	36	4.37	1.07	4.1×10^{-5}	4.0×10^{-2}	NA	NA
TMEM258	Muscle Skeletal	0.02	15	-5.74	1.40	4.2×10^{-5}	4.0×10^{-2}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
CARM1	Thyroid	0.03	24	-6.01	1.47	4.2×10^{-5}	4.1×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
AC074117.13	Skin Sun Exposed Lower leg	0.02	1	14.30	3.50	4.3×10^{-5}	4.1×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
EPOR	Heart Left Ventricle	0.03	18	5.54	1.36	4.3×10^{-5}	4.1×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
AC006126.4	Testis	0.12	22	-3.69	0.90	4.3×10^{-5}	4.1×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
AC012065.7	Esophagus Muscularis	0.14	52	2.88	0.71	4.4×10^{-5}	4.1×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
ZNF155	Minor Salivary Gland	0.08	62	-2.24	0.55	4.4×10^{-5}	4.1×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
POC5	Testis	0.15	30	-3.69	0.90	4.4×10^{-5}	4.2×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
ERCC2	Esophagus Gastroesophageal Junction	0.04	10	-8.54	2.09	4.5×10^{-5}	4.3×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
C18orf32	Brain Cerebellar Hemisphere	0.05	6	11.86	2.91	4.6×10^{-5}	4.3×10^{-2}	NA	rs77960347 pval=1×10^{-39} (Klarin, 30275531)
ZNF781	Colon Transverse	0.19	44	2.94	0.72	4.6×10^{-5}	4.3×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
ZNF283	Brain Cerebellum	0.14	81	-2.17	0.53	4.7×10^{-5}	4.4×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
MRPL45P2	Artery Coronary	0.10	17	4.30	1.06	4.7×10^{-5}	4.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
ZNF221	Ovary	0.11	25	-4.84	1.19	4.8×10^{-5}	4.4×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
MROH2A	Colon Transverse	0.12	34	3.86	0.95	4.8×10^{-5}	4.4×10^{-2}	NA	rs35754645 pval=3×10^{-13} (Klarin, 30275531)
TBKBP1	Artery Tibial	0.39	42	-1.87	0.46	4.8×10^{-5}	4.4×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
ITPRIP	Brain Anterior cingulate cortex BA24	0.06	28	-4.12	1.01	4.9×10^{-5}	4.5×10^{-2}	NA	NA
TXNL4B	Brain Substantia nigra	0.10	18	2.87	0.71	4.9×10^{-5}	4.5×10^{-2}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
UGT2B7	Liver	0.07	62	-2.34	0.58	5.0×10^{-5}	4.5×10^{-2}	NA	rs969114 pval=1×10^{-26} (Klarin, 30275531)
CETP	Lung	0.05	10	-7.19	1.77	5.0×10^{-5}	4.5×10^{-2}	NA	rs183130 pval=1×10^{-84} (Klarin, 30275531)
HAVCR1	Skin Not Sun Exposed Suprapubic	0.08	19	6.73	1.66	5.0×10^{-5}	4.5×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
POLK	Spleen	0.18	73	2.75	0.68	5.0×10^{-5}	4.5×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
TBKBP1	Stomach	0.15	19	-4.22	1.04	5.2×10^{-5}	4.6×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
CLINT1	Adipose Subcutaneous	0.02	16	-10.76	2.66	5.2×10^{-5}	4.6×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
SYPL2	Liver	0.45	44	-1.73	0.43	5.2×10^{-5}	4.6×10^{-2}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
ZNF512	DGN-WB	0.01	23	9.67	2.39	5.2×10^{-5}	4.6×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ABCA6	Brain Nucleus accumbens basal ganglia	0.11	17	3.61	0.89	5.2×10^{-5}	4.6×10^{-2}	rs740516 (pval=2.95×10^{-09})	rs77542162 pval=2×10^{-33} (Klarin, 30275531)
SEZ6L2	Thyroid	0.02	27	-5.24	1.30	5.3×10^{-5}	4.7×10^{-2}	NA	NA
MARK4	Muscle Skeletal	0.19	7	-3.00	0.74	5.3×10^{-5}	4.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
POLK	Ovary	0.10	11	8.13	2.02	5.4×10^{-5}	4.8×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
SLC22A1	Artery Tibial	0.02	9	-9.44	2.34	5.5×10^{-5}	4.8×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
ZNF225	DGN-WB	0.01	38	7.56	1.88	5.6×10^{-5}	4.9×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
BPGM	Artery Tibial	0.03	29	-5.01	1.24	5.7×10^{-5}	4.9×10^{-2}	NA	NA
TBKBP1	Heart Atrial Appendage	0.079	23	-3.90	0.97	5.7×10^{-5}	4.9×10^{-2}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)

Appendix VIII. Tissue-specific GReX results of the genes significantly associated with TG in BioVU

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
LPL	Nerve Tibial	0.14	33	-0.17	0.01	3.1×10^{-36}	8.0×10^{-31}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
LPL	Whole Blood	0.05	11	-0.25	0.02	4.2×10^{-35}	5.5×10^{-30}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
LPL	DGN-WB	0.30	66	-0.08	0.01	1.1×10^{-25}	9.5×10^{-21}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
LPL	Adipose Subcutaneous	0.07	24	-0.16	0.02	3.1×10^{-23}	2.0×10^{-18}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	Adipose Subcutaneous	0.05	29	-0.11	0.01	1.4×10^{-22}	7.2×10^{-18}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
ZNF259	Skin Sun Exposed Lower leg	0.02	21	-0.24	0.02	2.7×10^{-22}	1.2×10^{-17}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ZNF259	DGN-WB	0.02	24	-0.25	0.03	7.0×10^{-21}	2.6×10^{-16}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	Pancreas	0.17	18	-0.10	0.01	3.0×10^{-20}	9.7×10^{-16}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
RP11-373D23.3	Pituitary	0.06	7	0.25	0.03	4.9×10^{-20}	1.4×10^{-15}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Pituitary	0.07	13	-0.18	0.02	1.2×10^{-19}	3.1×10^{-15}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
EMILIN1	Uterus	0.07	12	-0.19	0.02	1.8×10^{-19}	4.4×10^{-15}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Esophagus Muscularis	0.12	30	-0.09	0.01	1.2×10^{-18}	2.5×10^{-14}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Skin Not Sun Exposed Suprapubic	0.30	34	-0.05	0.01	1.6×10^{-18}	3.2×10^{-14}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Thyroid	0.22	8	-0.07	0.01	4.7×10^{-18}	8.7×10^{-14}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Esophagus Mucosa	0.06	6	-0.16	0.02	5.0×10^{-18}	8.7×10^{-14}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
ZNF513	Brain Anterior cingulate cortex BA24	0.10	31	0.09	0.01	1.3×10^{-17}	2.1×10^{-13}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MLXIPL	Cells Transformed fibroblasts	0.15	36	-0.08	0.01	1.6×10^{-17}	2.4×10^{-13}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Minor Salivary Gland	0.08	12	-0.12	0.01	2.9×10^{-17}	4.2×10^{-13}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
BRE	Thyroid	0.04	8	0.21	0.02	6.0×10^{-17}	7.9×10^{-13}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GTF2IRD1	Skin Sun Exposed Lower leg	0.01	9	0.37	0.04	6.1×10^{-17}	7.9×10^{-13}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
ZNF513	Muscle Skeletal	0.01	1	1.04	0.13	8.9×10^{-17}	1.1×10^{-12}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
BCL7B	DGN-WB	0.00	3	0.63	0.08	1.0×10^{-16}	1.2×10^{-12}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
LZTS1	Uterus	0.09	49	0.08	0.01	1.7×10^{-16}	1.9×10^{-12}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	Skin Sun Exposed Lower leg	0.24	36	-0.05	0.01	2.4×10^{-16}	2.6×10^{-12}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Prostate	0.17	29	-0.08	0.01	2.7×10^{-16}	2.8×10^{-12}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
NRBP1	Esophagus Gastroesophageal Junction	0.05	22	0.15	0.02	7.4×10^{-16}	7.4×10^{-12}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
FNDC4	Thyroid	0.27	55	-0.05	0.01	2.5×10^{-15}	2.4×10^{-11}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GCKR	Thyroid	0.15	16	-0.09	0.01	3.2×10^{-15}	3.0×10^{-11}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
NRBP1	Artery Tibial	0.06	57	0.09	0.01	3.4×10^{-15}	3.0×10^{-11}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Esophagus Gastroesophageal Junction	0.17	16	-0.07	0.01	5.0×10^{-15}	4.3×10^{-11}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	Heart Left Ventricle	0.06	17	-0.12	0.02	5.2×10^{-15}	4.3×10^{-11}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
APOE	Skin Sun Exposed Lower leg	0.13	10	-0.10	0.01	1.7×10^{-14}	1.4×10^{-10}	rs584007 (pval=2.22×10^{-14})	APOE region
MPV17	Ovary	0.15	34	-0.12	0.02	2.1×10^{-14}	1.7×10^{-10}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
APOC1	Adrenal Gland	0.09	3	-0.18	0.02	7.9×10^{-14}	6.0×10^{-10}	rs584007 (pval=2.22×10^{-14})	APOE region

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MLXIPL	Breast Mammary Tissue	0.09	32	-0.06	0.01	1.0×10^{-13}	7.7×10^{-10}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
ATP6V1B2	Spleen	0.11	58	-0.06	0.01	1.2×10^{-13}	8.9×10^{-10}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	Lung	0.19	10	-0.08	0.01	3.3×10^{-13}	2.3×10^{-9}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
INTS10	DGN-WB	0.11	30	-0.15	0.02	4.7×10^{-13}	3.2×10^{-9}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
ZNF512	DGN-WB	0.01	23	0.22	0.03	8.8×10^{-13}	5.9×10^{-9}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
APOE	Skin Not Sun Exposed Suprapubic	0.18	23	-0.07	0.01	1.0×10^{-12}	6.7×10^{-9}	rs584007 (pval=2.22×10^{-14})	APOE region
GPN1	Muscle Skeletal	0.06	27	0.10	0.01	1.9×10^{-12}	1.2×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
SNX17	DGN-WB	0.01	19	-0.23	0.03	1.9×10^{-12}	1.2×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10OS	Prostate	0.17	19	-0.16	0.02	4.2×10^{-12}	2.6×10^{-8}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
GPN1	Testis	0.07	35	-0.09	0.01	4.4×10^{-12}	2.6×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Adipose Visceral Omentum	0.04	23	-0.12	0.02	7.4×10^{-12}	4.3×10^{-8}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
CCDC92	Breast Mammary Tissue	0.19	34	-0.07	0.01	7.7×10^{-12}	4.3×10^{-8}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Esophagus Mucosa	0.08	22	-0.10	0.02	1.2×10^{-11}	6.7×10^{-8}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
LPL	Skin Not Sun Exposed Suprapubic	0.04	11	-0.20	0.03	2.6×10^{-11}	1.4×10^{-7}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	Testis	0.07	16	-0.08	0.01	3.1×10^{-11}	1.6×10^{-7}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
DNAH10	DGN-WB	0.01	7	-0.45	0.07	4.4×10^{-11}	2.2×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
USP1	Adrenal Gland	0.06	27	0.09	0.01	4.4×10^{-11}	2.2×10^{-7}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
DNAH10OS	Esophagus Mucosa	0.08	14	-0.11	0.02	5.8×10^{-11}	2.9×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DNAH10OS	Esophagus Gastroesophageal Junction	0.27	45	-0.04	0.01	5.9×10^{-11}	2.9×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Pancreas	0.03	12	-0.17	0.03	6.8×10^{-11}	3.2×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Thyroid	0.09	15	-0.09	0.01	6.9×10^{-11}	3.2×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
ZNF664	DGN-WB	0.04	19	0.14	0.02	7.4×10^{-11}	3.3×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
AC074117.13	Skin Sun Exposed Lower leg	0.02	1	0.30	0.05	7.4×10^{-11}	3.3×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
NRBP1	Whole Blood	0.13	17	0.08	0.01	7.5×10^{-11}	3.3×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Skin Sun Exposed Lower leg	0.10	5	0.09	0.01	8.3×10^{-11}	3.6×10^{-7}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
ZNF664	Cells Transformed fibroblasts	0.13	15	0.10	0.02	9.0×10^{-11}	3.9×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
USP1	Nerve Tibial	0.03	5	0.21	0.03	9.1×10^{-11}	3.9×10^{-7}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
NRBP1	Small Intestine Terminal Ileum	0.05	16	0.10	0.02	1.2×10^{-10}	5.1×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10OS	Colon Sigmoid	0.22	31	-0.06	0.01	1.4×10^{-10}	5.6×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Adipose Subcutaneous	0.12	22	-0.09	0.01	1.5×10^{-10}	6.3×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Adrenal Gland	0.19	13	-0.08	0.01	1.7×10^{-10}	6.9×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
SIDT2	Nerve Tibial	0.05	25	-0.11	0.02	1.8×10^{-10}	6.9×10^{-7}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
DNAH10OS	Lung	0.13	8	-0.10	0.02	1.8×10^{-10}	7.1×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Skin Not Sun Exposed Suprapubic	0.02	14	-0.17	0.03	1.9×10^{-10}	7.2×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Skin Not Sun Exposed Suprapubic	0.05	6	-0.18	0.03	1.9×10^{-10}	7.2×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
TRIM74	Whole Blood	0.04	32	-0.09	0.01	2.2×10^{-10}	8.1×10^{-7}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
NRBP1	Skin Sun Exposed Lower leg	0.20	7	0.06	0.01	2.3×10^{-10}	8.3×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Whole Blood	0.07	19	0.10	0.02	2.6×10^{-10}	9.4×10^{-7}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
CAD	Stomach	0.06	26	0.08	0.01	2.8×10^{-10}	1.0×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10OS	Heart Atrial Appendage	0.10	16	-0.12	0.02	3.1×10^{-10}	1.1×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
NRBP1	Liver	0.05	1	0.16	0.03	3.2×10^{-10}	1.1×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
USP1	DGN-WB	0.00	1	0.86	0.14	3.4×10^{-10}	1.1×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
KRTCAP3	Brain Caudate basal ganglia	0.08	25	-0.07	0.01	3.5×10^{-10}	1.2×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Lung	0.02	2	0.31	0.05	3.6×10^{-10}	1.2×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
DNAH10OS	Nerve Tibial	0.13	21	-0.09	0.01	4.0×10^{-10}	1.3×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Adipose Visceral Omentum	0.10	19	-0.10	0.02	4.5×10^{-10}	1.5×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
NRBP1	Testis	0.08	7	0.13	0.02	4.6×10^{-10}	1.5×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CCDC92	Adipose Visceral Omentum	0.25	46	-0.05	0.01	4.7×10^{-10}	1.5×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
TRIM54	Brain Anterior cingulate cortex BA24	0.10	24	-0.07	0.01	5.0×10^{-10}	1.6×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Artery Aorta	0.03	13	0.17	0.03	6.0×10^{-10}	1.9×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
DNAH10OS	Brain Cortex	0.10	27	-0.08	0.01	6.3×10^{-10}	1.9×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
NRBP1	Colon Transverse	0.15	5	0.07	0.01	6.4×10^{-10}	1.9×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Artery Tibial	0.07	14	0.13	0.02	6.8×10^{-10}	2.0×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
ZNF664	Thyroid	0.14	21	0.07	0.01	6.8×10^{-10}	2.0×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
APOC4	Adrenal Gland	0.03	10	-0.12	0.02	6.9×10^{-10}	2.0×10^{-6}	rs584007 (pval=2.22×10^{-14})	APOE region
DOCK7	Skin Not Sun Exposed Suprapubic	0.03	6	0.18	0.03	7.3×10^{-10}	2.1×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
BUD13	DGN-WB	0.03	20	0.17	0.03	7.8×10^{-10}	2.2×10^{-6}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
HLA-DRB5	Breast Mammary Tissue	0.63	41	-0.05	0.01	7.9×10^{-10}	2.2×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DOCK7	DGN-WB	0.20	36	0.06	0.01	8.0×10^{-10}	2.2×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
NRBP1	Cells Transformed fibroblasts	0.20	19	0.07	0.01	8.0×10^{-10}	2.2×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Cells Transformed fibroblasts	0.27	54	0.05	0.01	1.0×10^{-9}	2.8×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
DNAH10OS	Heart Left Ventricle	0.14	28	-0.06	0.01	1.2×10^{-9}	3.3×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
MLXIPL	Heart Atrial Appendage	0.08	37	-0.05	0.01	1.3×10^{-9}	3.5×10^{-6}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
AP006216.11	Cells Transformed fibroblasts	0.04	14	-0.16	0.03	1.3×10^{-9}	3.5×10^{-6}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
DNAH10OS	Skin Sun Exposed Lower leg	0.17	28	-0.07	0.01	1.4×10^{-9}	3.6×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Esophagus Muscularis	0.37	25	-0.04	0.01	1.6×10^{-9}	4.1×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
NRBP1	Artery Aorta	0.06	13	0.09	0.01	1.7×10^{-9}	4.3×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Stomach	0.06	12	-0.10	0.02	1.8×10^{-9}	4.6×10^{-6}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
HLA-DRB5	Pituitary	0.53	38	-0.04	0.01	1.9×10^{-9}	4.9×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SIDT2	Thyroid	0.08	40	-0.08	0.01	2.0×10^{-9}	5.0×10^{-6}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
CCDC92	Heart Left Ventricle	0.30	36	-0.04	0.01	2.1×10^{-9}	5.2×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Artery Aorta	0.12	25	-0.07	0.01	2.2×10^{-9}	5.3×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HLA-DRB6	Brain Cortex	0.48	97	0.04	0.01	2.6×10^{-9}	6.2×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
APOB	Uterus	0.14	28	-0.06	0.01	2.6×10^{-9}	6.2×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1042034 pval=1×10^{-72} (Hoffmann, 29507422)
HLA-DRB5	Nerve Tibial	0.62	39	-0.05	0.01	2.9×10^{-9}	7.0×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC92	Nerve Tibial	0.19	18	-0.06	0.01	3.3×10^{-9}	7.7×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
ATP13A1	Artery Coronary	0.14	11	-0.13	0.02	3.5×10^{-9}	8.3×10^{-6}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
DNAH10OS	Colon Transverse	0.08	30	-0.10	0.02	3.6×10^{-9}	8.4×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC92	Prostate	0.17	13	-0.09	0.01	3.9×10^{-9}	8.9×10^{-6}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10	Artery Tibial	0.08	18	-0.09	0.02	5.2×10^{-9}	1.2×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
DNAH10OS	Thyroid	0.08	24	-0.08	0.01	6.5×10^{-9}	1.5×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
AGER	Heart Left Ventricle	0.03	6	0.17	0.03	7.0×10^{-9}	1.6×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DNAH10OS	Artery Tibial	0.26	47	-0.04	0.01	7.1×10^{-9}	1.6×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
NRBP1	DGN-WB	0.11	26	0.07	0.01	7.2×10^{-9}	1.6×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
PPM1G	Muscle Skeletal	0.02	24	0.10	0.02	7.4×10^{-9}	1.6×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GPN1	Heart Left Ventricle	0.06	19	0.10	0.02	9.4×10^{-9}	2.0×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10	Testis	0.08	40	-0.08	0.01	9.9×10^{-9}	2.1×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HLA-DRB5	Spleen	0.53	14	-0.05	0.01	1.1×10^{-8}	2.4×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DNAH10OS	Testis	0.07	35	-0.06	0.01	1.1×10^{-8}	2.4×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HLA-DRB5	Heart Atrial Appendage	0.56	43	-0.04	0.01	1.2×10^{-8}	2.4×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HLA-DRB5	Artery Tibial	0.66	73	-0.04	0.01	1.2×10^{-8}	2.5×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SNX17	Brain Putamen basal ganglia	0.07	9	-0.08	0.01	1.3×10^{-8}	2.7×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
NRBP1	Cells EBV-transformed lymphocytes	0.12	5	0.09	0.02	1.4×10^{-8}	3.0×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TRIM50	Thyroid	0.03	13	-0.14	0.02	1.5×10^{-8}	3.0×10^{-5}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
NRBP1	Skin Not Sun Exposed Suprapubic	0.24	30	0.04	0.01	1.5×10^{-8}	3.0×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Artery Aorta	0.64	58	-0.04	0.01	1.6×10^{-8}	3.1×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ATP13A1	Artery Aorta	0.14	18	-0.07	0.01	1.6×10^{-8}	3.2×10^{-5}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-DRB5	Esophagus Mucosa	0.60	34	-0.04	0.01	1.7×10^{-8}	3.4×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Adipose Visceral Omentum	0.66	33	-0.04	0.01	2.2×10^{-8}	4.3×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Stomach	0.59	79	-0.03	0.01	2.2×10^{-8}	4.3×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZNF664	Heart Atrial Appendage	0.09	29	-0.07	0.01	2.2×10^{-8}	4.3×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
APOC1	Skin Sun Exposed Lower leg	0.03	12	-0.11	0.02	2.5×10^{-8}	4.8×10^{-5}	rs584007 (pval=2.22×10^{-14})	APOE region
HLA-DRB5	Brain Hippocampus	0.49	25	-0.06	0.01	2.6×10^{-8}	4.9×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PPM1G	Adipose Subcutaneous	0.04	12	0.14	0.03	2.7×10^{-8}	5.0×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MLXIPL	Artery Aorta	0.05	1	-0.25	0.05	2.7×10^{-8}	5.1×10^{-5}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
CCDC92	Heart Atrial Appendage	0.14	16	-0.07	0.01	3.3×10^{-8}	6.1×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
AP006216.11	Nerve Tibial	0.07	9	-0.12	0.02	3.4×10^{-8}	6.3×10^{-5}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Artery Tibial	0.08	11	-0.11	0.02	3.5×10^{-8}	6.5×10^{-5}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DNAH10OS	Muscle Skeletal	0.13	33	-0.07	0.01	3.6×10^{-8}	6.6×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
ATP13A1	Esophagus Muscularis	0.10	5	-0.12	0.02	3.7×10^{-8}	6.6×10^{-5}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-DRB6	Small Intestine Terminal Ileum	0.34	46	0.04	0.01	4.1×10^{-8}	7.4×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
AP006216.11	Skin Not Sun Exposed Suprapubic	0.11	9	-0.08	0.01	4.2×10^{-8}	7.5×10^{-5}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
NRBP1	Thyroid	0.01	2	0.22	0.04	4.4×10^{-8}	7.7×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10OS	Breast Mammary Tissue	0.10	34	-0.08	0.02	4.6×10^{-8}	8.1×10^{-5}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HLA-DRB5	Colon Transverse	0.54	39	-0.04	0.01	4.6×10^{-8}	8.1×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SIDT2	Minor Salivary Gland	0.19	15	-0.10	0.02	4.7×10^{-8}	8.1×10^{-5}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Adipose Subcutaneous	0.12	11	-0.08	0.01	5.1×10^{-8}	8.7×10^{-5}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
KRTCAP3	Adrenal Gland	0.20	10	-0.06	0.01	5.6×10^{-8}	9.5×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Brain Amygdala	0.44	26	-0.04	0.01	5.7×10^{-8}	9.6×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Lung	0.63	48	-0.04	0.01	6.1×10^{-8}	1.0×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
UCN	DGN-WB	0.00	18	0.25	0.05	6.3×10^{-8}	1.1×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	Ovary	0.06	33	0.05	0.01	6.4×10^{-8}	1.1×10^{-4}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
KRTCAP3	Muscle Skeletal	0.06	13	-0.11	0.02	6.4×10^{-8}	1.1×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB9	Small Intestine Terminal Ileum	0.25	38	0.05	0.01	6.6×10^{-8}	1.1×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Skin Sun Exposed Lower leg	0.70	48	-0.04	0.01	7.2×10^{-8}	1.2×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Heart Left Ventricle	0.64	38	-0.04	0.01	8.2×10^{-8}	1.3×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
ATP13A1	Nerve Tibial	0.15	9	-0.07	0.01	8.3×10^{-8}	1.3×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
CCDC92	Whole Blood	0.08	9	-0.10	0.02	8.9×10^{-8}	1.4×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
ATP13A1	Skin Sun Exposed Lower leg	0.02	5	-0.22	0.04	9.1×10^{-8}	1.4×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
ATP13A1	Lung	0.02	2	-0.31	0.06	9.1×10^{-8}	1.4×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
DNAH10OS	Brain Anterior cingulate cortex BA24	0.15	24	-0.06	0.01	9.2×10^{-8}	1.4×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
ATP13A1	Spleen	0.14	6	-0.11	0.02	9.2×10^{-8}	1.4×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-DRB5	Brain Cerebellum	0.43	11	-0.07	0.01	1.0×10^{-7}	1.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Pancreas	0.64	59	-0.04	0.01	1.1×10^{-7}	1.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NRBP1	Lung	0.12	19	0.07	0.01	1.1×10^{-7}	1.6×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
LPL	Lung	0.03	59	-0.06	0.01	1.1×10^{-7}	1.7×10^{-4}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MRPL35P2	Esophagus Mucosa	0.02	5	0.19	0.04	1.2×10^{-7}	1.8×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
HLA-DRB5	Thyroid	0.71	60	-0.03	0.01	1.2×10^{-7}	1.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DNAH10	Brain Anterior cingulate cortex BA24	0.04	9	-0.13	0.02	1.3×10^{-7}	1.9×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
APOC1P1	Adipose Visceral Omentum	0.02	20	-0.14	0.03	1.4×10^{-7}	2.1×10^{-4}	rs584007 (pval=2.22×10^{-14})	APOE region
MRPL35P2	Spleen	0.11	10	0.10	0.02	1.5×10^{-7}	2.2×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
SNX17	Muscle Skeletal	0.43	44	0.03	0.01	1.6×10^{-7}	2.4×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Muscle Skeletal	0.66	18	-0.04	0.01	1.6×10^{-7}	2.4×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC92	Adipose Subcutaneous	0.19	26	-0.05	0.01	1.8×10^{-7}	2.6×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DNAH10	Adipose Visceral Omentum	0.13	18	-0.06	0.01	1.9×10^{-7}	2.7×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
PPM1G	Skin Sun Exposed Lower leg	0.05	11	0.13	0.02	1.9×10^{-7}	2.7×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Testis	0.70	38	-0.03	0.01	2.1×10^{-7}	3.0×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GPN1	Skin Not Sun Exposed Suprapubic	0.04	48	0.07	0.01	2.1×10^{-7}	3.0×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
NRBP1	Adipose Subcutaneous	0.14	28	0.06	0.01	2.1×10^{-7}	3.0×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
KRTCAP3	DGN-WB	0.40	40	-0.03	0.01	2.4×10^{-7}	3.3×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Small Intestine Terminal Ileum	0.40	44	-0.05	0.01	2.4×10^{-7}	3.4×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL35P2	Heart Atrial Appendage	0.05	17	0.10	0.02	2.4×10^{-7}	3.4×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
ZNF513	Brain Amygdala	0.06	48	0.05	0.01	2.4×10^{-7}	3.4×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
PPM1G	DGN-WB	0.00	7	0.32	0.06	2.6×10^{-7}	3.5×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HOMER3	DGN-WB	0.00	2	0.66	0.13	2.6×10^{-7}	3.6×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-DRB1	Uterus	0.06	27	-0.11	0.02	2.8×10^{-7}	3.9×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Adipose Subcutaneous	0.61	38	-0.04	0.01	2.9×10^{-7}	4.0×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL35P2	Thyroid	0.21	20	0.05	0.01	3.0×10^{-7}	4.1×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
PPM1G	Thyroid	0.08	8	0.09	0.02	3.2×10^{-7}	4.3×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MRPL35P2	Colon Transverse	0.12	36	0.06	0.01	3.3×10^{-7}	4.4×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
HLA-DRA	Muscle Skeletal	0.07	27	0.14	0.03	3.4×10^{-7}	4.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS1	Nerve Tibial	0.13	4	-0.07	0.01	3.6×10^{-7}	4.8×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MRPL35P2	Minor Salivary Gland	0.18	40	0.04	0.01	3.8×10^{-7}	4.9×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC92	Spleen	0.20	32	-0.05	0.01	3.8×10^{-7}	4.9×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
GPN1	Heart Atrial Appendage	0.05	19	0.11	0.02	4.0×10^{-7}	5.2×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Colon Sigmoid	0.61	107	-0.03	0.01	4.3×10^{-7}	5.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Brain Cerebellar Hemisphere	0.38	68	-0.03	0.01	4.3×10^{-7}	5.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC92	Artery Coronary	0.11	57	-0.05	0.01	4.5×10^{-7}	5.8×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HLA-DRB5	Uterus	0.42	33	-0.05	0.01	4.5×10^{-7}	5.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Liver	0.51	53	-0.04	0.01	4.5×10^{-7}	5.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS1	Pancreas	0.42	46	-0.03	0.01	4.7×10^{-7}	5.9×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
HLA-DRB5	Esophagus Muscularis	0.62	71	-0.04	0.01	4.7×10^{-7}	6.0×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RP11-109L13.1	Minor Salivary Gland	0.30	55	0.04	0.01	4.8×10^{-7}	6.0×10^{-4}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
FADS1	Brain Putamen basal ganglia	0.22	6	-0.07	0.01	4.9×10^{-7}	6.1×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
ATRAID	Heart Atrial Appendage	0.10	35	-0.06	0.01	4.9×10^{-7}	6.1×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ZNF572	Colon Transverse	0.02	1	0.20	0.04	5.2×10^{-7}	6.4×10^{-4}	rs28601761 (pval=2.33×10^{-23})	rs58253018 pval=2×10^{-182} (Klarin, 30275531)
FADS1	Brain Cerebellar Hemisphere	0.27	7	-0.05	0.01	5.2×10^{-7}	6.4×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
PCSK7	DGN-WB	0.10	24	0.06	0.01	5.2×10^{-7}	6.4×10^{-4}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
HLA-DRB1	Brain Nucleus accumbens basal ganglia	0.20	17	-0.07	0.01	5.4×10^{-7}	6.6×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL35P2	Adrenal Gland	0.13	18	0.07	0.01	5.8×10^{-7}	7.1×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
NRBF2	Cells Transformed fibroblasts	0.05	60	-0.06	0.01	5.9×10^{-7}	7.1×10^{-4}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC92	Pituitary	0.16	9	-0.08	0.02	5.9×10^{-7}	7.1×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HLA-B	Stomach	0.04	38	0.07	0.01	5.9×10^{-7}	7.1×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
MAU2	DGN-WB	0.13	25	0.05	0.01	6.1×10^{-7}	7.3×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-B	Esophagus Mucosa	0.19	59	0.05	0.01	6.4×10^{-7}	7.5×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
FADS1	Esophagus Mucosa	0.19	7	-0.05	0.01	7.3×10^{-7}	8.7×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
KRTCAP3	Brain Cortex	0.05	9	-0.09	0.02	7.5×10^{-7}	8.8×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
NRBP1	Esophagus Mucosa	0.07	18	0.08	0.02	7.7×10^{-7}	9.0×10^{-4}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GAB2	Muscle Skeletal	0.08	21	-0.08	0.02	7.9×10^{-7}	9.2×10^{-4}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
STAG3L3	Breast Mammary Tissue	0.11	21	-0.06	0.01	8.0×10^{-7}	9.3×10^{-4}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
GATAD2A	Esophagus Mucosa	0.04	17	-0.12	0.02	8.6×10^{-7}	1.0×10^{-3}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
TNXB	Adrenal Gland	0.22	46	0.06	0.01	8.7×10^{-7}	1.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZNF664	Heart Left Ventricle	0.05	10	-0.09	0.02	9.2×10^{-7}	1.1×10^{-3}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
RP11-109L13.1	Testis	0.42	51	0.03	0.01	9.5×10^{-7}	1.1×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	Adrenal Gland	0.05	54	-0.04	0.01	9.5×10^{-7}	1.1×10^{-3}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
ATG4C	Brain Cerebellum	0.17	43	-0.05	0.01	1.0×10^{-6}	1.1×10^{-3}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
UBXN4	Brain Hypothalamus	0.09	15	0.14	0.03	1.0×10^{-6}	1.1×10^{-3}	rs6704561 (pval=2.46×10^{-08})	NA
GPANK1	Nerve Tibial	0.03	72	0.06	0.01	1.0×10^{-6}	1.2×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
SLC44A4	Brain Hypothalamus	0.06	17	-0.07	0.01	1.0×10^{-6}	1.2×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
COBLL1	Thyroid	0.06	21	-0.09	0.02	1.1×10^{-6}	1.2×10^{-3}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
TAPBP	Artery Aorta	0.31	16	-0.04	0.01	1.1×10^{-6}	1.2×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NRBP1	Esophagus Muscularis	0.08	19	0.07	0.01	1.2×10^{-6}	1.3×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TNXA	Small Intestine Terminal Ileum	0.18	33	0.05	0.01	1.2×10^{-6}	1.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZBTB22	Skin Sun Exposed Lower leg	0.04	43	0.09	0.02	1.2×10^{-6}	1.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
KCNK3	Artery Aorta	0.04	17	-0.11	0.02	1.2×10^{-6}	1.4×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
METTL12	Brain Cerebellum	0.06	3	0.17	0.03	1.2×10^{-6}	1.4×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
DAXX	Liver	0.15	17	-0.06	0.01	1.3×10^{-6}	1.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
VPS37D	Adipose Subcutaneous	0.08	15	-0.06	0.01	1.4×10^{-6}	1.5×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
PAFAH1B2	Brain Cerebellum	0.14	33	-0.06	0.01	1.4×10^{-6}	1.5×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
HLA-DRB5	Whole Blood	0.61	53	-0.03	0.01	1.4×10^{-6}	1.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS1	Brain Cerebellum	0.44	19	-0.03	0.01	1.5×10^{-6}	1.6×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
OXCT2P1	Muscle Skeletal	0.13	18	0.05	0.01	1.5×10^{-6}	1.6×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
RP11-109L13.1	Uterus	0.42	46	0.03	0.01	1.5×10^{-6}	1.6×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
NRBP1	Breast Mammary Tissue	0.04	7	0.09	0.02	1.6×10^{-6}	1.6×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TNXA	Ovary	0.26	120	0.02	0.01	1.6×10^{-6}	1.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL35P2	Small Intestine Terminal Ileum	0.12	27	0.11	0.02	1.6×10^{-6}	1.7×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
CCDC92	Skin Sun Exposed Lower leg	0.09	59	-0.06	0.01	1.7×10^{-6}	1.7×10^{-3}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
RP11-452H21.4	Spleen	0.23	35	-0.05	0.01	1.7×10^{-6}	1.8×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
FADS1	Muscle Skeletal	0.14	30	-0.05	0.01	1.7×10^{-6}	1.8×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
ATRAID	Artery Coronary	0.17	16	-0.07	0.01	1.8×10^{-6}	1.8×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
AP006216.11	Adipose Subcutaneous	0.03	12	-0.11	0.02	1.8×10^{-6}	1.8×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
HLA-DRB5	Artery Coronary	0.64	39	-0.03	0.01	1.8×10^{-6}	1.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PABPC4	Adipose Subcutaneous	0.17	44	-0.05	0.01	1.9×10^{-6}	1.9×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
TAPBP	Esophagus Mucosa	0.17	28	-0.05	0.01	2.0×10^{-6}	2.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
C4A	Adrenal Gland	0.11	84	0.05	0.01	2.0×10^{-6}	2.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MAU2	Whole Blood	0.05	25	0.07	0.01	2.0×10^{-6}	2.0×10^{-3}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
DNAH10	Cells Transformed fibroblasts	0.14	20	-0.06	0.01	2.0×10^{-6}	2.0×10^{-3}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
PBX2	Brain Caudate basal ganglia	0.12	46	0.07	0.02	2.2×10^{-6}	2.2×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HYPK	Skin Not Sun Exposed Suprapubic	0.03	59	0.08	0.02	2.3×10^{-6}	2.3×10^{-3}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
SCN2A	Nerve Tibial	0.06	7	0.13	0.03	2.4×10^{-6}	2.4×10^{-3}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
OXCT2P1	Artery Tibial	0.26	63	0.03	0.01	2.4×10^{-6}	2.4×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
TAP2	Liver	0.04	20	0.10	0.02	2.5×10^{-6}	2.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GAB2	Skin Not Sun Exposed Suprapubic	0.06	4	0.18	0.04	2.7×10^{-6}	2.6×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
SIK3	Heart Left Ventricle	0.04	36	-0.08	0.02	2.8×10^{-6}	2.7×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
WSCD1	Heart Atrial Appendage	0.03	7	-0.11	0.02	2.9×10^{-6}	2.8×10^{-3}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MRPL35P2	Skin Not Sun Exposed Suprapubic	0.05	27	0.07	0.02	2.9×10^{-6}	2.8×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
TMEM258	Skin Sun Exposed Lower leg	0.05	7	0.12	0.03	2.9×10^{-6}	2.8×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
HLA-DRB5	Prostate	0.48	31	-0.04	0.01	2.9×10^{-6}	2.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RP11-452H21.4	Small Intestine Terminal Ileum	0.08	29	-0.07	0.01	2.9×10^{-6}	2.8×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
AC109829.1	Adipose Visceral Omentum	0.02	6	-0.18	0.04	3.0×10^{-6}	2.8×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB1	Testis	0.36	16	-0.04	0.01	3.0×10^{-6}	2.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GAB2	Artery Tibial	0.08	12	0.10	0.02	3.4×10^{-6}	3.2×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
ZNF259	Brain Cortex	0.04	49	-0.04	0.01	3.4×10^{-6}	3.2×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
GAB2	Liver	0.14	11	-0.06	0.01	3.6×10^{-6}	3.3×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
TAPBP	Breast Mammary Tissue	0.02	12	-0.13	0.03	3.6×10^{-6}	3.3×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
APOA1	DGN-WB	0.02	22	-0.14	0.03	3.7×10^{-6}	3.4×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
MRPL35P2	Artery Aorta	0.13	39	0.04	0.01	3.7×10^{-6}	3.5×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
RP11-109L13.1	Spleen	0.44	51	0.03	0.01	3.8×10^{-6}	3.5×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
AGER	Esophagus Gastroesophageal Junction	0.09	32	0.07	0.01	3.8×10^{-6}	3.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
STK32B	Brain Cortex	0.07	109	-0.03	0.01	3.8×10^{-6}	3.5×10^{-3}	rs115335747 (pval=3.10×10^{-08})	NA
AC074117.13	Nerve Tibial	0.02	13	0.12	0.03	3.9×10^{-6}	3.5×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GAB2	Esophagus Muscularis	0.06	14	0.09	0.02	3.9×10^{-6}	3.5×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
HLA-B	Brain Putamen basal ganglia	0.06	29	0.12	0.03	3.9×10^{-6}	3.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
TAPBP	Skin Sun Exposed Lower leg	0.06	46	-0.07	0.02	3.9×10^{-6}	3.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
OXCT2P1	Cells Transformed fibroblasts	0.21	13	0.04	0.01	4.1×10^{-6}	3.7×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
MRPL33	Ovary	0.10	21	0.05	0.01	4.2×10^{-6}	3.8×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MRPL35P2	Artery Tibial	0.13	13	0.06	0.01	4.3×10^{-6}	3.9×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
USP1	Esophagus Muscularis	0.04	41	0.09	0.02	4.4×10^{-6}	3.9×10^{-3}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
LINC00452	Lung	0.03	36	-0.07	0.01	4.4×10^{-6}	3.9×10^{-3}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
TAPBP	Uterus	0.21	56	-0.03	0.01	4.6×10^{-6}	4.1×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SIDT2	Spleen	0.24	67	-0.04	0.01	4.7×10^{-6}	4.1×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
FADS1	Brain Anterior cingulate cortex BA24	0.04	7	-0.09	0.02	4.8×10^{-6}	4.3×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
SNX17	Brain Amygdala	0.11	33	0.05	0.01	5.0×10^{-6}	4.4×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TAPBP	Artery Coronary	0.20	26	-0.05	0.01	5.1×10^{-6}	4.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZNF664	Whole Blood	0.04	51	0.05	0.01	5.1×10^{-6}	4.5×10^{-3}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CCDC40	Brain Caudate basal ganglia	0.13	56	-0.04	0.01	5.3×10^{-6}	4.6×10^{-3}	NA	NA
CAD	Whole Blood	0.07	27	0.09	0.02	5.5×10^{-6}	4.7×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
FADS1	Brain Frontal Cortex BA9	0.11	5	-0.06	0.01	5.5×10^{-6}	4.7×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
VPS37D	Artery Aorta	0.13	30	-0.04	0.01	5.7×10^{-6}	4.9×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
C2orf16	Thyroid	0.07	40	-0.06	0.01	5.9×10^{-6}	5.1×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
EGR2	DGN-WB	0.00	7	0.42	0.09	5.9×10^{-6}	5.1×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC40	Artery Coronary	0.30	38	-0.03	0.01	6.2×10^{-6}	5.2×10^{-3}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
FADS1	Thyroid	0.15	11	-0.06	0.01	6.3×10^{-6}	5.3×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
TNXB	Spleen	0.04	44	0.12	0.03	6.4×10^{-6}	5.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Ovary	0.54	29	-0.04	0.01	6.5×10^{-6}	5.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FAM35A	Artery Tibial	0.03	44	0.06	0.01	6.9×10^{-6}	5.8×10^{-3}	NA	NA
CCDC40	Small Intestine Terminal Ileum	0.33	13	-0.04	0.01	7.0×10^{-6}	5.8×10^{-3}	NA	NA
HLA-DRB5	Skin Not Sun Exposed Suprapubic	0.70	54	-0.03	0.01	7.0×10^{-6}	5.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PABPC4	Thyroid	0.12	7	-0.07	0.02	7.0×10^{-6}	5.8×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
FER	Colon Transverse	0.03	27	0.07	0.02	7.1×10^{-6}	5.9×10^{-3}	NA	NA
ZNF259	Adipose Visceral Omentum	0.02	52	-0.06	0.01	7.1×10^{-6}	5.9×10^{-3}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ZBTB22	DGN-WB	0.09	7	0.11	0.02	7.2×10^{-6}	5.9×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RXRB	Colon Sigmoid	0.06	19	0.25	0.05	7.3×10^{-6}	6.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZNF234	Spleen	0.10	57	0.03	0.01	7.5×10^{-6}	6.2×10^{-3}	rs584007 (pval=2.22×10^{-14})	APOE region
CCDC40	DGN-WB	0.23	5	-0.04	0.01	7.6×10^{-6}	6.2×10^{-3}	NA	NA
GAB2	Skin Sun Exposed Lower leg	0.07	36	0.06	0.01	7.6×10^{-6}	6.2×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
FADS1	Stomach	0.16	15	-0.05	0.01	7.8×10^{-6}	6.3×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
ZBTB22	Adipose Visceral Omentum	0.04	2	0.14	0.03	7.8×10^{-6}	6.3×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DAXX	Artery Aorta	0.34	9	-0.04	0.01	8.0×10^{-6}	6.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HCG27	Spleen	0.15	23	0.06	0.01	8.0×10^{-6}	6.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
TMEM258	Nerve Tibial	0.04	8	0.11	0.02	8.0×10^{-6}	6.4×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
LPL	Liver	0.04	27	-0.08	0.02	8.1×10^{-6}	6.5×10^{-3}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
SSUH2	Small Intestine Terminal Ileum	0.10	27	0.05	0.01	8.4×10^{-6}	6.7×10^{-3}	NA	NA
ATRAID	Artery Aorta	0.16	42	-0.04	0.01	8.5×10^{-6}	6.7×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TMEM64	Skin Sun Exposed Lower leg	0.08	52	0.07	0.01	8.6×10^{-6}	6.8×10^{-3}	NA	NA
PGS1	Artery Aorta	0.05	16	0.10	0.02	8.6×10^{-6}	6.8×10^{-3}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
FBXO22	Adrenal Gland	0.12	31	-0.06	0.01	8.7×10^{-6}	6.8×10^{-3}	NA	NA
PABPC4	Testis	0.02	5	-0.19	0.04	8.8×10^{-6}	6.8×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
FADS1	Adipose Visceral Omentum	0.04	6	-0.14	0.03	8.9×10^{-6}	6.9×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
HLA-B	Skin Sun Exposed Lower leg	0.11	29	0.05	0.01	8.9×10^{-6}	6.9×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
FADS1	Brain Substantia nigra	0.07	11	-0.11	0.02	9.0×10^{-6}	7.0×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
PABPC4	Esophagus Mucosa	0.11	11	-0.07	0.02	9.0×10^{-6}	7.0×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
OXCT2P1	Adipose Subcutaneous	0.18	16	0.04	0.01	9.4×10^{-6}	7.2×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
EIF2B4	DGN-WB	0.02	15	-0.13	0.03	9.4×10^{-6}	7.2×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ATP6V1B2	DGN-WB	0.00	12	-0.34	0.08	9.4×10^{-6}	7.2×10^{-3}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
ZBTB22	Esophagus Muscularis	0.03	8	0.11	0.03	9.6×10^{-6}	7.3×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
BMP8A	Artery Aorta	0.03	6	0.16	0.04	9.7×10^{-6}	7.4×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
USP35	Testis	0.09	15	-0.08	0.02	9.7×10^{-6}	7.4×10^{-3}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
CETP	Lung	0.05	10	0.10	0.02	1.0×10^{-5}	7.8×10^{-3}	NA	rs3764261 pval=3×10^{-27} (Spracklen, 28334899)
FADS1	Artery Tibial	0.02	20	-0.07	0.02	1.0×10^{-5}	7.9×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
TAPBP	Cells Transformed fibroblasts	0.11	7	-0.06	0.01	1.1×10^{-5}	8.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HLA-DRB5	Esophagus Gastroesophageal Junction	0.60	30	-0.04	0.01	1.1×10^{-5}	8.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GALNTL6	Colon Sigmoid	0.10	27	-0.07	0.02	1.1×10^{-5}	8.2×10^{-3}	NA	NA
SNX17	Heart Left Ventricle	0.07	12	0.07	0.02	1.1×10^{-5}	8.2×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CDSN	Skin Not Sun Exposed Suprapubic	0.12	37	0.06	0.01	1.1×10^{-5}	8.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
OXCT2P1	Prostate	0.21	23	0.04	0.01	1.1×10^{-5}	8.5×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
SNX17	Heart Atrial Appendage	0.04	20	0.07	0.02	1.1×10^{-5}	8.5×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MRPL33	Heart Atrial Appendage	0.04	28	0.07	0.02	1.2×10^{-5}	8.6×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10	Nerve Tibial	0.07	45	-0.05	0.01	1.2×10^{-5}	8.7×10^{-3}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
LYSMD1	Stomach	0.12	20	-0.06	0.01	1.2×10^{-5}	8.7×10^{-3}	NA	NA
HLA-DRB5	DGN-WB	0.85	121	-0.02	0.00	1.2×10^{-5}	8.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FKBPL	Whole Blood	0.04	90	0.07	0.02	1.2×10^{-5}	8.9×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PABPC4	Lung	0.07	7	-0.07	0.02	1.2×10^{-5}	9.0×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
MACF1	Thyroid	0.11	54	0.04	0.01	1.3×10^{-5}	9.1×10^{-3}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
XXbac-BPG248L24.12	Brain Cerebellar Hemisphere	0.47	58	-0.04	0.01	1.3×10^{-5}	9.1×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
C2CD4D	Skin Not Sun Exposed Suprapubic	0.06	37	-0.06	0.01	1.3×10^{-5}	9.2×10^{-3}	NA	NA
SYT7	Ovary	0.08	25	0.04	0.01	1.3×10^{-5}	9.3×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
CSGALNACT1	Whole Blood	0.39	46	-0.02	0.01	1.3×10^{-5}	9.4×10^{-3}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
TCF19	Prostate	0.15	14	-0.06	0.01	1.3×10^{-5}	9.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
CCDC40	Spleen	0.45	9	-0.03	0.01	1.3×10^{-5}	9.5×10^{-3}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
HLA-DRB5	Cells EBV-transformed lymphocytes	0.54	70	-0.03	0.01	1.4×10^{-5}	9.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SOCS4	Nerve Tibial	0.05	39	0.08	0.02	1.4×10^{-5}	9.8×10^{-3}	NA	NA
POU5F1	Brain Hypothalamus	0.11	27	0.05	0.01	1.4×10^{-5}	9.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
GPANK1	Artery Aorta	0.05	21	0.09	0.02	1.4×10^{-5}	9.9×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS1	Heart Left Ventricle	0.05	13	-0.09	0.02	1.4×10^{-5}	1.0×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
ZBTB22	Cells Transformed fibroblasts	0.06	23	0.14	0.03	1.4×10^{-5}	1.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC40	Minor Salivary Gland	0.16	8	-0.05	0.01	1.5×10^{-5}	1.0×10^{-2}	NA	NA
MRPL35P2	Pituitary	0.11	12	0.07	0.02	1.5×10^{-5}	1.1×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
FAM171A1	Skin Not Sun Exposed Suprapubic	0.04	33	-0.06	0.01	1.5×10^{-5}	1.1×10^{-2}	NA	NA
PPIEL	Skin Sun Exposed Lower leg	0.06	25	0.09	0.02	1.5×10^{-5}	1.1×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CETP	Artery Coronary	0.10	3	0.09	0.02	1.5×10^{-5}	1.1×10^{-2}	NA	rs3764261 pval=3×10^{-27} (Spracklen, 28334899)
HLA-B	Muscle Skeletal	0.06	22	0.10	0.02	1.6×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
TAPBP	Heart Atrial Appendage	0.09	5	-0.08	0.02	1.6×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
WDR46	Testis	0.23	7	-0.04	0.01	1.6×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RP11-420K8.2	Lung	0.01	5	-0.17	0.04	1.6×10^{-5}	1.1×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CCDC92	DGN-WB	0.08	30	-0.06	0.01	1.6×10^{-5}	1.1×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
AP006216.11	Artery Tibial	0.04	66	-0.05	0.01	1.6×10^{-5}	1.1×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
FADS1	Brain Cortex	0.11	11	-0.06	0.01	1.6×10^{-5}	1.1×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
PPM1G	Adipose Visceral Omentum	0.02	12	0.13	0.03	1.6×10^{-5}	1.1×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
DAXX	Cells Transformed fibroblasts	0.50	7	-0.02	0.01	1.7×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TMEM258	Uterus	0.15	17	0.05	0.01	1.7×10^{-5}	1.1×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
TMEM258	Cells Transformed fibroblasts	0.07	24	0.06	0.01	1.7×10^{-5}	1.1×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
NRBP1	Nerve Tibial	0.09	34	0.05	0.01	1.7×10^{-5}	1.1×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
OXCT2P1	Skin Not Sun Exposed Suprapubic	0.11	15	0.07	0.02	1.7×10^{-5}	1.1×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
RASA3	Breast Mammary Tissue	0.04	4	-0.11	0.03	1.7×10^{-5}	1.1×10^{-2}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
HLA-DRB5	Brain Frontal Cortex BA9	0.44	52	-0.03	0.01	1.7×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ATP6V1G2	Brain Caudate basal ganglia	0.08	37	0.05	0.01	1.7×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
CCDC40	Brain Cerebellar Hemisphere	0.51	18	-0.03	0.01	1.8×10^{-5}	1.2×10^{-2}	NA	NA
RPL15	Heart Left Ventricle	0.02	15	-0.14	0.03	1.8×10^{-5}	1.2×10^{-2}	NA	rs6792725 pval=4×10^{-08} (Hoffmann, 29507422)
RMI1	Nerve Tibial	0.02	6	0.17	0.04	1.8×10^{-5}	1.2×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
PSORS1C1	Muscle Skeletal	0.09	20	0.08	0.02	1.8×10^{-5}	1.2×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
MRPL33	Brain Caudate basal ganglia	0.04	7	0.26	0.06	1.8×10^{-5}	1.2×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
RP11-110I1.14	Brain Hippocampus	0.24	8	-0.05	0.01	1.8×10^{-5}	1.2×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
TFAM	Brain Hypothalamus	0.04	73	-0.04	0.01	1.9×10^{-5}	1.2×10^{-2}	rs3858121 (pval=2.05×10^{-08})	NA
OXCT2P1	Spleen	0.12	23	0.06	0.01	1.9×10^{-5}	1.2×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
TAPBP	Artery Tibial	0.36	42	-0.03	0.01	1.9×10^{-5}	1.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAPBP	Colon Sigmoid	0.10	53	-0.04	0.01	1.9×10^{-5}	1.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
XXbac-BPG299F13.14	Skin Not Sun Exposed Suprapubic	0.05	30	0.10	0.02	2.0×10^{-5}	1.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
GSTA2	Liver	0.32	29	0.03	0.01	2.0×10^{-5}	1.3×10^{-2}	NA	NA
ZBTB22	Adipose Subcutaneous	0.08	14	0.09	0.02	2.0×10^{-5}	1.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TMEM64	Whole Blood	0.02	14	-0.12	0.03	2.0×10^{-5}	1.3×10^{-2}	NA	NA
KATNAL2	Heart Left Ventricle	0.03	47	-0.06	0.01	2.0×10^{-5}	1.3×10^{-2}	NA	NA
ATRAID	Pituitary	0.10	16	-0.06	0.01	2.1×10^{-5}	1.3×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CCDC92	Lung	0.06	45	-0.05	0.01	2.1×10^{-5}	1.3×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
HMBS	Prostate	0.12	42	0.04	0.01	2.1×10^{-5}	1.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
HLA-DRB6	Liver	0.42	92	0.03	0.01	2.1×10^{-5}	1.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
THTPA	Skin Sun Exposed Lower leg	0.04	61	0.06	0.01	2.1×10^{-5}	1.3×10^{-2}	NA	NA
HLA-B	Adrenal Gland	0.08	14	0.08	0.02	2.1×10^{-5}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
UCN	Thyroid	0.02	2	0.21	0.05	2.2×10^{-5}	1.4×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
LMF1	Testis	0.09	38	-0.05	0.01	2.2×10^{-5}	1.4×10^{-2}	NA	NA
HLA-DRB6	Brain Frontal Cortex BA9	0.42	55	0.04	0.01	2.2×10^{-5}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	Brain Caudate basal ganglia	0.56	77	-0.03	0.01	2.2×10^{-5}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
WSCD1	DGN-WB	0.02	4	-0.14	0.03	2.2×10^{-5}	1.4×10^{-2}	NA	NA
HLA-DRB6	Testis	0.58	34	0.03	0.01	2.2×10^{-5}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
USP35	Colon Sigmoid	0.06	3	-0.12	0.03	2.2×10^{-5}	1.4×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
TAPBP	Heart Left Ventricle	0.14	7	-0.06	0.01	2.3×10^{-5}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
COPS7A	Adipose Subcutaneous	0.05	49	-0.05	0.01	2.3×10^{-5}	1.4×10^{-2}	NA	NA
HMBS	Skin Sun Exposed Lower leg	0.25	32	0.04	0.01	2.3×10^{-5}	1.4×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MCM6	Colon Transverse	0.06	4	-0.13	0.03	2.3×10^{-5}	1.4×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
CCDC40	Artery Aorta	0.47	14	-0.02	0.01	2.4×10^{-5}	1.4×10^{-2}	NA	NA
PSD3	Brain Cerebellum	0.23	107	-0.02	0.01	2.4×10^{-5}	1.4×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
HLA-DQB2	Skin Sun Exposed Lower leg	0.04	68	-0.07	0.02	2.4×10^{-5}	1.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAPBP	Brain Caudate basal ganglia	0.12	15	0.07	0.02	2.4×10^{-5}	1.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PPM1G	Esophagus Muscularis	0.11	23	0.04	0.01	2.4×10^{-5}	1.5×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
UBXN4	Skin Not Sun Exposed Suprapubic	0.06	10	0.10	0.02	2.4×10^{-5}	1.5×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
OXCT2P1	Thyroid	0.12	46	0.04	0.01	2.4×10^{-5}	1.5×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
RP11-109L13.1	Brain Putamen basal ganglia	0.41	72	0.02	0.01	2.5×10^{-5}	1.5×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
LINC01030	Thyroid	0.02	7	0.17	0.04	2.5×10^{-5}	1.5×10^{-2}	NA	NA
TAPBP	Adipose Visceral Omentum	0.12	10	-0.07	0.02	2.5×10^{-5}	1.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-B	Thyroid	0.07	59	0.06	0.01	2.6×10^{-5}	1.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
LZTS1	Minor Salivary Gland	0.10	41	0.04	0.01	2.6×10^{-5}	1.6×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
OXCT2P1	Esophagus Muscularis	0.23	18	0.04	0.01	2.6×10^{-5}	1.6×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PABPC4	Artery Tibial	0.19	14	-0.04	0.01	2.7×10^{-5}	1.6×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
DECR1	Pituitary	0.07	22	-0.06	0.02	2.7×10^{-5}	1.6×10^{-2}	NA	NA
NIPSNAP1	Brain Putamen basal ganglia	0.06	25	0.07	0.02	2.8×10^{-5}	1.6×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
GKAP1	Muscle Skeletal	0.06	30	0.09	0.02	2.8×10^{-5}	1.7×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
SFRP1	Liver	0.13	27	-0.05	0.01	2.8×10^{-5}	1.7×10^{-2}	NA	NA
DAXX	Lung	0.07	18	-0.07	0.02	3.0×10^{-5}	1.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
USO1	Pancreas	0.11	11	0.06	0.02	3.0×10^{-5}	1.7×10^{-2}	NA	NA
PABPC4	Small Intestine Terminal Ileum	0.09	16	-0.07	0.02	3.0×10^{-5}	1.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CCDC40	Esophagus Gastroesophageal Junction	0.25	17	-0.03	0.01	3.1×10^{-5}	1.8×10^{-2}	NA	NA
ATRAID	Breast Mammary Tissue	0.07	8	-0.07	0.02	3.1×10^{-5}	1.8×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB5	Brain Anterior cingulate cortex BA24	0.34	14	-0.05	0.01	3.1×10^{-5}	1.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GPN1	DGN-WB	0.00	2	0.46	0.11	3.2×10^{-5}	1.8×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CCDC40	Muscle Skeletal	0.17	34	-0.04	0.01	3.2×10^{-5}	1.8×10^{-2}	NA	NA
BMP8A	Artery Tibial	0.02	4	0.13	0.03	3.2×10^{-5}	1.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PABPC4	Breast Mammary Tissue	0.14	9	-0.06	0.01	3.2×10^{-5}	1.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CDSN	Skin Sun Exposed Lower leg	0.16	41	0.05	0.01	3.2×10^{-5}	1.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
HLA-DRB1	Brain Caudate basal ganglia	0.28	44	-0.05	0.01	3.3×10^{-5}	1.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL35P2	Esophagus Gastroesophageal Junction	0.10	8	0.08	0.02	3.3×10^{-5}	1.9×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
PSORS1C1	Esophagus Mucosa	0.55	54	0.02	0.00	3.4×10^{-5}	1.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
CCDC40	Breast Mammary Tissue	0.35	13	-0.03	0.01	3.5×10^{-5}	2.0×10^{-2}	NA	NA
EFHB	Testis	0.10	74	-0.04	0.01	3.5×10^{-5}	2.0×10^{-2}	NA	NA
NOTCH4	Nerve Tibial	0.20	76	-0.03	0.01	3.5×10^{-5}	2.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PPIP5K1	Brain Cortex	0.04	51	-0.04	0.01	3.5×10^{-5}	2.0×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
RMI1	Stomach	0.08	14	0.10	0.02	3.6×10^{-5}	2.0×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
CCDC40	Brain Nucleus accumbens basal ganglia	0.30	34	-0.04	0.01	3.6×10^{-5}	2.0×10^{-2}	NA	NA
LINC01030	Brain Nucleus accumbens basal ganglia	0.10	62	0.04	0.01	3.7×10^{-5}	2.1×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
PLEKHA5	Skin Sun Exposed Lower leg	0.04	24	0.08	0.02	3.8×10^{-5}	2.1×10^{-2}	NA	rs79719909 pval=3×10^{-17} (Hoffmann, 29507422)
CCDC40	Cells Transformed fibroblasts	0.48	12	-0.02	0.01	3.8×10^{-5}	2.2×10^{-2}	NA	NA
NIPSNAP1	Cells Transformed fibroblasts	0.19	28	0.04	0.01	3.9×10^{-5}	2.2×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
MACF1	Skin Sun Exposed Lower leg	0.09	7	-0.07	0.02	3.9×10^{-5}	2.2×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
MRPL35P2	Breast Mammary Tissue	0.15	51	0.04	0.01	3.9×10^{-5}	2.2×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC40	Whole Blood	0.19	44	-0.04	0.01	4.0×10^{-5}	2.2×10^{-2}	NA	NA
SIDT2	Whole Blood	0.27	6	-0.04	0.01	4.1×10^{-5}	2.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
SLC5A6	Pituitary	0.13	37	0.03	0.01	4.1×10^{-5}	2.3×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
OXCT2P1	Esophagus Mucosa	0.08	20	0.06	0.01	4.1×10^{-5}	2.3×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CCDC92	Colon Transverse	0.04	28	-0.06	0.01	4.1×10^{-5}	2.3×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
MRPL35P2	Brain Caudate basal ganglia	0.04	43	0.05	0.01	4.2×10^{-5}	2.3×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC40	Esophagus Mucosa	0.39	13	-0.03	0.01	4.2×10^{-5}	2.3×10^{-2}	NA	NA
OXCT2P1	Lung	0.26	32	0.03	0.01	4.3×10^{-5}	2.3×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
HLA-DRB1	Pituitary	0.08	34	-0.12	0.03	4.4×10^{-5}	2.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
USP35	Spleen	0.14	8	-0.08	0.02	4.4×10^{-5}	2.4×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
PTPN21	Heart Atrial Appendage	0.03	43	0.07	0.02	4.5×10^{-5}	2.4×10^{-2}	NA	NA
CCDC40	Brain Putamen basal ganglia	0.30	24	-0.03	0.01	4.5×10^{-5}	2.4×10^{-2}	NA	NA
MCM6	Esophagus Gastroesophageal Junction	0.04	3	-0.16	0.04	4.6×10^{-5}	2.5×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
FEM1C	Adipose Subcutaneous	0.09	35	-0.05	0.01	4.6×10^{-5}	2.5×10^{-2}	NA	NA
MYO1F	Heart Atrial Appendage	0.04	3	-0.13	0.03	4.6×10^{-5}	2.5×10^{-2}	rs116843064 (pval=1.05×10^{-09})	rs116843064 pval=6×10^{-134} (Klarin, 30275531)
MLF2	Adipose Visceral Omentum	0.08	46	0.05	0.01	4.7×10^{-5}	2.5×10^{-2}	NA	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
NUP62	DGN-WB	0.05	12	-0.09	0.02	4.7×10^{-5}	2.5×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
AP006621.5	Minor Salivary Gland	0.27	56	0.02	0.01	4.7×10^{-5}	2.5×10^{-2}	NA	NA
PSORS1C2	Spleen	0.22	44	0.05	0.01	4.7×10^{-5}	2.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
DNAH10	Whole Blood	0.10	15	-0.07	0.02	4.7×10^{-5}	2.5×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
C4A	Pancreas	0.21	70	0.06	0.01	4.8×10^{-5}	2.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC40	Brain Cerebellum	0.44	13	-0.03	0.01	4.9×10^{-5}	2.6×10^{-2}	NA	NA
ZNF664	Brain Frontal Cortex BA9	0.05	22	0.05	0.01	4.9×10^{-5}	2.6×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
SLC5A6	Muscle Skeletal	0.01	17	0.08	0.02	5.0×10^{-5}	2.6×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB1	Colon Transverse	0.02	65	-0.06	0.01	5.0×10^{-5}	2.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
OXCT2P1	Stomach	0.22	14	0.04	0.01	5.0×10^{-5}	2.6×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
RASA3	Heart Atrial Appendage	0.08	15	0.07	0.02	5.0×10^{-5}	2.6×10^{-2}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
TRIM54	Testis	0.03	6	0.11	0.03	5.1×10^{-5}	2.7×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
LINC00452	Nerve Tibial	0.06	36	-0.05	0.01	5.1×10^{-5}	2.7×10^{-2}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
HLA-DRB5	Brain Putamen basal ganglia	0.40	119	-0.02	0.01	5.1×10^{-5}	2.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CRLF3	Ovary	0.18	26	0.04	0.01	5.2×10^{-5}	2.7×10^{-2}	NA	NA
TTC28	Skin Sun Exposed Lower leg	0.01	27	0.10	0.02	5.2×10^{-5}	2.7×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
HCG27	Uterus	0.07	43	0.04	0.01	5.2×10^{-5}	2.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
C11orf10	DGN-WB	0.08	18	0.06	0.01	5.3×10^{-5}	2.7×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
INTS10	Whole Blood	0.06	34	-0.06	0.01	5.3×10^{-5}	2.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
CETP	Esophagus Mucosa	0.02	7	0.17	0.04	5.4×10^{-5}	2.8×10^{-2}	NA	rs3764261 pval=3×10^{-27} (Spracklen, 28334899)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
ATF6B	Skin Not Sun Exposed Suprapubic	0.14	59	-0.04	0.01	5.4×10^{-5}	2.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ZNF782	Brain Cortex	0.05	23	-0.07	0.02	5.4×10^{-5}	2.8×10^{-2}	NA	NA
OXCT2P1	Artery Coronary	0.08	12	0.05	0.01	5.5×10^{-5}	2.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
ATRAID	Pancreas	0.12	23	-0.07	0.02	5.5×10^{-5}	2.8×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MRPL35P2	Adipose Visceral Omentum	0.20	50	0.03	0.01	5.5×10^{-5}	2.8×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
ZNF512B	Brain Cerebellum	0.03	11	0.08	0.02	5.5×10^{-5}	2.8×10^{-2}	NA	NA
SLC38A11	Esophagus Gastroesophageal Junction	0.05	45	-0.04	0.01	5.5×10^{-5}	2.8×10^{-2}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
CSGALNACT1	Artery Aorta	0.13	35	-0.04	0.01	5.5×10^{-5}	2.8×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MYO1F	Esophagus Muscularis	0.08	3	-0.10	0.02	5.6×10^{-5}	2.8×10^{-2}	rs116843064 (pval=1.05×10^{-09})	rs116843064 pval=6×10^{-134} (Klarin, 30275531)
PABPC4	DGN-WB	0.10	19	-0.05	0.01	5.6×10^{-5}	2.9×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CCDC40	Adipose Subcutaneous	0.51	35	-0.02	0.01	5.8×10^{-5}	2.9×10^{-2}	NA	NA
PRRT1	Cells Transformed fibroblasts	0.02	12	0.15	0.04	5.8×10^{-5}	2.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HMBS	Thyroid	0.25	57	0.03	0.01	5.8×10^{-5}	2.9×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
RP11-109L13.1	Colon Sigmoid	0.60	28	0.02	0.01	5.8×10^{-5}	2.9×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
RP11-426L16.8	Brain Nucleus accumbens basal ganglia	0.11	45	0.03	0.01	5.9×10^{-5}	3.0×10^{-2}	NA	NA
DEF6	Pituitary	0.14	17	0.06	0.02	6.0×10^{-5}	3.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	NA
APOB	Skin Not Sun Exposed Suprapubic	0.19	12	-0.05	0.01	6.0×10^{-5}	3.0×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1042034 pval=1×10^{-72} (Hoffmann, 29507422)
NARS2	Brain Putamen basal ganglia	0.19	50	0.04	0.01	6.1×10^{-5}	3.0×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
HLA-DRB5	Adrenal Gland	0.41	87	-0.03	0.01	6.1×10^{-5}	3.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PABPC4	Adrenal Gland	0.10	22	-0.05	0.01	6.1×10^{-5}	3.0×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
CCDC40	Adipose Visceral Omentum	0.34	13	-0.03	0.01	6.1×10^{-5}	3.0×10^{-2}	NA	NA
NSUN5P2	Artery Coronary	0.28	39	-0.03	0.01	6.2×10^{-5}	3.0×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
GKAP1	DGN-WB	0.04	42	0.07	0.02	6.2×10^{-5}	3.1×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
PPIEL	Lung	0.11	21	0.05	0.01	6.2×10^{-5}	3.1×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
MAPK11	Esophagus Muscularis	0.02	21	-0.09	0.02	6.3×10^{-5}	3.1×10^{-2}	NA	NA
FADS1	DGN-WB	0.23	12	0.03	0.01	6.3×10^{-5}	3.1×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
VPS52	Lung	0.04	4	0.14	0.03	6.3×10^{-5}	3.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PSORS1C1	Heart Left Ventricle	0.41	72	0.03	0.01	6.3×10^{-5}	3.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
FADS2	Skin Sun Exposed Lower leg	0.03	13	0.08	0.02	6.3×10^{-5}	3.1×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
STRCP1	Brain Cerebellum	0.13	21	0.04	0.01	6.3×10^{-5}	3.1×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
CLINT1	Liver	0.03	40	0.05	0.01	6.4×10^{-5}	3.1×10^{-2}	NA	rs9715911 pval=5×10^{-38} (Klarin, 30275531)
ACYP2	Brain Cerebellum	0.21	19	0.04	0.01	6.5×10^{-5}	3.2×10^{-2}	NA	NA
CDPF1	Brain Anterior cingulate cortex BA24	0.06	58	0.04	0.01	6.6×10^{-5}	3.2×10^{-2}	NA	NA
CCDC40	Stomach	0.23	27	-0.03	0.01	6.6×10^{-5}	3.2×10^{-2}	NA	NA
IFT172	Adipose Subcutaneous	0.02	15	-0.09	0.02	6.6×10^{-5}	3.2×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DRB6	Pituitary	0.47	64	0.03	0.01	6.6×10^{-5}	3.2×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCDC40	Brain Cortex	0.39	29	-0.02	0.01	6.7×10^{-5}	3.2×10^{-2}	NA	NA
MYO1C	Nerve Tibial	0.02	68	0.04	0.01	6.7×10^{-5}	3.2×10^{-2}	NA	NA
GAB2	Esophagus Gastroesophageal Junction	0.13	19	0.05	0.01	6.8×10^{-5}	3.2×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
FADS1	Colon Sigmoid	0.05	17	-0.07	0.02	6.8×10^{-5}	3.3×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
HLA-DRB1	Cells Transformed fibroblasts	0.15	24	-0.07	0.02	6.9×10^{-5}	3.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
MRPL35P2	Lung	0.15	45	0.04	0.01	6.9×10^{-5}	3.3×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
HCG27	Esophagus Mucosa	0.24	28	0.04	0.01	6.9×10^{-5}	3.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
OXCT2P1	Skin Sun Exposed Lower leg	0.15	27	0.04	0.01	6.9×10^{-5}	3.3×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PDCD5	Brain Cerebellum	0.11	41	0.05	0.01	7.0×10^{-5}	3.3×10^{-2}	NA	rs12460070 pval=2×10^{-10} (Klarin, 30275531)
COPS7A	Nerve Tibial	0.11	16	-0.06	0.02	7.0×10^{-5}	3.3×10^{-2}	NA	NA
BMP8A	Esophagus Muscularis	0.09	29	0.05	0.01	7.0×10^{-5}	3.3×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CTSB	Colon Sigmoid	0.28	37	0.03	0.01	7.0×10^{-5}	3.3×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs709822 pval=5×10^{-13} (Klarin, 30275531)
ETNK1	Artery Aorta	0.05	26	-0.07	0.02	7.0×10^{-5}	3.3×10^{-2}	NA	NA
TUBGCP4	Brain Frontal Cortex BA9	0.08	85	0.04	0.01	7.1×10^{-5}	3.3×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
FAM153C	Brain Putamen basal ganglia	0.07	22	0.09	0.02	7.1×10^{-5}	3.3×10^{-2}	NA	NA
MYO1F	Skin Not Sun Exposed Suprapubic	0.04	18	-0.08	0.02	7.1×10^{-5}	3.3×10^{-2}	rs116843064 (pval=1.05×10^{-09})	rs116843064 pval=6×10^{-134} (Klarin, 30275531)
USP8P1	Whole Blood	0.19	11	0.04	0.01	7.2×10^{-5}	3.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
ADAL	Brain Putamen basal ganglia	0.40	53	-0.02	0.01	7.3×10^{-5}	3.4×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
KRTCAP3	Whole Blood	0.09	18	-0.06	0.01	7.3×10^{-5}	3.4×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ATRAID	Artery Tibial	0.18	29	-0.04	0.01	7.4×10^{-5}	3.4×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-B	Skin Not Sun Exposed Suprapubic	0.06	13	0.07	0.02	7.4×10^{-5}	3.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
PSORS1C1	Nerve Tibial	0.54	32	0.02	0.01	7.4×10^{-5}	3.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
C20orf112	Whole Blood	0.06	55	0.05	0.01	7.5×10^{-5}	3.5×10^{-2}	NA	rs6088793 pval=3×10^{-08} (Klarin, 30275531)
NSUN5	Artery Coronary	0.05	49	-0.03	0.01	7.5×10^{-5}	3.5×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
GIMAP8	Adrenal Gland	0.03	14	-0.10	0.02	7.5×10^{-5}	3.5×10^{-2}	NA	rs73165526 pval=2×10^{-09} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
PLB1	Lung	0.04	64	0.04	0.01	7.6×10^{-5}	3.5×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
REEP3	Skin Sun Exposed Lower leg	0.01	24	0.13	0.03	7.7×10^{-5}	3.5×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
YWHAZP4	Adipose Subcutaneous	0.04	30	-0.13	0.03	7.7×10^{-5}	3.5×10^{-2}	NA	rs13198641 pval=4×10^{-12} (Klarin, 30275531)
PPM1G	Brain Hippocampus	0.10	51	0.04	0.01	7.7×10^{-5}	3.5×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
OXCT2P1	Brain Nucleus accumbens basal ganglia	0.12	11	0.06	0.01	7.8×10^{-5}	3.6×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
HLA-DRA	Adipose Subcutaneous	0.12	14	0.06	0.02	7.8×10^{-5}	3.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
C2orf70	Pancreas	0.03	11	-0.08	0.02	7.9×10^{-5}	3.6×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MYO1F	Thyroid	0.08	1	-0.12	0.03	7.9×10^{-5}	3.6×10^{-2}	rs116843064 (pval=1.05×10^{-09})	rs116843064 pval=6×10^{-134} (Klarin, 30275531)
HLA-DPB1	Testis	0.05	59	0.04	0.01	7.9×10^{-5}	3.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SERINC4	DGN-WB	0.04	14	0.09	0.02	8.0×10^{-5}	3.6×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
ZNF229	Heart Atrial Appendage	0.04	36	-0.05	0.01	8.1×10^{-5}	3.6×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
NIPSNAP1	Esophagus Gastroesophageal Junction	0.19	38	0.03	0.01	8.1×10^{-5}	3.6×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
TTC40	Brain Cerebellar Hemisphere	0.04	11	-0.06	0.01	8.1×10^{-5}	3.6×10^{-2}	NA	rs1133400 pval=2×10^{-08} (Klarin, 30275531)
RNF40	Skin Sun Exposed Lower leg	0.01	1	-0.25	0.06	8.1×10^{-5}	3.7×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
NSUN5P2	Adrenal Gland	0.19	38	-0.03	0.01	8.2×10^{-5}	3.7×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
SIDT2	Pancreas	0.17	9	-0.05	0.01	8.2×10^{-5}	3.7×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
PATL2	Adrenal Gland	0.06	8	0.07	0.02	8.2×10^{-5}	3.7×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs138570705 pval=9×10^{-31} (Hoffmann, 29507422)
RPLP2	Heart Left Ventricle	0.06	11	0.07	0.02	8.3×10^{-5}	3.7×10^{-2}	NA	NA
TNXA	Testis	0.22	51	0.04	0.01	8.3×10^{-5}	3.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
NPC2	Nerve Tibial	0.07	50	-0.05	0.01	8.3×10^{-5}	3.7×10^{-2}	NA	NA
BCKDK	DGN-WB	0.08	16	-0.05	0.01	8.4×10^{-5}	3.7×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
PSORS1C2	Esophagus Mucosa	0.59	88	0.02	0.00	8.4×10^{-5}	3.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
MRPL35P2	Esophagus Muscularis	0.15	25	0.04	0.01	8.4×10^{-5}	3.7×10^{-2}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
EBAG9P1	Pituitary	0.05	7	0.08	0.02	8.4×10^{-5}	3.7×10^{-2}	NA	NA
TNIK	Vagina	0.21	51	-0.03	0.01	8.6×10^{-5}	3.8×10^{-2}	NA	rs11720145 pval=1×10^{-13} (Klarin, 30275531)
DXO	Adipose Subcutaneous	0.09	30	-0.05	0.01	8.6×10^{-5}	3.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAPBP	Muscle Skeletal	0.11	49	-0.04	0.01	8.6×10^{-5}	3.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAPBP	Brain Hypothalamus	0.07	11	0.11	0.03	8.6×10^{-5}	3.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PABPC4	Artery Aorta	0.05	48	-0.05	0.01	8.7×10^{-5}	3.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
OXCT2P1	Uterus	0.36	22	0.04	0.01	8.7×10^{-5}	3.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PNPLA2	Brain Cerebellar Hemisphere	0.08	26	-0.06	0.01	8.8×10^{-5}	3.9×10^{-2}	NA	NA
SLC5A6	Whole Blood	0.14	23	0.04	0.01	8.9×10^{-5}	3.9×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GKAP1	Artery Coronary	0.13	43	0.05	0.01	8.9×10^{-5}	3.9×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
GATAD2A	Skin Not Sun Exposed Suprapubic	0.04	5	-0.12	0.03	8.9×10^{-5}	3.9×10^{-2}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
CCDC40	Liver	0.36	9	-0.03	0.01	8.9×10^{-5}	3.9×10^{-2}	NA	NA
PABPC4	Skin Not Sun Exposed Suprapubic	0.19	21	-0.04	0.01	9.1×10^{-5}	3.9×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
SLC38A11	Minor Salivary Gland	0.15	8	-0.06	0.01	9.1×10^{-5}	3.9×10^{-2}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
BCL7B	Nerve Tibial	0.10	35	-0.05	0.01	9.2×10^{-5}	4.0×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
HMBS	Nerve Tibial	0.23	13	0.04	0.01	9.2×10^{-5}	4.0×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
IPO13	Muscle Skeletal	0.01	7	-0.16	0.04	9.4×10^{-5}	4.0×10^{-2}	NA	NA
RP3-449M8.6	Colon Sigmoid	0.09	14	0.05	0.01	9.5×10^{-5}	4.1×10^{-2}	NA	NA
CAD	Pituitary	0.12	33	0.05	0.01	9.6×10^{-5}	4.1×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
KAT8	Brain Anterior cingulate cortex BA24	0.20	45	0.03	0.01	9.6×10^{-5}	4.1×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
OXCT2P1	Adipose Visceral Omentum	0.20	41	0.03	0.01	9.6×10^{-5}	4.1×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CSNK2B	Esophagus Mucosa	0.08	40	0.06	0.01	9.6×10^{-5}	4.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CCNE2	Breast Mammary Tissue	0.04	3	-0.15	0.04	9.6×10^{-5}	4.1×10^{-2}	NA	NA
C6orf15	Pituitary	0.22	31	0.03	0.01	9.7×10^{-5}	4.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
OXCT2P1	Breast Mammary Tissue	0.11	12	0.06	0.01	9.8×10^{-5}	4.2×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
EBAG9P1	Esophagus Muscularis	0.11	18	0.05	0.01	9.8×10^{-5}	4.2×10^{-2}	NA	NA
CDC42SE1	Brain Frontal Cortex BA9	0.18	12	-0.07	0.02	9.9×10^{-5}	4.2×10^{-2}	NA	NA
PGS1	Cells Transformed fibroblasts	0.11	11	0.07	0.02	9.9×10^{-5}	4.2×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
TRIM50	Brain Caudate basal ganglia	0.08	33	-0.05	0.01	1.0×10^{-4}	4.2×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
HLA-DRB6	Pancreas	0.52	49	0.03	0.01	1.0×10^{-4}	4.2×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
SLC5A6	Nerve Tibial	0.13	52	0.03	0.01	1.0×10^{-4}	4.2×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
MCM6	DGN-WB	0.15	25	-0.06	0.01	1.0×10^{-4}	4.3×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
NARS2	Brain Hypothalamus	0.16	36	0.04	0.01	1.0×10^{-4}	4.3×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
HLA-E	Small Intestine Terminal Ileum	0.12	12	-0.11	0.03	1.0×10^{-4}	4.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs2247056 pval=2×10^{-15} (Teslovich, 20686565)
GKAP1	Thyroid	0.12	52	0.06	0.02	1.0×10^{-4}	4.3×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
BACE1	Whole Blood	0.05	33	-0.06	0.02	1.0×10^{-4}	4.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
GSTA2	Pancreas	0.06	24	0.07	0.02	1.0×10^{-4}	4.3×10^{-2}	NA	NA
SIDT2	Esophagus Muscularis	0.01	5	-0.22	0.06	1.0×10^{-4}	4.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
DNAH10OS	Brain Frontal Cortex BA9	0.15	38	-0.03	0.01	1.0×10^{-4}	4.3×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
STMN3	Esophagus Muscularis	0.07	11	0.09	0.02	1.0×10^{-4}	4.3×10^{-2}	NA	NA
PIDD	Adipose Visceral Omentum	0.17	31	0.03	0.01	1.1×10^{-4}	4.4×10^{-2}	NA	NA
HLA-B	Artery Tibial	0.19	39	0.04	0.01	1.1×10^{-4}	4.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
AP006621.1	Brain Putamen basal ganglia	0.47	46	0.02	0.01	1.1×10^{-4}	4.4×10^{-2}	NA	NA
BMP8A	Stomach	0.03	44	0.06	0.02	1.1×10^{-4}	4.4×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
CCHCR1	Cells Transformed fibroblasts	0.14	40	-0.05	0.01	1.1×10^{-4}	4.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
SUGP1	DGN-WB	0.02	22	0.10	0.03	1.1×10^{-4}	4.5×10^{-2}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
WDFY2	Nerve Tibial	0.31	22	0.03	0.01	1.1×10^{-4}	4.5×10^{-2}	NA	NA
WDFY2	Adipose Visceral Omentum	0.06	7	0.07	0.02	1.1×10^{-4}	4.5×10^{-2}	NA	NA
BMP8A	Testis	0.26	26	0.03	0.01	1.1×10^{-4}	4.5×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
SUPT7L	DGN-WB	0.01	19	-0.13	0.03	1.1×10^{-4}	4.5×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
AP006621.1	Spleen	0.55	46	0.02	0.01	1.1×10^{-4}	4.5×10^{-2}	NA	NA
GATAD2A	Skin Sun Exposed Lower leg	0.05	19	-0.08	0.02	1.1×10^{-4}	4.5×10^{-2}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
HLA-DRB6	Brain Hypothalamus	0.46	20	0.03	0.01	1.1×10^{-4}	4.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS2	Heart Atrial Appendage	0.19	16	0.04	0.01	1.1×10^{-4}	4.5×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
PCSK7	Cells Transformed fibroblasts	0.03	23	0.07	0.02	1.1×10^{-4}	4.5×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
SPAG9	Stomach	0.02	3	0.09	0.02	1.1×10^{-4}	4.5×10^{-2}	rs72836561 (pval=1.50×10^{-10})	NA
NIPSNAP1	Brain Frontal Cortex BA9	0.07	7	0.06	0.02	1.1×10^{-4}	4.5×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
RP11-109L13.1	Esophagus Muscularis	0.57	32	0.02	0.01	1.1×10^{-4}	4.5×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
CCDC40	Adrenal Gland	0.38	23	-0.03	0.01	1.1×10^{-4}	4.6×10^{-2}	NA	NA
AC114814.4	Adipose Visceral Omentum	0.03	3	0.35	0.09	1.1×10^{-4}	4.6×10^{-2}	NA	rs4663379 pval=1×10^{-09} (Hebbar, 30108155)
ATRAID	Adrenal Gland	0.16	14	-0.06	0.01	1.1×10^{-4}	4.6×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ZNF180	Artery Tibial	0.02	8	-0.13	0.04	1.2×10^{-4}	4.6×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
EXOSC10	Colon Sigmoid	0.05	8	-0.10	0.03	1.2×10^{-4}	4.6×10^{-2}	NA	rs55738118 pval=2×10^{-08} (Klarin, 30275531)
CTA-217C2.1	Breast Mammary Tissue	0.09	43	0.04	0.01	1.2×10^{-4}	4.6×10^{-2}	NA	NA
ARL14EP	Testis	0.40	30	-0.03	0.01	1.2×10^{-4}	4.6×10^{-2}	NA	NA
EFNA1	Thyroid	0.02	15	-0.10	0.02	1.2×10^{-4}	4.7×10^{-2}	NA	NA
HCG27	Small Intestine Terminal Ileum	0.10	65	0.05	0.01	1.2×10^{-4}	4.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
ATP6V0B	Whole Blood	0.12	5	0.06	0.02	1.2×10^{-4}	4.7×10^{-2}	NA	NA
RP11-1105O14.1	Heart Left Ventricle	0.22	14	-0.04	0.01	1.2×10^{-4}	4.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
KLRAP1	Brain Frontal Cortex BA9	0.05	46	-0.04	0.01	1.2×10^{-4}	4.7×10^{-2}	NA	NA
DCST2	Brain Substantia nigra	0.14	50	0.03	0.01	1.2×10^{-4}	4.7×10^{-2}	NA	rs6671166 pval=2×10^{-09} (Hoffmann, 29507422)
DARS	Colon Transverse	0.04	15	-0.14	0.04	1.2×10^{-4}	4.7×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
INTS10	Lung	0.01	32	-0.07	0.02	1.2×10^{-4}	4.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
CTSB	Colon Transverse	0.05	18	0.06	0.01	1.2×10^{-4}	4.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs709822 pval=5×10^{-13} (Klarin, 30275531)
CEND1	Heart Left Ventricle	0.14	10	0.05	0.01	1.2×10^{-4}	4.8×10^{-2}	NA	NA
RMI1	Cells Transformed fibroblasts	0.11	11	0.07	0.02	1.2×10^{-4}	4.8×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
RP11-109L13.1	Adrenal Gland	0.45	55	0.03	0.01	1.2×10^{-4}	4.8×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
BMP8A	Thyroid	0.03	12	0.12	0.03	1.2×10^{-4}	4.8×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)

Gene	Tissue	PrediXcan		SUGEN				Annotation	
		R^2	N SNPs	BETA	SE	P-value	FDR	GWAS	NHGRI-EBI
UCKL1	Thyroid	0.06	33	-0.06	0.02	1.2×10^{-4}	4.8×10^{-2}	NA	NA
HINFP	Liver	0.07	21	0.05	0.01	1.2×10^{-4}	4.9×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
ZNF180	Brain Cerebellum	0.23	23	-0.04	0.01	1.3×10^{-4}	4.9×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
PABPC4	Skin Sun Exposed Lower leg	0.20	19	-0.04	0.01	1.3×10^{-4}	4.9×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
HCG27	Heart Left Ventricle	0.20	37	0.04	0.01	1.3×10^{-4}	4.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
AP006621.1	Brain Hypothalamus	0.54	27	0.02	0.00	1.3×10^{-4}	4.9×10^{-2}	NA	NA
SYNGR2	Esophagus Mucosa	0.22	22	-0.04	0.01	1.3×10^{-4}	4.9×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
XXbac-BPG248L24.12	Brain Cerebellum	0.41	45	-0.04	0.01	1.3×10^{-4}	5.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
PABPC4	Cells Transformed fibroblasts	0.15	5	-0.05	0.01	1.3×10^{-4}	5.0×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
ATRAID	Cells EBV-transformed lymphocytes	0.24	18	-0.05	0.01	1.3×10^{-4}	5.0×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)

Appendix IX. Cross-tissue GReX results of the genes significantly associated with HDL-C in BioVU

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CETP	cross all tissues	8	4	83%	4.7×10^{-180}	1.1×10^{-175}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
NLRC5	cross all tissues	10	5	84%	3.9×10^{-117}	4.6×10^{-113}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
NLRC5	cross metabolic tissues	3	2	91%	4.8×10^{-48}	3.8×10^{-44}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LPL	cross all tissues	7	4	89%	1.2×10^{-44}	7.0×10^{-41}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
LIPC	cross metabolic tissues	6	3	90%	4.5×10^{-40}	2.1×10^{-36}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
LPL	cross metabolic tissues	4	3	94%	6.4×10^{-39}	2.5×10^{-35}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
LIPC	cross all tissues	17	6	82%	3.7×10^{-35}	1.3×10^{-31}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
MT1A	cross all tissues	20	7	81%	2.5×10^{-23}	7.5×10^{-20}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CPNE2	cross all tissues	12	7	85%	4.5×10^{-23}	1.2×10^{-19}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HERPUD1	cross metabolic tissues	3	2	92%	4.1×10^{-15}	9.7×10^{-12}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
MPHOSPH9	cross all tissues	16	6	82%	8.5×10^{-14}	1.8×10^{-10}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ABCB9	cross all tissues	20	6	81%	1.5×10^{-13}	2.9×10^{-10}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
MT2A	cross all tissues	5	4	91%	2.9×10^{-13}	5.2×10^{-10}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
HERPUD1	cross all tissues	10	4	86%	3.8×10^{-13}	6.4×10^{-10}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
LZTS1	cross all tissues	7	4	81%	1.9×10^{-12}	3.0×10^{-9}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
ARL6IP4	cross all tissues	12	4	85%	2.9×10^{-12}	4.3×10^{-9}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ARL6IP4	cross metabolic tissues	4	2	83%	$3.2×10^{-12}$	$4.4×10^{-9}$	rs7133378 (pval=$7.55×10^{-10}$)	rs4759375 pval=$2×10^{-24}$ (Klarin, 30275531)
CLPTM1	cross all tissues	6	4	85%	$6.5×10^{-12}$	$8.6×10^{-9}$	rs429358 (pval=$6.31×10^{-12}$)	APOE region
OGFOD2	cross all tissues	9	4	85%	$1.1×10^{-11}$	$1.3×10^{-8}$	rs7133378 (pval=$7.55×10^{-10}$)	rs4759375 pval=$2×10^{-24}$ (Klarin, 30275531)
ALDH1A2	cross metabolic tissues	3	2	90%	$1.4×10^{-11}$	$1.7×10^{-8}$	rs1077835 (pval=$1.69×10^{-21}$)	rs77250403 pval=$6×10^{-216}$ (Klarin, 30275531)
ZNF664	cross all tissues	12	6	84%	$3.0×10^{-11}$	$3.3×10^{-8}$	rs7133378 (pval=$7.55×10^{-10}$)	rs10773112 pval=$8×10^{-43}$ (Klarin, 30275531)
SETD8	cross all tissues	15	6	82%	$9.0×10^{-11}$	$9.7×10^{-8}$	rs7133378 (pval=$7.55×10^{-10}$)	rs4759375 pval=$2×10^{-24}$ (Klarin, 30275531)
DNAH10OS	cross all tissues	25	7	81%	$1.3×10^{-10}$	$1.4×10^{-7}$	rs7133378 (pval=$7.55×10^{-10}$)	rs10773112 pval=$8×10^{-43}$ (Klarin, 30275531)
BBS2	cross all tissues	41	13	80%	$1.5×10^{-10}$	$1.4×10^{-7}$	rs183130 (pval=$4.04×10^{-111}$)	rs56156922 pval=$1×10^{-300}$ (Hoffmann, 29507422)
NUDT21	cross all tissues	7	4	89%	$1.5×10^{-10}$	$1.4×10^{-7}$	rs183130 (pval=$4.04×10^{-111}$)	rs56156922 pval=$1×10^{-300}$ (Hoffmann, 29507422)
ZNF664	cross metabolic tissues	4	2	85%	$2.2×10^{-10}$	$2.0×10^{-7}$	rs7133378 (pval=$7.55×10^{-10}$)	rs10773112 pval=$8×10^{-43}$ (Klarin, 30275531)
ACP2	cross metabolic tissues	6	3	86%	$8.0×10^{-10}$	$7.0×10^{-7}$	NA	rs75393320 pval=$8×10^{-45}$ (Klarin, 30275531)
RBM6	cross metabolic tissues	8	2	91%	$1.3×10^{-9}$	$1.1×10^{-6}$	NA	rs111439884 pval=$3×10^{-16}$ (Klarin, 30275531)
LILRA3	cross metabolic tissues	8	2	83%	$1.9×10^{-9}$	$1.6×10^{-6}$	rs429358 (pval=$6.31×10^{-12}$)	APOE region
C12orf65	cross all tissues	15	6	82%	$2.3×10^{-9}$	$1.8×10^{-6}$	rs7133378 (pval=$7.55×10^{-10}$)	rs4759375 pval=$2×10^{-24}$ (Klarin, 30275531)
INTS10	cross metabolic tissues	3	2	81%	$2.6×10^{-9}$	$2.0×10^{-6}$	rs15285 (pval=$3.45×10^{-31}$)	rs79407615 pval=$3×10^{-293}$ (Klarin, 30275531)
CDK2AP1	cross metabolic tissues	6	3	88%	$3.2×10^{-9}$	$2.3×10^{-6}$	rs7133378 (pval=$7.55×10^{-10}$)	rs4759375 pval=$2×10^{-24}$ (Klarin, 30275531)
DNAH10OS	cross metabolic tissues	3	1	82%	$3.8×10^{-9}$	$2.7×10^{-6}$	rs7133378 (pval=$7.55×10^{-10}$)	rs10773112 pval=$8×10^{-43}$ (Klarin, 30275531)
CCDC92	cross all tissues	24	10	81%	$6.7×10^{-9}$	$4.7×10^{-6}$	rs7133378 (pval=$7.55×10^{-10}$)	rs10773112 pval=$8×10^{-43}$ (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
MT3	cross all tissues	6	4	93%	8.1×10^{-9}	5.5×10^{-6}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
ABCB9	cross metabolic tissues	5	2	87%	2.5×10^{-8}	1.7×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PARP15	cross metabolic tissues	5	3	81%	4.2×10^{-8}	2.7×10^{-5}	NA	rs7614016 pval=1×10^{-09} (Hoffmann, 29507422)
RSPRY1	cross all tissues	9	4	81%	4.4×10^{-8}	2.7×10^{-5}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CCDC92	cross metabolic tissues	6	3	87%	6.4×10^{-8}	3.9×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
SETD8	cross metabolic tissues	4	1	82%	7.9×10^{-8}	4.7×10^{-5}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ZNF76	cross all tissues	6	2	86%	1.8×10^{-7}	1.0×10^{-4}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
LCAT	cross all tissues	12	4	82%	1.8×10^{-7}	1.0×10^{-4}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
ACP2	cross all tissues	23	8	81%	1.8×10^{-7}	1.0×10^{-4}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
NUP93	cross all tissues	8	4	81%	2.0×10^{-7}	1.1×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
DNAH10	cross all tissues	10	5	82%	2.4×10^{-7}	1.3×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
SIDT2	cross all tissues	17	5	82%	2.5×10^{-7}	1.3×10^{-4}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
ACYP2	cross all tissues	27	10	81%	2.9×10^{-7}	1.5×10^{-4}	NA	NA
SLC39A13	cross all tissues	19	7	83%	3.4×10^{-7}	1.7×10^{-4}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
PITPNM2	cross all tissues	6	2	80%	3.4×10^{-7}	1.7×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
RNASEH2C	cross metabolic tissues	7	3	84%	4.0×10^{-7}	1.9×10^{-4}	NA	rs12801636 pval=4×10^{-10} (Spracklen, 28334899)
SLC12A4	cross all tissues	8	4	82%	5.6×10^{-7}	2.6×10^{-4}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
RNASET2	cross metabolic tissues	6	2	86%	7.3×10^{-7}	3.3×10^{-4}	NA	NA
NRN1L	cross all tissues	5	2	85%	1.0×10^{-6}	4.4×10^{-4}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CDK2AP1	cross all tissues	28	8	82%	1.0×10^{-6}	4.4×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ACD	cross metabolic tissues	3	2	84%	1.1×10^{-6}	4.8×10^{-4}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
DNAH10	cross metabolic tissues	3	2	97%	1.1×10^{-6}	4.8×10^{-4}	rs7133378 (pval=7.55×10^{-10})	rs10773112 pval=8×10^{-43} (Klarin, 30275531)
ADAM10	cross all tissues	18	8	81%	1.4×10^{-6}	5.6×10^{-4}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
IKZF4	cross metabolic tissues	4	3	91%	1.4×10^{-6}	5.9×10^{-4}	NA	NA
AMFR	cross all tissues	22	11	81%	1.5×10^{-6}	5.9×10^{-4}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
B4GALT2	cross all tissues	6	4	88%	1.5×10^{-6}	5.9×10^{-4}	NA	NA
FAM205A	cross all tissues	6	3	85%	1.7×10^{-6}	6.5×10^{-4}	NA	NA
RP11-166B2.1	cross metabolic tissues	7	2	85%	1.8×10^{-6}	6.8×10^{-4}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
NR1H3	cross all tissues	19	8	83%	2.1×10^{-6}	7.8×10^{-4}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
POLR2M	cross all tissues	21	9	82%	2.3×10^{-6}	8.5×10^{-4}	rs1077835 (pval=1.69×10^{-21})	rs77250403 pval=6×10^{-216} (Klarin, 30275531)
RNASET2	cross all tissues	23	8	82%	2.5×10^{-6}	9.1×10^{-4}	NA	NA
P2RX7	cross all tissues	8	4	83%	2.5×10^{-6}	9.1×10^{-4}	rs7133378 (pval=7.55×10^{-10})	NA
RNF123	cross metabolic tissues	3	2	94%	3.0×10^{-6}	1.1×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
APOA1	cross all tissues	8	4	82%	3.1×10^{-6}	1.1×10^{-3}	rs964184 (pval=3.66×10^{-12})	rs3741297 pval=3×10^{-157} (Kanai, 29403010)
IRS1	cross metabolic tissues	4	3	92%	4.3×10^{-6}	1.5×10^{-3}	NA	rs2203452 pval=9×10^{-52} (Klarin, 30275531)
ENKD1	cross all tissues	5	3	89%	5.2×10^{-6}	1.8×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
MT1A	cross metabolic tissues	4	2	82%	5.8×10^{-6}	1.9×10^{-3}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
F2	cross all tissues	6	3	86%	5.9×10^{-6}	1.9×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
PARD6A	cross all tissues	6	3	86%	6.1×10^{-6}	2.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
MT1X	cross all tissues	14	5	81%	6.4×10^{-6}	2.1×10^{-3}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
N6AMT1	cross all tissues	21	8	83%	8.2×10^{-6}	2.6×10^{-3}	NA	NA
RBM6	cross all tissues	48	9	82%	1.1×10^{-5}	3.3×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ZNF285B	cross all tissues	8	4	86%	1.1×10^{-5}	3.4×10^{-3}	rs429358 (pval=6.31×10^{-12})	APOE region
CSGALNACT1	cross metabolic tissues	6	3	84%	1.2×10^{-5}	3.7×10^{-3}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
DEF6	cross all tissues	11	3	80%	1.2×10^{-5}	3.7×10^{-3}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
TSNAXIP1	cross all tissues	18	5	81%	1.4×10^{-5}	4.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
COQ10A	cross all tissues	8	4	86%	1.4×10^{-5}	4.2×10^{-3}	NA	NA
PPP1R18	cross all tissues	16	8	81%	1.6×10^{-5}	4.5×10^{-3}	NA	NA
OGFOD1	cross all tissues	15	6	81%	1.6×10^{-5}	4.6×10^{-3}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
YWHAB	cross metabolic tissues	4	2	86%	1.7×10^{-5}	4.7×10^{-3}	NA	rs1800961 pval=2×10^{-65} (Klarin, 30275531)
INTS10	cross all tissues	18	7	81%	1.7×10^{-5}	4.8×10^{-3}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
SLC39A13	cross metabolic tissues	6	4	90%	1.8×10^{-5}	5.0×10^{-3}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
IKZF4	cross all tissues	9	4	83%	1.9×10^{-5}	5.2×10^{-3}	NA	NA
FGFR1OP	cross all tissues	14	5	82%	2.1×10^{-5}	5.6×10^{-3}	NA	NA
RWDD2B	cross metabolic tissues	6	2	87%	2.1×10^{-5}	5.7×10^{-3}	NA	NA
SLC12A4	cross metabolic tissues	4	2	80%	2.4×10^{-5}	6.2×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
ERVFRD-1	cross all tissues	7	3	85%	2.5×10^{-5}	6.4×10^{-3}	NA	NA
SPATA5L1	cross metabolic tissues	7	2	83%	2.7×10^{-5}	6.9×10^{-3}	NA	NA
SNRPC	cross metabolic tissues	6	3	84%	2.7×10^{-5}	7.0×10^{-3}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
GFOD2	cross all tissues	8	4	85%	2.8×10^{-5}	7.0×10^{-3}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
UHRF1BP1	cross metabolic tissues	8	2	81%	3.0×10^{-5}	7.4×10^{-3}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
UBA7	cross all tissues	18	5	81%	3.1×10^{-5}	7.6×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
hsa-mir-8072	cross all tissues	32	8	81%	3.1×10^{-5}	7.7×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
GPER1	cross metabolic tissues	4	2	81%	3.2×10^{-5}	7.7×10^{-3}	NA	NA
UBA7	cross metabolic tissues	4	2	94%	3.2×10^{-5}	7.7×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ABCA1	cross metabolic tissues	3	3	100%	3.2×10^{-5}	7.7×10^{-3}	NA	rs4149307 pval=3×10^{-93} (Klarin, 30275531)
RP11-119D9.1	cross all tissues	5	3	93%	3.5×10^{-5}	8.1×10^{-3}	NA	NA
C12orf65	cross metabolic tissues	3	2	90%	3.5×10^{-5}	8.1×10^{-3}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
PHF14	cross all tissues	14	6	82%	3.5×10^{-5}	8.1×10^{-3}	NA	NA
AL133458.1	cross metabolic tissues	5	3	85%	3.6×10^{-5}	8.3×10^{-3}	NA	NA
PIWIL2	cross all tissues	37	11	80%	3.9×10^{-5}	8.8×10^{-3}	rs15285 (pval=3.45×10^{-31})	NA
POLR2J2	cross metabolic tissues	8	2	88%	4.0×10^{-5}	8.9×10^{-3}	NA	NA
POLR2J2	cross metabolic tissues	8	2	88%	4.0×10^{-5}	8.9×10^{-3}	NA	NA
PGS1	cross all tissues	19	7	81%	4.1×10^{-5}	8.9×10^{-3}	NA	rs12601079 pval=8×10^{-35} (Klarin, 30275531)
N6AMT1	cross metabolic tissues	5	2	85%	4.1×10^{-5}	8.9×10^{-3}	NA	NA
MAD2L1	cross all tissues	9	5	85%	4.1×10^{-5}	8.9×10^{-3}	NA	NA
SEMA3F	cross all tissues	14	6	83%	4.5×10^{-5}	9.6×10^{-3}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
PARP15	cross all tissues	21	9	83%	4.5×10^{-5}	9.6×10^{-3}	NA	rs7614016 pval=1×10^{-09} (Hoffmann, 29507422)
C12orf43	cross metabolic tissues	8	4	83%	4.8×10^{-5}	1.0×10^{-2}	rs7133378 (pval=7.55×10^{-10})	NA
TCTN2	cross all tissues	39	14	80%	4.8×10^{-5}	1.0×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
NR1H3	cross metabolic tissues	4	3	92%	4.9×10^{-5}	1.0×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
LTN1	cross all tissues	5	3	86%	4.9×10^{-5}	1.0×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
IGFBP2	cross metabolic tissues	5	3	85%	5.0×10^{-5}	1.0×10^{-2}	NA	NA
RASA4B	cross metabolic tissues	6	3	85%	5.1×10^{-5}	1.0×10^{-2}	NA	NA
SPDYE6	cross all tissues	31	11	81%	5.1×10^{-5}	1.0×10^{-2}	NA	NA
PINLYP	cross metabolic tissues	5	3	91%	5.4×10^{-5}	1.1×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
ZNF76	cross metabolic tissues	3	1	88%	5.5×10^{-5}	1.1×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
NBPF3	cross all tissues	49	7	81%	5.6×10^{-5}	1.1×10^{-2}	NA	NA
NOP56	cross metabolic tissues	4	3	89%	5.6×10^{-5}	1.1×10^{-2}	NA	NA
RP11-384F7.2	cross all tissues	7	4	84%	5.8×10^{-5}	1.1×10^{-2}	NA	NA
ACD	cross all tissues	6	4	83%	5.8×10^{-5}	1.1×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
HLA-B	cross all tissues	34	12	81%	5.9×10^{-5}	1.1×10^{-2}	NA	NA
RERE	cross all tissues	18	7	82%	6.7×10^{-5}	1.2×10^{-2}	NA	rs149963466 pval=3×10^{-08} (Nagy, 28270201)
GATC	cross all tissues	41	15	81%	6.8×10^{-5}	1.3×10^{-2}	rs7133378 (pval=7.55×10^{-10})	NA
DPEP3	cross all tissues	5	3	88%	7.2×10^{-5}	1.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
MST1R	cross metabolic tissues	5	3	90%	7.3×10^{-5}	1.3×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
USP35	cross all tissues	16	6	85%	7.4×10^{-5}	1.3×10^{-2}	NA	NA
PIWIL2	cross metabolic tissues	5	2	88%	7.4×10^{-5}	1.3×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
RPL23P2	cross all tissues	16	7	82%	8.1×10^{-5}	1.4×10^{-2}	NA	NA
HIST1H2BK	cross all tissues	8	4	81%	8.4×10^{-5}	1.5×10^{-2}	NA	NA
PRSS16	cross all tissues	20	5	80%	8.4×10^{-5}	1.5×10^{-2}	NA	NA
C7orf50	cross metabolic tissues	4	2	82%	8.4×10^{-5}	1.5×10^{-2}	NA	NA
DAP	cross metabolic tissues	8	3	82%	8.5×10^{-5}	1.5×10^{-2}	NA	NA
RNF123	cross all tissues	33	10	81%	9.1×10^{-5}	1.6×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
AMFR	cross metabolic tissues	4	3	90%	9.4×10^{-5}	1.6×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PABPC4	cross metabolic tissues	5	2	81%	9.8×10^{-5}	1.7×10^{-2}	NA	rs3768321 pval=1×10^{-36} (Klarin, 30275531)
POMT1	cross metabolic tissues	5	2	81%	9.9×10^{-5}	1.7×10^{-2}	NA	NA
GEMIN7	cross all tissues	40	15	81%	9.9×10^{-5}	1.7×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
FAM129A	cross all tissues	10	5	85%	1.0×10^{-4}	1.7×10^{-2}	NA	rs10911505 pval=1×10^{-08} (Klarin, 30275531)
LILRA3	cross all tissues	32	11	81%	1.0×10^{-4}	1.7×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
MTL5	cross metabolic tissues	6	3	84%	1.1×10^{-4}	1.8×10^{-2}	NA	NA
DGKG	cross all tissues	5	4	93%	1.1×10^{-4}	1.8×10^{-2}	NA	rs112545201 pval=3×10^{-19} (Hoffmann, 29507422)
TMEM252	cross metabolic tissues	3	2	83%	1.1×10^{-4}	1.8×10^{-2}	NA	NA
TPK1	cross metabolic tissues	8	3	80%	1.2×10^{-4}	1.9×10^{-2}	NA	NA
MST1R	cross all tissues	25	9	81%	1.2×10^{-4}	1.9×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
NARS2	cross all tissues	37	6	81%	1.2×10^{-4}	1.9×10^{-2}	NA	NA
PSMC3	cross metabolic tissues	6	3	81%	1.3×10^{-4}	2.0×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
RXRG	cross metabolic tissues	3	2	86%	1.3×10^{-4}	2.0×10^{-2}	NA	NA
C6orf25	cross all tissues	5	3	87%	1.4×10^{-4}	2.1×10^{-2}	NA	rs28366301 pval=8×10^{-11} (Kanai, 29403010)
POLR2J	cross all tissues	13	5	81%	1.4×10^{-4}	2.1×10^{-2}	NA	NA
CYB561D1	cross all tissues	5	2	80%	1.4×10^{-4}	2.1×10^{-2}	NA	rs3832016 pval=4×10^{-29} (Klarin, 30275531)
AC005003.1	cross all tissues	6	3	86%	1.4×10^{-4}	2.1×10^{-2}	NA	NA
SERPINH1	cross metabolic tissues	3	2	92%	1.4×10^{-4}	2.1×10^{-2}	NA	rs34696509 pval=2×10^{-13} (Klarin, 30275531)
MT1DP	cross all tissues	5	3	86%	1.4×10^{-4}	2.2×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
MT1G	cross all tissues	13	5	81%	1.5×10^{-4}	2.2×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
CTRL	cross all tissues	6	3	84%	1.5×10^{-4}	2.2×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
MRFAP1	cross all tissues	6	2	86%	1.6×10^{-4}	2.3×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CCDC25	cross metabolic tissues	6	2	84%	1.6×10^{-4}	2.3×10^{-2}	rs15285 (pval=3.45×10^{-31})	NA
SH2D4A	cross all tissues	11	6	84%	1.6×10^{-4}	2.3×10^{-2}	rs15285 (pval=3.45×10^{-31})	rs79407615 pval=3×10^{-293} (Klarin, 30275531)
DEF6	cross metabolic tissues	3	1	81%	1.7×10^{-4}	2.4×10^{-2}	NA	rs9368830 pval=4×10^{-21} (Klarin, 30275531)
KIAA1715	cross metabolic tissues	6	3	80%	1.7×10^{-4}	2.4×10^{-2}	NA	NA
RILPL2	cross all tissues	16	7	81%	1.7×10^{-4}	2.4×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
LST1	cross metabolic tissues	4	3	89%	1.7×10^{-4}	2.4×10^{-2}	NA	NA
IMPDH1	cross metabolic tissues	3	2	92%	1.7×10^{-4}	2.4×10^{-2}	NA	rs7778167 pval=2×10^{-11} (Kanai, 29403010)
APOE	cross all tissues	7	4	85%	1.7×10^{-4}	2.4×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
CD320	cross all tissues	10	5	82%	1.7×10^{-4}	2.4×10^{-2}	rs116843064 (pval=1.17×10^{-09})	rs116843064 pval=3×10^{-137} (Klarin, 30275531)
HCG27	cross metabolic tissues	8	3	85%	1.8×10^{-4}	2.5×10^{-2}	NA	NA
KCNIP2	cross all tissues	5	4	91%	1.8×10^{-4}	2.5×10^{-2}	NA	NA
ABCA1	cross all tissues	6	4	86%	2.0×10^{-4}	2.7×10^{-2}	NA	rs4149307 pval=3×10^{-93} (Klarin, 30275531)
TMC4	cross all tissues	40	13	81%	2.1×10^{-4}	2.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
C1QTNF4	cross all tissues	29	6	81%	2.1×10^{-4}	2.8×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
PSMC3	cross all tissues	26	7	81%	2.1×10^{-4}	2.8×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
ERCC2	cross all tissues	22	9	82%	2.1×10^{-4}	2.8×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
CELSR2	cross all tissues	21	7	80%	2.2×10^{-4}	2.9×10^{-2}	NA	rs3832016 pval=4×10^{-29} (Klarin, 30275531)
C4A	cross all tissues	44	16	80%	2.2×10^{-4}	2.9×10^{-2}	NA	rs28366301 pval=8×10^{-11} (Kanai, 29403010)
ELP2	cross metabolic tissues	4	2	90%	2.2×10^{-4}	2.9×10^{-2}	NA	NA
LCAT	cross metabolic tissues	5	3	86%	2.3×10^{-4}	3.0×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
RFNG	cross all tissues	10	4	81%	2.4×10^{-4}	3.1×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CACNA1H	cross all tissues	10	5	81%	2.4×10^{-4}	3.1×10^{-2}	NA	NA
MAK	cross all tissues	5	3	90%	2.4×10^{-4}	3.1×10^{-2}	NA	NA
NARS2	cross metabolic tissues	7	2	85%	2.4×10^{-4}	3.1×10^{-2}	NA	NA
RP11-766N7.3	cross all tissues	13	5	83%	2.4×10^{-4}	3.1×10^{-2}	NA	NA
CENPH	cross metabolic tissues	4	3	89%	2.5×10^{-4}	3.2×10^{-2}	NA	NA
COQ7	cross all tissues	23	7	82%	2.5×10^{-4}	3.2×10^{-2}	NA	NA
HCAR3	cross all tissues	7	2	81%	2.5×10^{-4}	3.2×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
DARS	cross all tissues	13	5	85%	2.6×10^{-4}	3.2×10^{-2}	NA	NA
MYBPC3	cross metabolic tissues	3	2	93%	2.6×10^{-4}	3.2×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
LRWD1	cross metabolic tissues	7	3	88%	2.6×10^{-4}	3.3×10^{-2}	NA	NA
IFITM4P	cross all tissues	41	12	82%	2.7×10^{-4}	3.3×10^{-2}	NA	NA
WDR6	cross all tissues	40	8	80%	2.8×10^{-4}	3.5×10^{-2}	NA	rs111439884 pval=3×10^{-16} (Klarin, 30275531)
ADCYAP1R1	cross all tissues	8	4	84%	2.9×10^{-4}	3.5×10^{-2}	NA	NA
ZNF334	cross all tissues	33	8	80%	2.9×10^{-4}	3.5×10^{-2}	NA	rs6065906 pval=5×10^{-40} (Willer, 24097068)
TSNAXIP1	cross metabolic tissues	3	2	94%	2.9×10^{-4}	3.5×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
MAGOHB	cross all tissues	9	5	86%	2.9×10^{-4}	3.5×10^{-2}	NA	NA
CD3EAP	cross all tissues	24	9	82%	3.0×10^{-4}	3.5×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
ETHE1	cross metabolic tissues	6	3	85%	3.0×10^{-4}	3.5×10^{-2}	rs429358 (pval=6.31×10^{-12})	APOE region
MYO1F	cross all tissues	14	5	82%	3.0×10^{-4}	3.5×10^{-2}	rs116843064 (pval=1.17×10^{-09})	rs116843064 pval=3×10^{-137} (Klarin, 30275531)
UPB1	cross all tissues	27	7	81%	3.0×10^{-4}	3.5×10^{-2}	NA	NA
UBE2Z	cross metabolic tissues	4	2	90%	3.1×10^{-4}	3.6×10^{-2}	rs72836561 (pval=3.63×10^{-09})	NA
TMEM89	cross all tissues	6	3	83%	3.1×10^{-4}	3.6×10^{-2}	NA	rs6808104 pval=7×10^{-09} (Klarin, 30275531)
DDX55	cross all tissues	43	13	81%	3.2×10^{-4}	3.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
SMTNL2	cross all tissues	8	4	83%	3.2×10^{-4}	3.7×10^{-2}	NA	NA
PDE6D	cross all tissues	6	4	89%	3.2×10^{-4}	3.7×10^{-2}	NA	NA
RWDD2B	cross all tissues	36	8	81%	3.4×10^{-4}	3.9×10^{-2}	NA	NA
CWF19L1	cross metabolic tissues	8	2	86%	3.4×10^{-4}	3.9×10^{-2}	NA	rs1408579 pval=7×10^{-11} (Klarin, 30275531)
RP11-175I17.2	cross all tissues	24	8	80%	3.5×10^{-4}	3.9×10^{-2}	NA	rs553682607 pval=1×10^{-15} (Klarin, 30275531)
CTC-498M16.4	cross all tissues	10	4	81%	3.5×10^{-4}	3.9×10^{-2}	NA	NA
SYT7	cross all tissues	9	5	85%	3.5×10^{-4}	3.9×10^{-2}	NA	rs174550 pval=6×10^{-30} (Spracklen, 28334899)
NPC1	cross metabolic tissues	5	2	85%	3.5×10^{-4}	3.9×10^{-2}	NA	rs1788783 pval=8×10^{-14} (Klarin, 30275531)
HOXD1	cross metabolic tissues	3	3	100%	3.5×10^{-4}	3.9×10^{-2}	NA	NA
HLA-C	cross metabolic tissues	8	4	84%	3.7×10^{-4}	4.0×10^{-2}	NA	NA
GNAO1	cross metabolic tissues	3	2	86%	3.7×10^{-4}	4.0×10^{-2}	rs183130 (pval=4.04×10^{-111})	rs56156922 pval=1×10^{-300} (Hoffmann, 29507422)
XXbac-BPG248L24.12	cross all tissues	34	13	80%	3.7×10^{-4}	4.0×10^{-2}	NA	NA
RP11-166B2.1	cross all tissues	47	11	80%	3.7×10^{-4}	4.0×10^{-2}	NA	rs7188861 pval=7×10^{-09} (Surakka, 25961943)
DARS	cross metabolic tissues	3	2	97%	3.8×10^{-4}	4.1×10^{-2}	NA	NA
NUTM2E	cross metabolic tissues	3	2	92%	3.8×10^{-4}	4.1×10^{-2}	NA	NA
PABPC1P4	cross all tissues	11	5	81%	3.9×10^{-4}	4.1×10^{-2}	NA	NA
OIP5	cross all tissues	15	7	81%	3.9×10^{-4}	4.1×10^{-2}	NA	NA
OXCT2P1	cross metabolic tissues	3	2	86%	4.0×10^{-4}	4.2×10^{-2}	NA	rs3768321 pval=1×10^{-36} (Klarin, 30275531)
GDE1	cross all tissues	11	5	84%	4.0×10^{-4}	4.2×10^{-2}	NA	NA
RPS6KA4	cross all tissues	6	3	87%	4.1×10^{-4}	4.2×10^{-2}	NA	rs71468663 pval=2×10^{-15} (Klarin, 30275531)
VEGFB	cross all tissues	14	6	80%	4.1×10^{-4}	4.2×10^{-2}	NA	rs71468663 pval=2×10^{-15} (Klarin, 30275531)
DUS2	cross all tissues	14	5	82%	4.1×10^{-4}	4.3×10^{-2}	NA	rs56070533 pval=9×10^{-95} (Klarin, 30275531)
AOAH	cross metabolic tissues	6	3	81%	4.2×10^{-4}	4.3×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Eexplained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
RASA4B	cross all tissues	24	10	81%	4.3×10^{-4}	4.4×10^{-2}	NA	NA
CENPQ	cross metabolic tissues	6	3	83%	4.3×10^{-4}	4.4×10^{-2}	NA	NA
DDB2	cross all tissues	9	5	86%	4.3×10^{-4}	4.4×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
LRWD1	cross all tissues	35	8	81%	4.4×10^{-4}	4.5×10^{-2}	NA	NA
ZBTB42	cross metabolic tissues	3	2	82%	4.5×10^{-4}	4.5×10^{-2}	NA	rs2494748 pval=3×10^{-26} (Klarin, 30275531)
ATP5G1	cross all tissues	14	5	81%	4.5×10^{-4}	4.5×10^{-2}	rs72836561 (pval=3.63×10^{-09})	NA
PLSCR1	cross metabolic tissues	5	3	90%	4.5×10^{-4}	4.5×10^{-2}	NA	NA
PCNXL3	cross metabolic tissues	5	2	81%	4.6×10^{-4}	4.6×10^{-2}	NA	rs12801636 pval=4×10^{-10} (Spracklen, 28334899)
LTBP2	cross all tissues	7	3	86%	4.6×10^{-4}	4.6×10^{-2}	NA	rs13379043 pval=1×10^{-08} (Klarin, 30275531)
VPS37B	cross all tissues	6	2	89%	4.6×10^{-4}	4.6×10^{-2}	rs7133378 (pval=7.55×10^{-10})	rs4759375 pval=2×10^{-24} (Klarin, 30275531)
ICOSLG	cross metabolic tissues	6	4	87%	4.7×10^{-4}	4.6×10^{-2}	NA	rs235314 pval=3×10^{-10} (Kanai, 29403010)
ERBB4	cross all tissues	13	7	82%	4.7×10^{-4}	4.6×10^{-2}	NA	rs1047891 pval=9×10^{-10} (Willer, 24097068)
ACADS	cross all tissues	23	9	82%	4.8×10^{-4}	4.7×10^{-2}	rs7133378 (pval=7.55×10^{-10})	NA
MLF2	cross metabolic tissues	7	4	85%	4.9×10^{-4}	4.8×10^{-2}	NA	rs10743940 pval=7×10^{-09} (Spracklen, 28334899)
PACSIN3	cross all tissues	19	6	81%	4.9×10^{-4}	4.8×10^{-2}	NA	rs75393320 pval=8×10^{-45} (Klarin, 30275531)
CCDC85B	cross all tissues	5	3	87%	5.1×10^{-4}	4.9×10^{-2}	NA	rs12801636 pval=4×10^{-10} (Spracklen, 28334899)
TMPRSS5	cross all tissues	24	8	81%	5.1×10^{-4}	4.9×10^{-2}	rs964184 (pval=3.66×10^{-12})	NA
RGS12	cross metabolic tissues	3	2	81%	5.1×10^{-4}	5.0×10^{-2}	NA	NA
KCNJ6	cross all tissues	6	4	88%	5.2×10^{-4}	5.0×10^{-2}	NA	NA

Appendix X. Cross-tissue GReX results of the genes significantly associated with LDL-C in BioVU

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PSRC1	cross metabolic tissues	8	3	0.86	8.8×10^{-93}	2.1×10^{-88}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SORT1	cross all tissues	9	4	0.85	1.8×10^{-87}	2.1×10^{-83}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	cross metabolic tissues	6	3	0.86	1.6×10^{-86}	1.3×10^{-82}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	cross all tissues	32	11	0.81	1.9×10^{-84}	1.1×10^{-80}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	cross all tissues	21	7	0.80	3.7×10^{-76}	1.7×10^{-72}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SORT1	cross metabolic tissues	3	1	0.85	3.1×10^{-56}	1.2×10^{-52}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
GEMIN7	cross all tissues	40	15	0.81	5.4×10^{-40}	1.8×10^{-36}	rs7412 (pval=3.55×10^{-178})	APOE region
APOB	cross all tissues	12	5	0.84	1.0×10^{-35}	3.0×10^{-32}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
SARS	cross all tissues	5	3	0.81	1.5×10^{-28}	3.9×10^{-25}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
DOCK6	cross all tissues	15	5	0.80	8.8×10^{-23}	2.1×10^{-19}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
CEACAM19	cross all tissues	40	17	0.81	1.1×10^{-21}	2.3×10^{-18}	rs7412 (pval=3.55×10^{-178})	APOE region
P2RY11	cross all tissues	26	11	0.81	7.2×10^{-18}	1.4×10^{-14}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PCSK9	cross all tissues	8	4	0.87	7.2×10^{-17}	1.3×10^{-13}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
GSTM3	cross all tissues	48	14	0.80	6.7×10^{-16}	1.1×10^{-12}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CLCC1	cross all tissues	15	4	0.81	4.0×10^{-15}	6.3×10^{-12}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ZNF112	cross all tissues	22	7	0.82	7.6×10^{-15}	1.1×10^{-11}	rs7412 (pval=3.55×10^{-178})	APOE region
GSTM1	cross all tissues	37	18	0.81	8.2×10^{-15}	1.1×10^{-11}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SYPL2	cross all tissues	29	10	0.81	1.0×10^{-14}	1.4×10^{-11}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ZNF155	cross all tissues	33	14	0.80	2.2×10^{-14}	2.7×10^{-11}	rs7412 (pval=3.55×10^{-178})	APOE region
SMARCA4	cross all tissues	10	5	0.82	1.5×10^{-13}	1.8×10^{-10}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ATXN7L2	cross all tissues	15	7	0.83	1.5×10^{-12}	1.7×10^{-9}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
PVRL2	cross metabolic tissues	6	3	0.88	1.7×10^{-12}	1.9×10^{-9}	rs7412 (pval=3.55×10^{-178})	APOE region
PVRL2	cross all tissues	18	7	0.82	2.0×10^{-12}	2.1×10^{-9}	rs7412 (pval=3.55×10^{-178})	APOE region
ATXN7L2	cross metabolic tissues	3	2	0.92	5.4×10^{-12}	5.3×10^{-9}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ZNF285B	cross all tissues	8	4	0.86	3.0×10^{-11}	2.9×10^{-8}	rs7412 (pval=3.55×10^{-178})	APOE region
AC067959.1	cross all tissues	13	5	0.84	3.1×10^{-11}	2.9×10^{-8}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
CEACAM19	cross metabolic tissues	7	4	0.85	5.1×10^{-11}	4.3×10^{-8}	rs7412 (pval=3.55×10^{-178})	APOE region
SPC24	cross all tissues	23	10	0.83	5.2×10^{-11}	4.3×10^{-8}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ZNF235	cross all tissues	17	7	0.81	5.3×10^{-11}	4.3×10^{-8}	rs7412 (pval=3.55×10^{-178})	APOE region
GSTM2	cross all tissues	24	12	0.82	6.7×10^{-11}	5.3×10^{-8}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
HPR	cross all tissues	25	7	0.81	1.1×10^{-10}	8.3×10^{-8}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
DMPK	cross all tissues	20	9	0.82	1.2×10^{-10}	8.9×10^{-8}	rs7412 (pval=3.55×10^{-178})	APOE region
WTAP	cross all tissues	30	9	0.82	5.0×10^{-10}	3.6×10^{-7}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
ST3GAL4	cross metabolic tissues	5	3	0.86	6.4×10^{-10}	4.4×10^{-7}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
ANKDD1B	cross all tissues	13	7	0.83	7.8×10^{-10}	5.3×10^{-7}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
ST3GAL4	cross all tissues	16	8	0.83	8.0×10^{-10}	5.3×10^{-7}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
AP1M2	cross all tissues	13	5	0.82	1.3×10^{-9}	8.1×10^{-7}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
KLC3	cross all tissues	10	5	0.84	2.1×10^{-9}	1.3×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
GEMIN7	cross metabolic tissues	6	2	0.84	2.2×10^{-9}	1.3×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
KRI1	cross all tissues	48	10	0.80	2.4×10^{-9}	1.4×10^{-6}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
FADS2	cross all tissues	28	9	0.81	2.5×10^{-9}	1.5×10^{-6}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
TXNL4B	cross all tissues	16	8	0.82	2.9×10^{-9}	1.7×10^{-6}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
GSTM1	cross metabolic tissues	7	4	0.84	3.3×10^{-9}	1.8×10^{-6}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
ERCC1	cross all tissues	23	8	0.82	6.0×10^{-9}	3.2×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
KANK2	cross all tissues	22	9	0.81	7.9×10^{-9}	4.2×10^{-6}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ZNF404	cross all tissues	41	14	0.81	1.2×10^{-8}	6.2×10^{-6}	rs7412 (pval=3.55×10^{-178})	APOE region
FTH1	cross all tissues	6	4	0.87	1.4×10^{-8}	7.0×10^{-6}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
HP	cross all tissues	12	5	0.83	1.6×10^{-8}	8.0×10^{-6}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
TMEM258	cross all tissues	19	9	0.82	2.6×10^{-8}	1.3×10^{-5}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
C19orf52	cross all tissues	5	3	0.89	3.1×10^{-8}	1.5×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.2	cross all tissues	42	13	0.80	3.5×10^{-8}	1.6×10^{-5}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
FADS1	cross all tissues	24	9	0.81	4.0×10^{-8}	1.8×10^{-5}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
C19orf52	cross metabolic tissues	3	2	0.94	5.5×10^{-8}	2.5×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
GSTM4	cross all tissues	36	14	0.81	7.5×10^{-8}	3.3×10^{-5}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
SLC22A3	cross all tissues	25	10	0.81	7.6×10^{-8}	3.3×10^{-5}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RP11-295M18.2	cross metabolic tissues	6	2	0.83	9.5×10^{-8}	4.0×10^{-5}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
IGF2R	cross metabolic tissues	4	2	0.85	1.0×10^{-7}	4.3×10^{-5}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
SMARCA4	cross metabolic tissues	3	2	0.83	1.3×10^{-7}	5.2×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
FADS2	cross metabolic tissues	6	2	0.86	1.3×10^{-7}	5.2×10^{-5}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
CETP	cross all tissues	8	4	0.83	1.6×10^{-7}	6.3×10^{-5}	NA	rs3764261 pval=2×10^{-34} (Willer, 24097068)
CD3EAP	cross all tissues	24	9	0.82	1.8×10^{-7}	7.0×10^{-5}	rs7412 (pval=3.55×10^{-178})	APOE region
TYK2	cross all tissues	16	8	0.82	1.8×10^{-7}	7.0×10^{-5}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
PKN3	cross all tissues	11	5	0.85	2.4×10^{-7}	9.2×10^{-5}	rs532436 (pval=2.31×10^{-11})	NA
GSTM2	cross metabolic tissues	6	4	0.85	3.6×10^{-7}	1.3×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
HMGCR	cross all tissues	8	3	0.85	5.0×10^{-7}	1.8×10^{-4}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
MRPL45P2	cross metabolic tissues	5	2	0.85	5.9×10^{-7}	2.1×10^{-4}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
DOCK7	cross metabolic tissues	4	2	0.83	6.1×10^{-7}	2.2×10^{-4}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
CLPTM1	cross all tissues	6	4	0.85	7.0×10^{-7}	2.4×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM258	cross metabolic tissues	3	2	0.82	7.9×10^{-7}	2.7×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
RP11-295M18.6	cross all tissues	41	13	0.80	9.3×10^{-7}	3.2×10^{-4}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
PCSK9	cross metabolic tissues	3	1	0.84	1.2×10^{-6}	3.8×10^{-4}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
RP11-288H12.3	cross all tissues	16	8	0.81	1.2×10^{-6}	3.8×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
AMIGO1	cross all tissues	37	11	0.82	1.2×10^{-6}	3.9×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ZNF283	cross metabolic tissues	5	3	0.91	1.3×10^{-6}	4.0×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
C2orf43	cross all tissues	45	13	0.81	1.3×10^{-6}	4.2×10^{-4}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
MYBPHL	cross all tissues	9	4	0.86	1.4×10^{-6}	4.3×10^{-4}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RP11-295M18.6	cross metabolic tissues	6	3	0.86	1.4×10^{-6}	4.3×10^{-4}	NA	rs2642438 pval=9×10^{-24} (Hoffmann, 29507422)
MAU2	cross metabolic tissues	5	3	0.83	2.0×10^{-6}	6.2×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
FUT2	cross all tissues	19	7	0.81	2.3×10^{-6}	7.0×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
FADS1	cross metabolic tissues	4	2	0.86	2.5×10^{-6}	7.3×10^{-4}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
NTN5	cross all tissues	20	7	0.82	2.6×10^{-6}	7.7×10^{-4}	rs7412 (pval=3.55×10^{-178})	APOE region
ATP13A1	cross all tissues	14	6	0.84	2.7×10^{-6}	7.9×10^{-4}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
SLC22A3	cross metabolic tissues	6	3	0.81	2.8×10^{-6}	7.9×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RAB8A	cross metabolic tissues	5	3	0.87	2.8×10^{-6}	7.9×10^{-4}	rs17248727 (pval=4.40×10^{-51})	NA
SLC22A1	cross all tissues	16	8	0.82	2.9×10^{-6}	8.0×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RP11-288H12.3	cross metabolic tissues	3	2	0.80	2.9×10^{-6}	8.0×10^{-4}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
PLEC	cross all tissues	38	12	0.81	3.2×10^{-6}	8.8×10^{-4}	NA	rs7832643 pval=2×10^{-17} (Spracklen, 28334899)
IGF2R	cross all tissues	16	8	0.83	6.2×10^{-6}	1.7×10^{-3}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ZNF283	cross all tissues	28	10	0.81	6.8×10^{-6}	1.8×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
ATP13A1	cross metabolic tissues	4	3	0.89	8.1×10^{-6}	2.1×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
TBKBP1	cross all tissues	36	10	0.82	8.3×10^{-6}	2.2×10^{-3}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
ABCA6	cross all tissues	10	4	0.83	9.0×10^{-6}	2.3×10^{-3}	rs740516 (pval=3.11×10^{-10})	rs77542162 pval=4×10^{-52} (Klarin, 30275531)
ERCC2	cross all tissues	22	9	0.82	1.0×10^{-5}	2.6×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
SYPL2	cross metabolic tissues	4	2	0.80	1.0×10^{-5}	2.6×10^{-3}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
CCDC159	cross all tissues	5	4	0.89	1.4×10^{-5}	3.5×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
CARM1	cross all tissues	11	5	0.86	1.4×10^{-5}	3.5×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
SEC1P	cross all tissues	22	7	0.81	1.6×10^{-5}	4.0×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF20	cross all tissues	10	4	0.84	1.6×10^{-5}	4.0×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs2738464 pval=4×10^{-40} (Kanai, 29403010)
ACAT1	cross all tissues	24	9	0.80	1.8×10^{-5}	4.3×10^{-3}	NA	NA
ZNF284	cross all tissues	19	6	0.82	1.8×10^{-5}	4.3×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
DKFZP761J1410	cross all tissues	21	8	0.82	1.9×10^{-5}	4.4×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
TBKBP1	cross metabolic tissues	8	3	0.86	2.1×10^{-5}	5.0×10^{-3}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
GTF3C3	cross all tissues	5	3	0.83	2.2×10^{-5}	5.0×10^{-3}	NA	NA

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ZNF491	cross all tissues	6	4	0.91	2.3×10^{-5}	5.2×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
POLK	cross all tissues	18	7	0.83	2.4×10^{-5}	5.4×10^{-3}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
FADS3	cross all tissues	10	4	0.81	2.4×10^{-5}	5.5×10^{-3}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
AP1G1	cross all tissues	13	6	0.81	2.5×10^{-5}	5.5×10^{-3}	rs2287997 (pval=2.93×10^{-08})	rs5471 pval=5×10^{-57} (Klarin, 30275531)
NTN5	cross metabolic tissues	3	1	0.84	2.6×10^{-5}	5.7×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
SIRT6	cross all tissues	30	7	0.81	2.7×10^{-5}	5.8×10^{-3}	rs17248727 (pval=4.40×10^{-51})	NA
TGDS	cross metabolic tissues	3	2	0.98	3.5×10^{-5}	7.5×10^{-3}	NA	NA
GALNT3	cross metabolic tissues	6	3	0.84	3.5×10^{-5}	7.5×10^{-3}	NA	NA
MRPL45P2	cross all tissues	24	7	0.81	3.6×10^{-5}	7.5×10^{-3}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)
EXOC3L2	cross all tissues	9	5	0.82	3.8×10^{-5}	7.9×10^{-3}	rs7412 (pval=3.55×10^{-178})	APOE region
HAVCR1	cross metabolic tissues	4	2	0.88	4.4×10^{-5}	9.2×10^{-3}	rs12657266 (pval=1.33×10^{-09})	rs6882076 pval=1×10^{-33} (Spracklen, 28334899)
KEAP1	cross all tissues	12	7	0.83	4.6×10^{-5}	9.4×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
MAU2	cross all tissues	12	6	0.82	4.6×10^{-5}	9.4×10^{-3}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
DOK7	cross metabolic tissues	5	3	0.85	4.6×10^{-5}	9.4×10^{-3}	NA	rs6818397 pval=3×10^{-09} (Spracklen, 28334899)
RAB3D	cross all tissues	11	6	0.85	5.2×10^{-5}	1.0×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
EML3	cross all tissues	31	11	0.81	5.3×10^{-5}	1.1×10^{-2}	rs174601 (pval=2.14×10^{-08})	rs174546 pval=1×10^{-58} (Hoffmann, 29507422)
NPEPPS	cross metabolic tissues	5	3	0.89	5.3×10^{-5}	1.1×10^{-2}	NA	rs8078686 pval=2×10^{-25} (Hoffmann, 29507422)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PNLDC1	cross all tissues	33	11	0.82	5.8×10^{-5}	1.1×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
CDKN2D	cross all tissues	14	6	0.84	6.0×10^{-5}	1.2×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
SLC44A2	cross all tissues	12	5	0.82	6.0×10^{-5}	1.2×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
ITPR2	cross all tissues	13	6	0.81	6.8×10^{-5}	1.3×10^{-2}	NA	NA
RHCE	cross metabolic tissues	7	3	0.87	7.2×10^{-5}	1.4×10^{-2}	NA	rs11802413 pval=2×10^{-18} (Spracklen, 28334899)
C1orf194	cross all tissues	14	6	0.82	7.5×10^{-5}	1.4×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
RGL3	cross all tissues	18	6	0.80	7.5×10^{-5}	1.4×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
WDFY2	cross metabolic tissues	6	3	0.84	7.8×10^{-5}	1.4×10^{-2}	NA	NA
DNAH11	cross metabolic tissues	6	3	0.87	8.2×10^{-5}	1.5×10^{-2}	NA	rs73066485 pval=2×10^{-16} (Klarin, 30275531)
POC5	cross all tissues	31	9	0.81	8.2×10^{-5}	1.5×10^{-2}	rs3846662 (pval=2.61×10^{-10})	rs12916 pval=3×10^{-95} (Spracklen, 28334899)
MARK4	cross metabolic tissues	3	1	0.90	8.3×10^{-5}	1.5×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
LRRC25	cross all tissues	17	8	0.82	8.7×10^{-5}	1.6×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
NUDCD3	cross all tissues	35	10	0.81	8.8×10^{-5}	1.6×10^{-2}	NA	rs17725246 pval=2×10^{-22} (Klarin, 30275531)
AGPAT4	cross metabolic tissues	5	3	0.88	9.0×10^{-5}	1.6×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
TGDS	cross all tissues	6	2	0.84	9.2×10^{-5}	1.6×10^{-2}	NA	NA
CHMP4A	cross all tissues	7	4	0.81	9.2×10^{-5}	1.6×10^{-2}	NA	rs8017377 pval=3×10^{-15} (Willer, 24097068)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PTBP3	cross all tissues	12	5	0.84	9.3×10^{-5}	1.6×10^{-2}	NA	NA
RP11-991C1.1	cross all tissues	5	3	0.82	9.5×10^{-5}	1.6×10^{-2}	NA	rs17580 pval=1×10^{-18} (Klarin, 30275531)
RP1-111B22.3	cross all tissues	7	3	0.84	9.9×10^{-5}	1.7×10^{-2}	NA	NA
WI2-81516$\times10^{3}$.1	cross all tissues	9	6	0.87	9.9×10^{-5}	1.7×10^{-2}	NA	NA
RP11-421M1.8	cross metabolic tissues	4	2	0.85	1.1×10^{-4}	1.8×10^{-2}	NA	NA
NYNRIN	cross metabolic tissues	6	4	0.89	1.1×10^{-4}	1.9×10^{-2}	NA	rs8017377 pval=3×10^{-15} (Willer, 24097068)
CTSG	cross all tissues	5	4	0.92	1.1×10^{-4}	1.9×10^{-2}	NA	rs8017377 pval=3×10^{-15} (Willer, 24097068)
RP11-426C22.6	cross metabolic tissues	4	2	0.81	1.1×10^{-4}	1.9×10^{-2}	NA	NA
P2RY11	cross metabolic tissues	7	4	0.88	1.2×10^{-4}	2.0×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
RP11-288H12.4	cross all tissues	5	4	0.90	1.3×10^{-4}	2.1×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RP3-449M8.9	cross metabolic tissues	3	2	0.95	1.3×10^{-4}	2.1×10^{-2}	NA	NA
SNX17	cross all tissues	9	4	0.82	1.4×10^{-4}	2.3×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs780094 pval=3×10^{-21} (Klarin, 30275531)
MAMSTR	cross metabolic tissues	3	2	0.89	1.5×10^{-4}	2.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
GYLTL1B	cross metabolic tissues	3	2	0.91	1.7×10^{-4}	2.7×10^{-2}	NA	rs73461870 pval=3×10^{-08} (Klarin, 30275531)
BCAM	cross all tissues	5	3	0.86	1.8×10^{-4}	2.8×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ABCA5	cross metabolic tissues	3	2	0.88	1.8×10^{-4}	2.8×10^{-2}	rs740516 (pval=3.11×10^{-10})	rs77542162 pval=4×10^{-52} (Klarin, 30275531)
AC012065.7	cross all tissues	15	7	0.82	1.9×10^{-4}	2.9×10^{-2}	rs580889 (pval=9.61×10^{-36})	rs577584 pval=1×10^{-229} (Klarin, 30275531)
GALNT6	cross metabolic tissues	3	2	0.92	1.9×10^{-4}	2.9×10^{-2}	NA	rs1521516 pval=3×10^{-12} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ZNF230	cross all tissues	7	5	0.89	1.9×10^{-4}	2.9×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ACAT1	cross metabolic tissues	5	2	0.81	1.9×10^{-4}	2.9×10^{-2}	NA	NA
YJEFN3	cross all tissues	17	8	0.84	1.9×10^{-4}	2.9×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
OSBPL3	cross all tissues	14	7	0.82	2.0×10^{-4}	2.9×10^{-2}	NA	rs4722551 pval=9×10^{-18} (Klarin, 30275531)
RNASE6	cross all tissues	12	5	0.83	2.0×10^{-4}	2.9×10^{-2}	NA	NA
ZNF90	cross all tissues	21	9	0.83	2.0×10^{-4}	2.9×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs10401969 pval=3×10^{-54} (Willer, 24097068)
AMIGO1	cross metabolic tissues	6	2	0.85	2.0×10^{-4}	3.0×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
AC012309.5	cross metabolic tissues	5	2	0.83	2.1×10^{-4}	3.0×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
DCPS	cross metabolic tissues	6	4	0.89	2.1×10^{-4}	3.0×10^{-2}	rs73632745 (pval=8.25×10^{-09})	rs10893499 pval=1×10^{-22} (Hoffmann, 29507422)
RNASE6	cross metabolic tissues	5	2	0.83	2.2×10^{-4}	3.1×10^{-2}	NA	NA
ACP5	cross all tissues	22	7	0.81	2.2×10^{-4}	3.1×10^{-2}	rs17248727 (pval=4.40×10^{-51})	rs143020224 pval=1×10^{-300} (Klarin, 30275531)
TMEM50A	cross all tissues	14	6	0.82	2.3×10^{-4}	3.3×10^{-2}	NA	rs11802413 pval=2×10^{-18} (Spracklen, 28334899)
SYMPK	cross all tissues	19	8	0.82	2.4×10^{-4}	3.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ZNF571	cross all tissues	9	4	0.85	2.5×10^{-4}	3.5×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
PKN3	cross metabolic tissues	3	2	0.96	2.5×10^{-4}	3.5×10^{-2}	rs532436 (pval=2.31×10^{-11})	NA
SPATC1	cross all tissues	9	5	0.86	2.5×10^{-4}	3.5×10^{-2}	NA	rs7832643 pval=2×10^{-17} (Spracklen, 28334899)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CD3EAP	cross metabolic tissues	5	3	0.89	2.6×10^{-4}	3.5×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
ZBTB32	cross metabolic tissues	6	2	0.81	2.6×10^{-4}	3.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
TMEM57	cross all tissues	10	5	0.80	2.6×10^{-4}	3.6×10^{-2}	NA	rs11802413 pval=2×10^{-18} (Spracklen, 28334899)
LIN37	cross metabolic tissues	3	2	0.81	2.6×10^{-4}	3.6×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
C2orf73	cross all tissues	10	3	0.81	3.0×10^{-4}	4.1×10^{-2}	NA	NA
USP1	cross metabolic tissues	3	2	0.98	3.0×10^{-4}	4.1×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs2131925 pval=3×10^{-32} (Willer, 24097068)
SLC22A1	cross metabolic tissues	5	3	0.87	3.2×10^{-4}	4.3×10^{-2}	rs10455872 (pval=2.99×10^{-29})	rs186696265 pval=3×10^{-69} (Hoffmann, 29507422)
RP11-495P10.3	cross all tissues	6	3	0.87	3.2×10^{-4}	4.3×10^{-2}	NA	NA
TRAPPC12	cross metabolic tissues	5	3	0.86	3.3×10^{-4}	4.3×10^{-2}	NA	NA
POMP	cross metabolic tissues	3	2	0.88	3.3×10^{-4}	4.3×10^{-2}	NA	NA
GSTM5	cross all tissues	47	16	0.81	3.3×10^{-4}	4.3×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)
MAMSTR	cross all tissues	17	7	0.83	3.4×10^{-4}	4.4×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
PPM1N	cross all tissues	29	10	0.81	3.5×10^{-4}	4.5×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
PGAP1	cross all tissues	6	3	0.84	3.5×10^{-4}	4.5×10^{-2}	NA	NA
TMEM59	cross metabolic tissues	3	2	0.83	3.5×10^{-4}	4.5×10^{-2}	1:55505647:G:T (pval=6.46×10^{-45})	rs11591147 pval=3×10^{-257} (Klarin, 30275531)
RAB8A	cross all tissues	12	5	0.83	3.6×10^{-4}	4.6×10^{-2}	rs17248727 (pval=4.40×10^{-51})	NA
RP13-631K18.5	cross all tissues	9	4	0.84	3.6×10^{-4}	4.6×10^{-2}	NA	NA
ISCA2	cross all tissues	5	2	0.88	3.6×10^{-4}	4.6×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PPFIA3	cross all tissues	8	4	0.84	3.8×10^{-4}	4.7×10^{-2}	rs7412 (pval=3.55×10^{-178})	APOE region
RP11-243A14.1	cross all tissues	7	4	0.82	3.8×10^{-4}	4.7×10^{-2}	NA	NA
HMGN2P19	cross all tissues	21	6	0.83	4.0×10^{-4}	4.9×10^{-2}	NA	NA
TAF13	cross metabolic tissues	6	3	0.86	4.0×10^{-4}	5.0×10^{-2}	rs629301 (pval=5.66×10^{-57})	rs611917 pval=1×10^{-300} (Klarin, 30275531)

Appendix XI. Cross-tissue GReX results of the genes significantly associated with TC in BioVU

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PSRC1	cross metabolic tissues	8	3	86%	7.7×10^{-69}	1.8×10^{-64}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SORT1	cross all tissues	9	4	85%	5.5×10^{-66}	6.5×10^{-62}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	cross metabolic tissues	6	3	86%	1.4×10^{-64}	1.1×10^{-60}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
PSRC1	cross all tissues	32	11	81%	2.5×10^{-62}	1.5×10^{-58}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
CELSR2	cross all tissues	21	7	80%	1.1×10^{-53}	5.3×10^{-50}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SORT1	cross metabolic tissues	3	1	85%	3.0×10^{-42}	1.2×10^{-38}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
APOB	cross all tissues	12	5	84%	8.8×10^{-34}	3.0×10^{-30}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
GEMIN7	cross all tissues	40	15	81%	8.3×10^{-20}	2.5×10^{-16}	rs7412 (pval=1.55×10^{-90})	APOE region
SARS	cross all tissues	5	3	81%	1.1×10^{-19}	2.9×10^{-16}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
DOCK6	cross all tissues	15	5	80%	6.1×10^{-18}	1.4×10^{-14}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
DOCK7	cross metabolic tissues	4	2	83%	2.7×10^{-16}	5.7×10^{-13}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
LIPC	cross all tissues	17	6	82%	2.0×10^{-15}	3.9×10^{-12}	rs10468017 (pval=6.54×10^{-13})	rs7350789 pval=4×10^{-78} (Klarin, 30275531)
LIPC	cross metabolic tissues	6	3	90%	5.1×10^{-15}	9.4×10^{-12}	rs10468017 (pval=6.54×10^{-13})	rs7350789 pval=4×10^{-78} (Klarin, 30275531)
P2RY11	cross all tissues	26	11	81%	6.3×10^{-14}	1.1×10^{-10}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATP13A1	cross all tissues	14	6	84%	1.1×10^{-13}	1.8×10^{-10}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
HPR	cross all tissues	25	7	81%	2.4×10^{-13}	3.6×10^{-10}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CEACAM19	cross all tissues	40	17	81%	2.5×10^{-12}	3.4×10^{-9}	rs7412 (pval=1.55×10^{-90})	APOE region
ANKDD1B	cross all tissues	13	7	83%	5.1×10^{-12}	6.8×10^{-9}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
AC067959.1	cross all tissues	13	5	84%	4.1×10^{-11}	5.1×10^{-8}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
USP1	cross metabolic tissues	3	2	98%	5.4×10^{-11}	6.4×10^{-8}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
SNX17	cross all tissues	9	4	82%	7.3×10^{-11}	8.2×10^{-8}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
TXNL4B	cross all tissues	16	8	82%	1.7×10^{-10}	1.8×10^{-7}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
AP1M2	cross all tissues	13	5	82%	1.7×10^{-10}	1.8×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
SMARCA4	cross all tissues	10	5	82%	2.0×10^{-10}	1.9×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
MAU2	cross metabolic tissues	5	3	83%	3.7×10^{-10}	3.5×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ATP13A1	cross metabolic tissues	4	3	89%	4.0×10^{-10}	3.7×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
USP1	cross all tissues	8	4	86%	4.6×10^{-10}	4.0×10^{-7}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
HP	cross all tissues	12	5	83%	5.6×10^{-10}	4.7×10^{-7}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
KRI1	cross all tissues	48	10	80%	5.7×10^{-10}	4.7×10^{-7}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
CLCC1	cross all tissues	15	4	81%	6.2×10^{-10}	4.9×10^{-7}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ZNF155	cross all tissues	33	14	80%	1.2×10^{-9}	9.3×10^{-7}	rs7412 (pval=1.55×10^{-90})	APOE region
C2orf43	cross all tissues	45	13	81%	2.3×10^{-9}	1.7×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
SYPL2	cross all tissues	29	10	81%	3.7×10^{-9}	2.6×10^{-6}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
DOCK7	cross all tissues	19	6	82%	4.0×10^{-9}	2.7×10^{-6}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
GSTM1	cross all tissues	37	18	81%	4.0×10^{-9}	2.7×10^{-6}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ZNF513	cross all tissues	6	2	84%	6.9×10^{-9}	4.5×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ZNF112	cross all tissues	22	7	82%	7.9×10^{-9}	5.0×10^{-6}	rs7412 (pval=1.55×10^{-90})	APOE region
GSTM3	cross all tissues	48	14	80%	9.3×10^{-9}	5.8×10^{-6}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
EMILIN1	cross all tissues	5	3	87%	1.0×10^{-8}	6.0×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
GCKR	cross all tissues	5	3	80%	1.0×10^{-8}	6.0×10^{-6}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
SPC24	cross all tissues	23	10	83%	1.1×10^{-8}	6.6×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
MAU2	cross all tissues	12	6	82%	1.4×10^{-8}	7.9×10^{-6}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
KRTCAP3	cross all tissues	17	7	82%	4.9×10^{-8}	2.7×10^{-5}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
PVRL2	cross metabolic tissues	6	3	88%	6.5×10^{-8}	3.5×10^{-5}	rs7412 (pval=1.55×10^{-90})	APOE region
MRPL45P2	cross metabolic tissues	5	2	85%	1.0×10^{-7}	5.3×10^{-5}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
PCSK9	cross all tissues	8	4	87%	1.1×10^{-7}	5.5×10^{-5}	1:55505647:G:T (pval=2.47×10^{-31})	rs11591147 pval=8×10^{-175} (Klarin, 30275531)
AP1G1	cross all tissues	13	6	81%	1.1×10^{-7}	5.7×10^{-5}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
HMGCR	cross all tissues	8	3	85%	1.6×10^{-7}	7.9×10^{-5}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
ZNF285B	cross all tissues	8	4	86%	1.8×10^{-7}	8.5×10^{-5}	rs7412 (pval=1.55×10^{-90})	APOE region
KANK2	cross all tissues	22	9	81%	2.0×10^{-7}	9.6×10^{-5}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ATXN7L2	cross all tissues	15	7	83%	2.6×10^{-7}	1.2×10^{-4}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ST3GAL4	cross all tissues	16	8	83%	3.1×10^{-7}	1.4×10^{-4}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
GALNT6	cross metabolic tissues	3	2	92%	3.1×10^{-7}	1.4×10^{-4}	NA	NA

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ABCA1	cross metabolic tissues	3	3	100%	3.6×10^{-7}	1.6×10^{-4}	rs62568182 (pval=4.62×10^{-10})	rs1883025 pval=4×10^{-64} (Spracklen, 28334899)
WTAP	cross all tissues	30	9	82%	4.9×10^{-7}	2.1×10^{-4}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
RP11-288H12.3	cross all tissues	16	8	81%	4.9×10^{-7}	2.1×10^{-4}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
DOK7	cross metabolic tissues	5	3	85%	7.7×10^{-7}	3.2×10^{-4}	NA	rs59950280 pval=4×10^{-12} (Klarin, 30275531)
GPN1	cross all tissues	8	4	83%	8.6×10^{-7}	3.5×10^{-4}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
POC5	cross all tissues	31	9	81%	9.0×10^{-7}	3.6×10^{-4}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
DMPK	cross all tissues	20	9	82%	1.2×10^{-6}	4.9×10^{-4}	rs7412 (pval=1.55×10^{-90})	APOE region
PPM1G	cross metabolic tissues	5	3	91%	1.7×10^{-6}	6.8×10^{-4}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
CEACAM19	cross metabolic tissues	7	4	85%	1.8×10^{-6}	6.8×10^{-4}	rs7412 (pval=1.55×10^{-90})	APOE region
ALDH1A2	cross metabolic tissues	3	2	90%	1.9×10^{-6}	7.3×10^{-4}	rs10468017 (pval=6.54×10^{-13})	rs7350789 pval=4×10^{-78} (Klarin, 30275531)
C19orf52	cross metabolic tissues	3	2	94%	2.3×10^{-6}	8.4×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
ABCA6	cross all tissues	10	4	83%	2.3×10^{-6}	8.6×10^{-4}	rs740516 (pval=2.95×10^{-09})	rs77542162 pval=2×10^{-33} (Klarin, 30275531)
C19orf52	cross all tissues	5	3	89%	2.5×10^{-6}	9.2×10^{-4}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
RAB8A	cross metabolic tissues	5	3	87%	3.0×10^{-6}	1.1×10^{-3}	rs17248727 (pval=7.18×10^{-41})	NA
TBKBP1	cross all tissues	36	10	82%	3.1×10^{-6}	1.1×10^{-3}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
FADS2	cross all tissues	28	9	81%	3.1×10^{-6}	1.1×10^{-3}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
NPEPPS	cross metabolic tissues	5	3	89%	3.2×10^{-6}	1.1×10^{-3}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
GPER1	cross metabolic tissues	4	2	81%	3.2×10^{-6}	1.1×10^{-3}	NA	rs2362529 pval=8×10^{-19} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ATXN7L2	cross metabolic tissues	3	2	92%	3.2×10^{-6}	1.1×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
SLC44A2	cross all tissues	12	5	82%	3.2×10^{-6}	1.1×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
NLRC5	cross all tissues	10	5	84%	4.1×10^{-6}	1.3×10^{-3}	NA	rs183130 pval=1×10^{-84} (Klarin, 30275531)
DNAH11	cross metabolic tissues	6	3	87%	4.2×10^{-6}	1.3×10^{-3}	NA	rs66476925 pval=9×10^{-19} (Klarin, 30275531)
GSTM2	cross all tissues	24	12	82%	4.6×10^{-6}	1.4×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
TYK2	cross all tissues	16	8	82%	4.7×10^{-6}	1.4×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
CETP	cross all tissues	8	4	83%	4.7×10^{-6}	1.4×10^{-3}	NA	rs183130 pval=1×10^{-84} (Klarin, 30275531)
ST3GAL4	cross metabolic tissues	5	3	86%	4.7×10^{-6}	1.4×10^{-3}	rs964184 (pval=2.84×10^{-13})	rs68055275 pval=3×10^{-18} (Klarin, 30275531)
ATG4C	cross all tissues	7	4	91%	7.2×10^{-6}	2.1×10^{-3}	1:55505647:G:T (pval=2.47×10^{-31})	rs995000 pval=6×10^{-112} (Klarin, 30275531)
RP11-288H12.3	cross metabolic tissues	3	2	80%	7.2×10^{-6}	2.1×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
SLC22A1	cross all tissues	16	8	82%	7.3×10^{-6}	2.1×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
SMARCA4	cross metabolic tissues	3	2	83%	8.5×10^{-6}	2.4×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
NRBP1	cross all tissues	21	5	81%	9.6×10^{-6}	2.7×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
ZNF404	cross all tissues	41	14	81%	1.1×10^{-5}	3.0×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
KRTCAP3	cross metabolic tissues	6	3	90%	1.2×10^{-5}	3.2×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
PVRL2	cross all tissues	18	7	82%	1.2×10^{-5}	3.2×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
CHMP4A	cross all tissues	7	4	81%	1.2×10^{-5}	3.3×10^{-3}	NA	rs11621792 pval=3×10^{-12} (Hoffmann, 29507422)
NRBP1	cross metabolic tissues	5	2	89%	1.3×10^{-5}	3.4×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
UGT2B7	cross all tissues	11	4	82%	1.3×10^{-5}	3.5×10^{-3}	NA	rs969114 pval=1×10^{-26} (Klarin, 30275531)
MKRN2	cross metabolic tissues	7	3	84%	1.4×10^{-5}	3.6×10^{-3}	NA	rs7616006 pval=1×10^{-18} (Spracklen, 28334899)
CD3EAP	cross all tissues	24	9	82%	1.4×10^{-5}	3.6×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
TBKBP1	cross metabolic tissues	8	3	86%	1.5×10^{-5}	3.8×10^{-3}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
SEZ6L2	cross all tissues	8	4	88%	1.5×10^{-5}	3.9×10^{-3}	NA	NA
RP11-495P10.3	cross all tissues	6	3	87%	1.6×10^{-5}	3.9×10^{-3}	NA	NA
ITPR2	cross all tissues	13	6	81%	1.6×10^{-5}	3.9×10^{-3}	NA	NA
IGF2R	cross metabolic tissues	4	2	85%	1.6×10^{-5}	3.9×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
ZNF283	cross all tissues	28	10	81%	1.9×10^{-5}	4.5×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
MRPL45P2	cross all tissues	24	7	81%	1.9×10^{-5}	4.5×10^{-3}	NA	rs8078686 pval=2×10^{-22} (Hoffmann, 29507422)
RP11-439M11.1	cross metabolic tissues	4	3	90%	1.9×10^{-5}	4.6×10^{-3}	NA	NA
IGF2R	cross all tissues	16	8	83%	2.2×10^{-5}	5.1×10^{-3}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
AIM1L	cross all tissues	7	4	86%	2.3×10^{-5}	5.3×10^{-3}	NA	rs10903129 pval=3×10^{-16} (Spracklen, 28334899)
ABCA1	cross all tissues	6	4	86%	2.3×10^{-5}	5.4×10^{-3}	rs62568182 (pval=4.62×10^{-10})	rs1883025 pval=4×10^{-64} (Spracklen, 28334899)
HMGN2P19	cross all tissues	21	6	83%	2.4×10^{-5}	5.4×10^{-3}	NA	NA
GSTM1	cross metabolic tissues	7	4	84%	2.5×10^{-5}	5.7×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
ABCA9	cross all tissues	8	4	86%	2.6×10^{-5}	5.7×10^{-3}	rs740516 (pval=2.95×10^{-09})	rs77542162 pval=2×10^{-33} (Klarin, 30275531)
FTH1	cross all tissues	6	4	87%	2.6×10^{-5}	5.7×10^{-3}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
CDPF1	cross all tissues	10	5	83%	2.7×10^{-5}	5.9×10^{-3}	NA	rs4253772 pval=1×10^{-08} (Willer, 24097068)
HKR1	cross metabolic tissues	5	3	85%	2.9×10^{-5}	6.3×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
GSTM4	cross all tissues	36	14	81%	2.9×10^{-5}	6.3×10^{-3}	rs629301 (pval=1.57×10^{-42})	rs7528419 pval=1×10^{-300} (Klarin, 30275531)
YJEFN3	cross all tissues	17	8	84%	3.0×10^{-5}	6.4×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
FADS1	cross all tissues	24	9	81%	3.3×10^{-5}	7.0×10^{-3}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
AC012065.7	cross all tissues	15	7	82%	3.4×10^{-5}	7.1×10^{-3}	rs580889 (pval=9.52×10^{-34})	rs10692845 pval=6×10^{-209} (Klarin, 30275531)
POLK	cross all tissues	18	7	83%	3.9×10^{-5}	8.2×10^{-3}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
C18orf32	cross all tissues	13	6	80%	4.5×10^{-5}	9.2×10^{-3}	NA	rs77960347 pval=1×10^{-39} (Klarin, 30275531)
GATAD2A	cross all tissues	6	2	81%	4.7×10^{-5}	9.5×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
ZNF235	cross all tissues	17	7	81%	4.7×10^{-5}	9.6×10^{-3}	rs7412 (pval=1.55×10^{-90})	APOE region
TRAPPC12	cross metabolic tissues	5	3	86%	4.8×10^{-5}	9.6×10^{-3}	NA	NA
AP1M2	cross metabolic tissues	4	2	84%	4.9×10^{-5}	9.8×10^{-3}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
OR7D2	cross metabolic tissues	7	4	86%	5.2×10^{-5}	1.0×10^{-2}	rs17248727 (pval=7.18×10^{-41})	NA
ZNF283	cross metabolic tissues	5	3	91%	5.4×10^{-5}	1.1×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
DOK7	cross all tissues	20	8	82%	5.5×10^{-5}	1.1×10^{-2}	NA	rs59950280 pval=4×10^{-12} (Klarin, 30275531)
CDIPT	cross all tissues	6	4	88%	5.8×10^{-5}	1.1×10^{-2}	NA	NA
ITPRIP	cross all tissues	6	3	86%	6.3×10^{-5}	1.2×10^{-2}	NA	NA
HKR1	cross all tissues	8	4	82%	6.8×10^{-5}	1.3×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
UGT2B17	cross all tissues	10	5	84%	6.8×10^{-5}	1.3×10^{-2}	NA	rs969114 pval=1×10^{-26} (Klarin, 30275531)
SLC22A3	cross all tissues	25	10	81%	7.2×10^{-5}	1.3×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
GALNT6	cross all tissues	20	8	82%	7.8×10^{-5}	1.4×10^{-2}	NA	NA
UBE2L3	cross all tissues	12	5	81%	8.3×10^{-5}	1.5×10^{-2}	NA	rs5754102 pval=1×10^{-12} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
PKN3	cross all tissues	11	5	85%	8.6×10^{-5}	1.6×10^{-2}	rs532436 (pval=1.12×10^{-10})	NA
HAVCR1	cross metabolic tissues	4	2	88%	9.0×10^{-5}	1.6×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
AC012309.5	cross metabolic tissues	5	2	83%	9.3×10^{-5}	1.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
TMEM57	cross all tissues	10	5	80%	9.3×10^{-5}	1.7×10^{-2}	NA	rs10903129 pval=3×10^{-16} (Spracklen, 28334899)
TMEM258	cross all tissues	19	9	82%	9.5×10^{-5}	1.7×10^{-2}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
ERCC1	cross all tissues	23	8	82%	9.6×10^{-5}	1.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
RP11-458D21.1	cross all tissues	14	3	82%	9.7×10^{-5}	1.7×10^{-2}	NA	NA
LRRC57	cross all tissues	30	8	80%	1.0×10^{-4}	1.8×10^{-2}	NA	NA
STK17A	cross metabolic tissues	4	2	87%	1.0×10^{-4}	1.8×10^{-2}	NA	rs17725246 pval=3×10^{-19} (Klarin, 30275531)
NF1	cross metabolic tissues	3	2	87%	1.0×10^{-4}	1.8×10^{-2}	NA	rs7214248 pval=7×10^{-10} (Klarin, 30275531)
CLINT1	cross all tissues	8	5	85%	1.1×10^{-4}	1.8×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
SIRT6	cross all tissues	30	7	81%	1.1×10^{-4}	1.8×10^{-2}	rs17248727 (pval=7.18×10^{-41})	NA
CCDC159	cross all tissues	5	4	89%	1.1×10^{-4}	1.9×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
GTF3C3	cross all tissues	5	3	83%	1.2×10^{-4}	1.9×10^{-2}	NA	NA
TMEM258	cross metabolic tissues	3	2	82%	1.2×10^{-4}	2.0×10^{-2}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
MKRN2	cross all tissues	37	16	81%	1.2×10^{-4}	2.0×10^{-2}	NA	rs7616006 pval=1×10^{-18} (Spracklen, 28334899)
CARM1	cross all tissues	11	5	86%	1.2×10^{-4}	2.0×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
RHCE	cross metabolic tissues	7	3	87%	1.3×10^{-4}	2.1×10^{-2}	NA	rs10903129 pval=3×10^{-16} (Spracklen, 28334899)
TGDS	cross metabolic tissues	3	2	98%	1.3×10^{-4}	2.1×10^{-2}	NA	NA
HGFAC	cross all tissues	11	5	81%	1.3×10^{-4}	2.1×10^{-2}	NA	rs59950280 pval=4×10^{-12} (Klarin, 30275531)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
SLC44A2	cross metabolic tissues	4	2	87%	1.3×10^{-4}	2.1×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs8106503 pval=2×10^{-281} (Klarin, 30275531)
COX19	cross all tissues	7	4	84%	1.4×10^{-4}	2.1×10^{-2}	NA	rs2362529 pval=8×10^{-19} (Klarin, 30275531)
ZNF20	cross all tissues	10	4	84%	1.4×10^{-4}	2.1×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs2738464 pval=8×10^{-49} (Kanai, 29403010)
WDFY2	cross metabolic tissues	6	3	84%	1.4×10^{-4}	2.1×10^{-2}	NA	NA
LRRC57	cross metabolic tissues	6	2	88%	1.4×10^{-4}	2.2×10^{-2}	NA	NA
PPM1G	cross all tissues	11	4	82%	1.5×10^{-4}	2.3×10^{-2}	rs580889 (pval=9.52×10^{-34})	rs1260326 pval=3×10^{-160} (Klarin, 30275531)
HCG9	cross metabolic tissues	6	3	82%	1.8×10^{-4}	2.8×10^{-2}	NA	NA
GNB1L	cross all tissues	20	10	80%	1.9×10^{-4}	2.8×10^{-2}	NA	NA
RP11-20D14.6	cross all tissues	8	3	80%	1.9×10^{-4}	2.8×10^{-2}	NA	rs4883201 pval=5×10^{-11} (Spracklen, 28334899)
ACOT11	cross metabolic tissues	3	2	88%	1.9×10^{-4}	2.8×10^{-2}	1:55505647:G:T (pval=2.47×10^{-31})	rs11591147 pval=8×10^{-175} (Klarin, 30275531)
SNHG8	cross all tissues	35	12	81%	1.9×10^{-4}	2.8×10^{-2}	NA	NA
CLINT1	cross metabolic tissues	3	2	84%	2.0×10^{-4}	3.0×10^{-2}	rs12657266 (pval=2.09×10^{-14})	rs6882076 pval=2×10^{-43} (Spracklen, 28334899)
HAPLN4	cross all tissues	20	8	83%	2.1×10^{-4}	3.0×10^{-2}	rs17248727 (pval=7.18×10^{-41})	rs10401969 pval=4×10^{-77} (Willer, 24097068)
AP1AR	cross all tissues	17	3	80%	2.1×10^{-4}	3.1×10^{-2}	NA	NA
PINLYP	cross metabolic tissues	5	3	91%	2.2×10^{-4}	3.2×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
BMPR2	cross all tissues	9	4	83%	2.3×10^{-4}	3.3×10^{-2}	NA	rs72926986 pval=2×10^{-27} (Klarin, 30275531)
MROH2A	cross all tissues	7	5	88%	2.5×10^{-4}	3.5×10^{-2}	NA	rs35754645 pval=3×10^{-13} (Klarin, 30275531)
M6PR	cross metabolic tissues	6	3	86%	2.5×10^{-4}	3.6×10^{-2}	NA	rs4883201 pval=5×10^{-11} (Spracklen, 28334899)
RP11-295M18.2	cross all tissues	42	13	80%	2.6×10^{-4}	3.6×10^{-2}	NA	rs2642438 pval=1×10^{-22} (Spracklen, 28334899)
NTN5	cross metabolic tissues	3	1	84%	2.6×10^{-4}	3.6×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
ALG1L10P	cross all tissues	9	5	86%	2.6×10^{-4}	3.6×10^{-2}	NA	rs4883201 pval=5×10^{-11} (Spracklen, 28334899)

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CYP2W1	cross all tissues	12	5	82%	2.6×10^{-4}	3.6×10^{-2}	NA	rs2362529 pval=8×10^{-19} (Klarin, 30275531)
NTN5	cross all tissues	20	7	82%	2.7×10^{-4}	3.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
NBPF12	cross metabolic tissues	4	3	89%	2.7×10^{-4}	3.7×10^{-2}	NA	NA
POC5	cross metabolic tissues	7	3	88%	2.8×10^{-4}	3.8×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
SOBP	cross all tissues	5	3	81%	2.8×10^{-4}	3.8×10^{-2}	NA	NA
KRT80	cross all tissues	10	5	82%	2.9×10^{-4}	3.8×10^{-2}	NA	NA
APOBEC3H	cross all tissues	8	3	82%	2.9×10^{-4}	3.8×10^{-2}	NA	NA
MRPL21	cross metabolic tissues	7	2	83%	2.9×10^{-4}	3.8×10^{-2}	NA	NA
ENC1	cross all tissues	12	5	81%	2.9×10^{-4}	3.8×10^{-2}	rs42854 (pval=9.62×10^{-11})	rs12916 pval=7×10^{-94} (Klarin, 30275531)
POMP	cross metabolic tissues	3	2	88%	3.0×10^{-4}	3.9×10^{-2}	NA	NA
RASL12	cross all tissues	9	4	86%	3.1×10^{-4}	4.1×10^{-2}	rs10468017 (pval=6.54×10^{-13})	NA
CYP4F12	cross all tissues	25	9	81%	3.2×10^{-4}	4.1×10^{-2}	rs17248727 (pval=7.18×10^{-41})	NA
DHODH	cross all tissues	40	13	80%	3.3×10^{-4}	4.2×10^{-2}	rs2287997 (pval=1.75×10^{-09})	rs5471 pval=1×10^{-70} (Klarin, 30275531)
PHF11	cross metabolic tissues	4	2	87%	3.3×10^{-4}	4.3×10^{-2}	NA	rs4942859 pval=3×10^{-08} (Klarin, 30275531)
PPP5C	cross metabolic tissues	5	2	91%	3.4×10^{-4}	4.3×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
FADS2	cross metabolic tissues	6	2	86%	3.4×10^{-4}	4.3×10^{-2}	NA	rs1535 pval=1×10^{-43} (Spracklen, 28334899)
RAF1	cross all tissues	8	5	87%	3.4×10^{-4}	4.3×10^{-2}	NA	rs7616006 pval=1×10^{-18} (Spracklen, 28334899)
SPRYD4	cross metabolic tissues	6	2	83%	3.6×10^{-4}	4.5×10^{-2}	NA	NA
LILRA3	cross metabolic tissues	8	2	83%	3.6×10^{-4}	4.5×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
TRIB2	cross metabolic tissues	3	2	84%	3.6×10^{-4}	4.5×10^{-2}	rs580889 (pval=9.52×10^{-34})	NA
PGAP1	cross all tissues	6	3	84%	3.7×10^{-4}	4.5×10^{-2}	NA	NA
PCSK6	cross all tissues	8	5	82%	3.7×10^{-4}	4.5×10^{-2}	NA	NA

Gene	Model	N tissue	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CTD-2162K18.4	cross all tissues	22	7	81%	3.7×10^{-4}	4.6×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
ZNF781	cross metabolic tissues	7	4	85%	3.8×10^{-4}	4.7×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
SLC22A3	cross metabolic tissues	6	3	81%	3.9×10^{-4}	4.7×10^{-2}	rs74617384 (pval=1.80×10^{-22})	rs186696265 pval=5×10^{-64} (Hoffmann, 29507422)
PSMC3	cross metabolic tissues	6	3	81%	3.9×10^{-4}	4.7×10^{-2}	NA	rs555328608 pval=1×10^{-09} (Klarin, 30275531)
CTSG	cross all tissues	5	4	92%	3.9×10^{-4}	4.7×10^{-2}	NA	rs11621792 pval=3×10^{-12} (Hoffmann, 29507422)
NYNRIN	cross metabolic tissues	6	4	89%	3.9×10^{-4}	4.7×10^{-2}	NA	rs11621792 pval=3×10^{-12} (Hoffmann, 29507422)
HMGN2P19	cross metabolic tissues	3	1	85%	3.9×10^{-4}	4.7×10^{-2}	NA	NA
NFKBIB	cross metabolic tissues	6	3	88%	4.0×10^{-4}	4.8×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
PLIN3	cross metabolic tissues	4	3	92%	4.1×10^{-4}	4.8×10^{-2}	rs17248727 (pval=7.18×10^{-41})	NA
TMEM56	cross metabolic tissues	3	2	90%	4.1×10^{-4}	4.8×10^{-2}	NA	NA
ZNF571	cross all tissues	9	4	85%	4.2×10^{-4}	4.9×10^{-2}	rs7412 (pval=1.55×10^{-90})	APOE region
C1orf106	cross all tissues	10	4	82%	4.3×10^{-4}	5.0×10^{-2}	NA	NA

Appendix XII. Cross-tissue GReX results of the genes significantly associated with TG in BioVU

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
LPL	cross all tissues	7	4	89%	1.3×10^{-56}	3.2×10^{-52}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
LPL	cross metabolic tissues	4	3	94%	2.2×10^{-50}	2.6×10^{-46}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
MLXIPL	cross all tissues	21	9	81%	4.1×10^{-30}	3.3×10^{-26}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MLXIPL	cross metabolic tissues	4	3	92%	3.7×10^{-27}	2.2×10^{-23}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
NRBP1	cross all tissues	21	5	81%	9.7×10^{-23}	4.6×10^{-19}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
RP11-109L13.1	cross all tissues	48	6	81%	1.5×10^{-21}	5.7×10^{-18}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
SNX17	cross all tissues	9	4	82%	2.9×10^{-19}	9.7×10^{-16}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
EMILIN1	cross all tissues	5	3	87%	6.1×10^{-19}	1.8×10^{-15}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GPN1	cross all tissues	8	4	83%	8.2×10^{-19}	2.2×10^{-15}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
KRTCAP3	cross all tissues	17	7	82%	6.1×10^{-18}	1.4×10^{-14}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ZNF513	cross all tissues	6	2	84%	1.5×10^{-16}	3.2×10^{-13}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
GCKR	cross all tissues	5	3	80%	8.2×10^{-16}	1.6×10^{-12}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DOCK7	cross metabolic tissues	4	2	83%	5.1×10^{-15}	9.3×10^{-12}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
CCDC92	cross metabolic tissues	6	3	87%	8.4×10^{-15}	1.4×10^{-11}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
INTS10	cross metabolic tissues	3	2	81%	6.0×10^{-14}	9.5×10^{-11}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
ZNF664	cross all tissues	12	6	84%	6.5×10^{-14}	9.6×10^{-11}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
CCDC92	cross all tissues	24	10	81%	1.0×10^{-13}	1.4×10^{-10}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
BCL7B	cross all tissues	12	4	81%	1.0×10^{-13}	1.4×10^{-10}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
LZTS1	cross all tissues	7	4	81%	1.9×10^{-13}	2.4×10^{-10}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
DNAH10OS	cross all tissues	25	7	81%	9.4×10^{-13}	1.1×10^{-9}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
KRTCAP3	cross metabolic tissues	6	3	90%	1.9×10^{-12}	2.1×10^{-9}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
PCSK7	cross all tissues	10	6	85%	2.0×10^{-12}	2.1×10^{-9}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
NRBP1	cross metabolic tissues	5	2	89%	3.9×10^{-12}	4.0×10^{-9}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ZNF259	cross all tissues	6	3	85%	7.7×10^{-12}	7.6×10^{-9}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
APOE	cross all tissues	7	4	85%	1.5×10^{-11}	1.4×10^{-8}	rs584007 (pval=2.22×10^{-14})	APOE region
PPM1G	cross all tissues	11	4	82%	1.9×10^{-11}	1.7×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
SIDT2	cross all tissues	17	5	82%	2.9×10^{-11}	2.5×10^{-8}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ATP13A1	cross all tissues	14	6	84%	3.0×10^{-11}	2.5×10^{-8}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
APOB	cross all tissues	12	5	84%	3.0×10^{-11}	2.5×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1042034 pval=1×10^{-72} (Hoffmann, 29507422)
DNAH10	cross all tissues	10	5	82%	3.6×10^{-11}	2.8×10^{-8}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
PCSK7	cross metabolic tissues	3	2	86%	3.7×10^{-11}	2.9×10^{-8}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
BRE	cross all tissues	5	3	83%	5.2×10^{-11}	3.9×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
INTS10	cross all tissues	18	7	81%	7.1×10^{-11}	5.1×10^{-8}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
ZNF664	cross metabolic tissues	4	2	85%	7.8×10^{-11}	5.4×10^{-8}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
SLC5A6	cross all tissues	23	11	81%	8.7×10^{-11}	5.9×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ATRAID	cross all tissues	35	11	81%	1.4×10^{-10}	9.5×10^{-8}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
USP1	cross metabolic tissues	3	2	98%	2.5×10^{-10}	1.6×10^{-7}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
PPM1G	cross metabolic tissues	5	3	91%	2.6×10^{-10}	1.6×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CAD	cross all tissues	18	5	83%	3.2×10^{-10}	1.9×10^{-7}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
ATP13A1	cross metabolic tissues	4	3	89%	4.7×10^{-10}	2.8×10^{-7}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
DNAH10OS	cross metabolic tissues	3	1	82%	6.0×10^{-10}	3.5×10^{-7}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
MRPL35P2	cross all tissues	28	10	82%	8.9×10^{-10}	5.0×10^{-7}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
OXCT2P1	cross metabolic tissues	3	2	86%	1.0×10^{-9}	5.7×10^{-7}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
VPS37D	cross all tissues	10	5	86%	2.0×10^{-9}	1.1×10^{-6}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
TBL2	cross all tissues	31	13	82%	2.1×10^{-9}	1.1×10^{-6}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
SLC4A1AP	cross all tissues	10	5	82%	2.7×10^{-9}	1.4×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
C4A	cross all tissues	44	16	80%	3.4×10^{-9}	1.7×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	cross all tissues	48	8	80%	5.8×10^{-9}	2.9×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NSUN5P2	cross all tissues	45	12	80%	6.4×10^{-9}	3.1×10^{-6}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
AGER	cross all tissues	22	10	82%	6.7×10^{-9}	3.2×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MLF2	cross metabolic tissues	7	4	85%	7.3×10^{-9}	3.4×10^{-6}	NA	NA
USP1	cross all tissues	8	4	86%	7.9×10^{-9}	3.6×10^{-6}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
CCDC40	cross all tissues	45	15	81%	1.2×10^{-8}	5.2×10^{-6}	NA	NA

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
ZBTB22	cross all tissues	9	4	87%	1.4×10^{-8}	6.1×10^{-6}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MRPL33	cross all tissues	8	4	86%	1.5×10^{-8}	6.6×10^{-6}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TAPBP	cross all tissues	25	9	82%	3.2×10^{-8}	1.4×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
FADS1	cross all tissues	24	9	81%	3.4×10^{-8}	1.4×10^{-5}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
HLA-DRB1	cross all tissues	44	13	82%	3.6×10^{-8}	1.5×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
C4A	cross metabolic tissues	7	3	83%	4.7×10^{-8}	1.9×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NRBF2	cross all tissues	10	6	83%	5.2×10^{-8}	2.1×10^{-5}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
CCDC40	cross metabolic tissues	8	4	86%	6.2×10^{-8}	2.4×10^{-5}	NA	NA
PABPC4	cross metabolic tissues	5	2	81%	6.3×10^{-8}	2.4×10^{-5}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
MAU2	cross metabolic tissues	5	3	83%	6.6×10^{-8}	2.5×10^{-5}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
GAB2	cross metabolic tissues	4	3	94%	9.4×10^{-8}	3.5×10^{-5}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
MRPL35P2	cross metabolic tissues	5	2	81%	1.2×10^{-7}	4.5×10^{-5}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
TBL2	cross metabolic tissues	7	4	82%	1.3×10^{-7}	4.7×10^{-5}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
TNXA	cross all tissues	29	12	81%	1.7×10^{-7}	5.8×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB5	cross metabolic tissues	8	1	84%	1.9×10^{-7}	6.7×10^{-5}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
CAD	cross metabolic tissues	6	3	83%	2.4×10^{-7}	8.4×10^{-5}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
FADS1	cross metabolic tissues	4	2	86%	2.8×10^{-7}	9.4×10^{-5}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
OXCT2P1	cross all tissues	37	14	81%	2.9×10^{-7}	9.6×10^{-5}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
NARS2	cross metabolic tissues	7	2	85%	3.0×10^{-7}	9.9×10^{-5}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
NARS2	cross all tissues	37	6	81%	3.4×10^{-7}	1.1×10^{-4}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
ATF6B	cross all tissues	29	12	81%	4.5×10^{-7}	1.4×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DRB6	cross all tissues	47	9	81%	5.6×10^{-7}	1.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
LY6G5C	cross all tissues	35	9	81%	6.1×10^{-7}	1.9×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DAXX	cross all tissues	9	5	87%	6.4×10^{-7}	2.0×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DAXX	cross metabolic tissues	6	4	83%	6.8×10^{-7}	2.1×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GPANK1	cross all tissues	15	8	80%	7.0×10^{-7}	2.1×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DOCK7	cross all tissues	19	6	82%	7.7×10^{-7}	2.3×10^{-4}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
CSGALNACT1	cross metabolic tissues	6	3	84%	8.7×10^{-7}	2.6×10^{-4}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
ZNF234	cross all tissues	19	7	81%	1.0×10^{-6}	3.0×10^{-4}	rs584007 (pval=2.22×10^{-14})	APOE region
PABPC4	cross all tissues	23	8	81%	1.3×10^{-6}	3.7×10^{-4}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
ZNF76	cross all tissues	6	2	86%	1.4×10^{-6}	3.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	NA
WBSCR27	cross all tissues	49	7	81%	1.4×10^{-6}	3.8×10^{-4}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
PSORS1C2	cross all tissues	32	8	81%	1.4×10^{-6}	3.8×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
FADS2	cross metabolic tissues	6	2	86%	1.8×10^{-6}	4.8×10^{-4}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
DNAH10	cross metabolic tissues	3	2	97%	2.1×10^{-6}	5.8×10^{-4}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
CD300LF	cross all tissues	10	5	86%	2.2×10^{-6}	5.9×10^{-4}	NA	NA
POM121	cross all tissues	21	9	82%	2.3×10^{-6}	6.0×10^{-4}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
HMBS	cross metabolic tissues	7	3	84%	2.3×10^{-6}	6.0×10^{-4}	rs964184 (pval=1.43×10^{-71})	NA

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
TRIM50	cross all tissues	7	3	85%	2.5×10^{-6}	6.5×10^{-4}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
LINC00452	cross all tissues	7	4	86%	2.7×10^{-6}	6.9×10^{-4}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
BMP8A	cross all tissues	18	8	83%	2.8×10^{-6}	7.1×10^{-4}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PAFAH1B2	cross all tissues	10	5	85%	3.2×10^{-6}	7.9×10^{-4}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
ABHD11	cross all tissues	28	9	81%	3.3×10^{-6}	8.2×10^{-4}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
B3GALT4	cross all tissues	9	5	83%	3.7×10^{-6}	9.1×10^{-4}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MAU2	cross all tissues	12	6	82%	4.1×10^{-6}	9.8×10^{-4}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
MLF2	cross all tissues	20	8	82%	4.5×10^{-6}	1.1×10^{-3}	NA	NA
RP11-373D23.3	cross all tissues	19	8	81%	5.0×10^{-6}	1.2×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
BCL7B	cross metabolic tissues	4	2	84%	5.6×10^{-6}	1.3×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
CD151	cross metabolic tissues	8	2	84%	5.8×10^{-6}	1.3×10^{-3}	NA	NA
PNKD	cross metabolic tissues	6	3	86%	5.9×10^{-6}	1.4×10^{-3}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
VPS37D	cross metabolic tissues	3	2	85%	6.2×10^{-6}	1.4×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
PPIP5K1	cross all tissues	7	4	81%	6.3×10^{-6}	1.4×10^{-3}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
TAP2	cross all tissues	36	15	82%	6.4×10^{-6}	1.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAP2	cross all tissues	36	15	82%	6.4×10^{-6}	1.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TMEM258	cross all tissues	19	9	82%	6.7×10^{-6}	1.5×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
MCM6	cross metabolic tissues	4	3	88%	6.7×10^{-6}	1.5×10^{-3}	rs6704561 (pval=2.46×10^{-08})	NA
NSUN5P2	cross metabolic tissues	7	3	85%	6.9×10^{-6}	1.5×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
CETP	cross all tissues	8	4	83%	7.1×10^{-6}	1.5×10^{-3}	NA	rs3764261 pval=3×10^{-27} (Spracklen, 28334899)
COBLL1	cross all tissues	9	5	84%	7.4×10^{-6}	1.6×10^{-3}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
AC104135.3	cross metabolic tissues	7	2	86%	7.8×10^{-6}	1.6×10^{-3}	NA	NA
ZBTB22	cross metabolic tissues	3	1	90%	9.8×10^{-6}	2.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PNPLA2	cross all tissues	13	6	85%	9.8×10^{-6}	2.0×10^{-3}	NA	NA
NRBF2	cross metabolic tissues	3	3	100%	1.1×10^{-5}	2.3×10^{-3}	rs3858121 (pval=2.05×10^{-08})	rs5785580 pval=1×10^{-26} (Klarin, 30275531)
XXbac-BPG248L24.12	cross all tissues	34	13	80%	1.2×10^{-5}	2.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
GSTA1	cross all tissues	15	6	81%	1.2×10^{-5}	2.5×10^{-3}	NA	NA
HLA-DQB2	cross all tissues	48	14	81%	1.3×10^{-5}	2.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PBX2	cross all tissues	5	3	81%	1.3×10^{-5}	2.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ATRAID	cross metabolic tissues	6	3	88%	1.4×10^{-5}	2.7×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
HLA-DQB1	cross all tissues	48	12	81%	1.4×10^{-5}	2.7×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DUSP3	cross all tissues	8	4	82%	1.5×10^{-5}	2.9×10^{-3}	rs72836561 (pval=1.50×10^{-10})	rs72836561 pval=8×10^{-84} (Klarin, 30275531)
SYT7	cross all tissues	9	5	85%	1.5×10^{-5}	2.9×10^{-3}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
ZBTB9	cross all tissues	6	3	86%	1.6×10^{-5}	3.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
LY6G5B	cross all tissues	40	14	81%	1.6×10^{-5}	3.1×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ABHD1	cross all tissues	5	3	88%	1.7×10^{-5}	3.2×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
SCN3A	cross all tissues	12	6	82%	1.7×10^{-5}	3.2×10^{-3}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
BAG6	cross all tissues	32	13	80%	1.8×10^{-5}	3.3×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TMEM106B	cross metabolic tissues	4	3	89%	1.8×10^{-5}	3.3×10^{-3}	NA	rs3173615 pval=7×10^{-09} (Klarin, 30275531)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
AP006621.1	cross metabolic tissues	7	2	83%	1.9×10^{-5}	3.4×10^{-3}	NA	NA
GATAD2A	cross all tissues	6	2	81%	2.1×10^{-5}	3.7×10^{-3}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
GPBAR1	cross all tissues	10	4	83%	2.1×10^{-5}	3.7×10^{-3}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
AC104135.2	cross metabolic tissues	7	2	86%	2.1×10^{-5}	3.7×10^{-3}	NA	NA
DOC2GP	cross metabolic tissues	6	3	83%	2.2×10^{-5}	3.8×10^{-3}	NA	NA
FER	cross all tissues	9	5	83%	2.3×10^{-5}	4.0×10^{-3}	NA	NA
ADAL	cross metabolic tissues	7	2	83%	2.5×10^{-5}	4.3×10^{-3}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
ATG4C	cross all tissues	7	4	91%	2.5×10^{-5}	4.3×10^{-3}	rs7531579 (pval=3.13×10^{-11})	rs995000 pval=3×10^{-92} (Spracklen, 28334899)
RP11-166B2.1	cross metabolic tissues	7	2	85%	2.6×10^{-5}	4.5×10^{-3}	NA	NA
LINC00565	cross all tissues	11	6	85%	2.6×10^{-5}	4.5×10^{-3}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
TRIM2	cross metabolic tissues	5	3	88%	2.9×10^{-5}	4.8×10^{-3}	NA	NA
KAT8	cross metabolic tissues	6	2	81%	2.9×10^{-5}	4.8×10^{-3}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
FAM205A	cross all tissues	6	3	85%	3.0×10^{-5}	4.9×10^{-3}	NA	rs3843935 pval=6×10^{-11} (Klarin, 30275531)
TMEM64	cross all tissues	7	3	85%	3.0×10^{-5}	4.9×10^{-3}	NA	NA
LIPC	cross metabolic tissues	6	3	90%	3.0×10^{-5}	4.9×10^{-3}	NA	rs1800588 pval=6×10^{-51} (Kanai, 29403010)
COPS7A	cross all tissues	8	5	87%	3.0×10^{-5}	4.9×10^{-3}	NA	NA
FBXO22	cross metabolic tissues	4	2	81%	3.2×10^{-5}	5.2×10^{-3}	NA	NA
TUBGCP4	cross metabolic tissues	3	2	87%	3.6×10^{-5}	5.7×10^{-3}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
B3GALT4	cross metabolic tissues	4	2	85%	3.6×10^{-5}	5.7×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HLA-DMB	cross all tissues	9	5	83%	3.6×10^{-5}	5.7×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
ADAL	cross all tissues	47	13	81%	3.7×10^{-5}	5.8×10^{-3}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
HLA-DRA	cross metabolic tissues	4	3	91%	3.7×10^{-5}	5.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
GUF1	cross metabolic tissues	8	4	86%	3.7×10^{-5}	5.8×10^{-3}	NA	NA
CTSB	cross metabolic tissues	6	3	82%	3.8×10^{-5}	5.9×10^{-3}	rs1059611 (pval=4.06×10^{-38})	rs709822 pval=5×10^{-13} (Klarin, 30275531)
HINFP	cross metabolic tissues	5	3	89%	3.9×10^{-5}	6.0×10^{-3}	rs964184 (pval=1.43×10^{-71})	NA
C2orf16	cross all tissues	7	5	85%	4.0×10^{-5}	6.1×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
RP11-56A10.1	cross all tissues	5	2	85%	4.1×10^{-5}	6.2×10^{-3}	NA	NA
LCN1P1	cross all tissues	7	4	82%	4.2×10^{-5}	6.3×10^{-3}	NA	NA
EBAG9P1	cross all tissues	24	8	81%	4.3×10^{-5}	6.4×10^{-3}	NA	NA
LY6G6C	cross all tissues	5	3	84%	4.4×10^{-5}	6.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RP3-449M8.9	cross metabolic tissues	3	2	95%	4.4×10^{-5}	6.5×10^{-3}	NA	NA
STAG3L2	cross metabolic tissues	7	4	84%	4.5×10^{-5}	6.6×10^{-3}	rs13233571 (pval=2.76×10^{-18})	rs139441335 pval=2×10^{-16} (Klarin, 30275531)
STAM2	cross all tissues	14	5	80%	4.6×10^{-5}	6.7×10^{-3}	NA	NA
KHK	cross all tissues	31	9	82%	4.7×10^{-5}	6.8×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
TRIM5	cross metabolic tissues	4	3	90%	5.1×10^{-5}	7.4×10^{-3}	NA	NA
HLA-DRB9	cross all tissues	26	9	82%	5.3×10^{-5}	7.5×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MT2A	cross all tissues	5	4	91%	5.6×10^{-5}	7.9×10^{-3}	NA	rs3764261 pval=3×10^{-27} (Spracklen, 28334899)
TAPBP	cross metabolic tissues	4	2	80%	5.6×10^{-5}	7.9×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
VPS52	cross all tissues	8	4	84%	5.7×10^{-5}	8.0×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
AC019172.2	cross all tissues	9	5	82%	5.9×10^{-5}	8.2×10^{-3}	NA	NA
PRRT1	cross all tissues	14	5	80%	6.1×10^{-5}	8.4×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NOTCH4	cross all tissues	37	13	82%	6.4×10^{-5}	8.8×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
NTNG2	cross metabolic tissues	3	2	82%	6.5×10^{-5}	8.8×10^{-3}	NA	NA
SERPINH1	cross metabolic tissues	3	2	92%	7.1×10^{-5}	9.6×10^{-3}	NA	NA

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
PSORS1C1	cross all tissues	41	11	81%	7.1×10^{-5}	9.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
PPP1R18	cross all tissues	16	8	81%	7.2×10^{-5}	9.6×10^{-3}	rs13191810 (pval=1.63×10^{-11})	rs2247056 pval=2×10^{-15} (Teslovich, 20686565)
SLC5A6	cross metabolic tissues	3	2	86%	7.2×10^{-5}	9.6×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
RP4-794H19.4	cross all tissues	11	5	82%	7.3×10^{-5}	9.6×10^{-3}	rs7531579 (pval=3.13×10^{-11})	NA
KCNK3	cross all tissues	9	5	83%	7.3×10^{-5}	9.6×10^{-3}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
DBNDD1	cross metabolic tissues	7	4	88%	7.6×10^{-5}	1.0×10^{-2}	NA	NA
CDC42SE1	cross all tissues	13	5	85%	7.9×10^{-5}	1.0×10^{-2}	NA	NA
TAP2	cross metabolic tissues	7	4	85%	8.1×10^{-5}	1.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TAP2	cross metabolic tissues	7	4	85%	8.1×10^{-5}	1.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
HYPK	cross all tissues	9	5	84%	8.1×10^{-5}	1.0×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
HCG22	cross all tissues	32	9	81%	8.2×10^{-5}	1.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
BCKDK	cross all tissues	5	2	81%	8.7×10^{-5}	1.1×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
TTC40	cross all tissues	10	6	85%	9.0×10^{-5}	1.1×10^{-2}	NA	rs1133400 pval=2×10^{-08} (Klarin, 30275531)
STAG3L3	cross all tissues	35	10	81%	9.0×10^{-5}	1.1×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
RP11-452H21.4	cross all tissues	6	3	88%	9.1×10^{-5}	1.1×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
CADM1	cross all tissues	9	5	86%	9.4×10^{-5}	1.2×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
THOC3	cross metabolic tissues	8	4	88%	9.6×10^{-5}	1.2×10^{-2}	NA	NA
TMBIM1	cross metabolic tissues	4	2	92%	9.9×10^{-5}	1.2×10^{-2}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
IFT172	cross all tissues	8	5	84%	9.9×10^{-5}	1.2×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
CLINT1	cross metabolic tissues	3	2	84%	1.0×10^{-4}	1.2×10^{-2}	NA	rs9715911 pval=5×10^{-38} (Klarin, 30275531)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
NUDT5	cross metabolic tissues	3	2	89%	1.0×10^{-4}	1.2×10^{-2}	NA	NA
ZNF259	cross metabolic tissues	4	2	87%	1.1×10^{-4}	1.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
HLA-B	cross all tissues	34	12	81%	1.1×10^{-4}	1.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
PPDPF	cross all tissues	27	12	80%	1.1×10^{-4}	1.4×10^{-2}	NA	NA
SERPINH1	cross all tissues	8	4	83%	1.2×10^{-4}	1.4×10^{-2}	NA	NA
MPHOSPH9	cross all tissues	16	6	82%	1.3×10^{-4}	1.5×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
RP11-271K11.5	cross all tissues	16	5	81%	1.3×10^{-4}	1.5×10^{-2}	NA	NA
DSCC1	cross all tissues	44	13	81%	1.4×10^{-4}	1.6×10^{-2}	rs28601761 (pval=2.33×10^{-23})	NA
BACE1	cross metabolic tissues	3	2	86%	1.4×10^{-4}	1.6×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
TNXA	cross metabolic tissues	5	3	87%	1.4×10^{-4}	1.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RPS18	cross all tissues	36	16	80%	1.4×10^{-4}	1.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TMBIM1	cross all tissues	21	6	82%	1.4×10^{-4}	1.6×10^{-2}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
COX20	cross all tissues	6	3	87%	1.4×10^{-4}	1.6×10^{-2}	NA	NA
DNAH17	cross all tissues	14	5	82%	1.4×10^{-4}	1.6×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
PSD3	cross all tissues	18	9	80%	1.5×10^{-4}	1.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
GTF3C4	cross all tissues	5	2	82%	1.5×10^{-4}	1.7×10^{-2}	NA	NA
HMBS	cross all tissues	41	13	81%	1.5×10^{-4}	1.7×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
NUP62	cross metabolic tissues	6	3	88%	1.5×10^{-4}	1.7×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
CSGALNACT1	cross all tissues	40	15	80%	1.6×10^{-4}	1.7×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs1569209 pval=1×10^{-300} (Klarin, 30275531)
COPS7A	cross metabolic tissues	4	3	89%	1.6×10^{-4}	1.7×10^{-2}	NA	NA
SYNGR2	cross all tissues	12	4	80%	1.6×10^{-4}	1.7×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
DARS	cross metabolic tissues	3	2	97%	1.6×10^{-4}	1.7×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
SLC38A11	cross all tissues	23	8	80%	1.6×10^{-4}	1.7×10^{-2}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
NME5	cross all tissues	25	9	80%	1.6×10^{-4}	1.8×10^{-2}	NA	NA
RP11-85G21.3	cross metabolic tissues	3	2	88%	1.6×10^{-4}	1.8×10^{-2}	NA	NA
GNPDA2	cross metabolic tissues	8	3	84%	1.6×10^{-4}	1.8×10^{-2}	NA	NA
CDPF1	cross all tissues	10	5	83%	1.7×10^{-4}	1.8×10^{-2}	NA	NA
PARP15	cross metabolic tissues	5	3	81%	1.7×10^{-4}	1.8×10^{-2}	NA	NA
BTBD9	cross all tissues	19	7	80%	1.7×10^{-4}	1.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	NA
ACYP2	cross all tissues	27	10	81%	1.7×10^{-4}	1.8×10^{-2}	NA	NA
RERE	cross all tissues	18	7	82%	1.7×10^{-4}	1.8×10^{-2}	NA	NA
ZNF233	cross metabolic tissues	4	2	87%	1.8×10^{-4}	1.8×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
RASGEF1A	cross all tissues	14	6	81%	1.8×10^{-4}	1.9×10^{-2}	NA	NA
CACNA1H	cross all tissues	10	5	81%	1.8×10^{-4}	1.9×10^{-2}	NA	NA
WDR76	cross all tissues	5	4	91%	1.9×10^{-4}	1.9×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
EFNA1	cross all tissues	9	5	86%	1.9×10^{-4}	1.9×10^{-2}	NA	NA
SBDSP1	cross all tissues	15	6	84%	1.9×10^{-4}	1.9×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
MRE11A	cross metabolic tissues	8	2	86%	1.9×10^{-4}	1.9×10^{-2}	NA	NA
INTU	cross all tissues	5	2	83%	1.9×10^{-4}	1.9×10^{-2}	NA	NA
TMC6	cross all tissues	19	8	81%	1.9×10^{-4}	2.0×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
CSNK2B	cross all tissues	10	6	84%	1.9×10^{-4}	2.0×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TBXAS1	cross all tissues	5	3	84%	2.0×10^{-4}	2.0×10^{-2}	NA	NA
FAM35A	cross all tissues	31	10	82%	2.0×10^{-4}	2.0×10^{-2}	NA	NA
MSANTD1	cross all tissues	5	3	85%	2.0×10^{-4}	2.0×10^{-2}	rs115335747 (pval=3.10×10^{-08})	rs13108218 pval=1×10^{-16} (Klarin, 30275531)
ZNF180	cross metabolic tissues	4	2	97%	2.0×10^{-4}	2.0×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
AP006621.5	cross metabolic tissues	7	2	84%	2.0×10^{-4}	2.0×10^{-2}	NA	NA
DHRS4	cross all tissues	25	12	81%	2.1×10^{-4}	2.0×10^{-2}	NA	NA
ARL6IP4	cross metabolic tissues	4	2	83%	2.1×10^{-4}	2.1×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs4765127 pval=1×10^{-18} (Hoffmann, 29507422)
GSTA1	cross metabolic tissues	3	2	91%	2.1×10^{-4}	2.1×10^{-2}	NA	NA
LRGUK	cross metabolic tissues	8	3	83%	2.1×10^{-4}	2.1×10^{-2}	NA	NA
DNAJC30	cross all tissues	11	5	80%	2.2×10^{-4}	2.1×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
RP11-37B2.1	cross all tissues	33	13	82%	2.2×10^{-4}	2.1×10^{-2}	NA	NA
WDFY2	cross all tissues	19	9	82%	2.3×10^{-4}	2.2×10^{-2}	NA	NA
RP11-7F17.3	cross all tissues	19	7	83%	2.3×10^{-4}	2.2×10^{-2}	NA	rs12431415 pval=2×10^{-08} (Hoffmann, 29507422)
FADS2	cross all tissues	28	9	81%	2.3×10^{-4}	2.2×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
DOC2GP	cross all tissues	25	8	81%	2.3×10^{-4}	2.2×10^{-2}	NA	NA
ATXN7L3B	cross all tissues	7	4	84%	2.3×10^{-4}	2.2×10^{-2}	NA	NA
SIDT2	cross metabolic tissues	4	1	89%	2.3×10^{-4}	2.2×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
RP11-66B24.1	cross all tissues	5	3	88%	2.4×10^{-4}	2.2×10^{-2}	NA	rs11247287 pval=3×10^{-08} (Klarin, 30275531)
PLB1	cross all tissues	16	7	83%	2.4×10^{-4}	2.2×10^{-2}	rs1260326 (pval=2.43×10^{-29})	rs1260326 pval=1×10^{-300} (Hoffmann, 29507422)
IPO13	cross all tissues	6	3	90%	2.4×10^{-4}	2.3×10^{-2}	NA	NA
PGS1	cross all tissues	19	7	81%	2.5×10^{-4}	2.3×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
POU5F1	cross all tissues	42	17	80%	2.5×10^{-4}	2.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
KAT8	cross all tissues	40	11	82%	2.5×10^{-4}	2.3×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
ISCA2	cross all tissues	5	2	88%	2.5×10^{-4}	2.3×10^{-2}	NA	NA
XXbac-BPG299F13.14	cross all tissues	11	6	83%	2.5×10^{-4}	2.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
BRI3	cross all tissues	18	7	83%	2.6×10^{-4}	2.3×10^{-2}	NA	NA
GATAD2A	cross metabolic tissues	3	2	96%	2.6×10^{-4}	2.3×10^{-2}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
DARS	cross all tissues	13	5	85%	2.6×10^{-4}	2.3×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
PRPF6	cross all tissues	21	10	81%	2.6×10^{-4}	2.4×10^{-2}	NA	NA
INCENP	cross metabolic tissues	5	3	89%	2.6×10^{-4}	2.4×10^{-2}	NA	rs174537 pval=2×10^{-86} (Klarin, 30275531)
DXO	cross all tissues	16	7	81%	2.7×10^{-4}	2.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TUBGCP4	cross all tissues	14	6	80%	2.7×10^{-4}	2.4×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
RNASET2	cross all tissues	23	8	82%	2.7×10^{-4}	2.4×10^{-2}	NA	rs62436827 pval=7×10^{-09} (Ko, 24886709)
JMJD8	cross metabolic tissues	5	3	84%	2.8×10^{-4}	2.4×10^{-2}	NA	NA
GKAP1	cross all tissues	16	6	82%	2.8×10^{-4}	2.5×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
LST1	cross metabolic tissues	4	3	89%	2.8×10^{-4}	2.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
GSTA2	cross all tissues	6	3	85%	2.9×10^{-4}	2.5×10^{-2}	NA	NA
G3BP2	cross metabolic tissues	5	3	87%	2.9×10^{-4}	2.5×10^{-2}	NA	NA
STMN3	cross metabolic tissues	3	2	89%	2.9×10^{-4}	2.5×10^{-2}	NA	NA
TTC28	cross all tissues	13	7	83%	2.9×10^{-4}	2.5×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
ARHGDIG	cross metabolic tissues	3	3	100%	2.9×10^{-4}	2.5×10^{-2}	NA	NA
NIPSNAP1	cross metabolic tissues	6	4	88%	3.0×10^{-4}	2.5×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
LMF1	cross all tissues	39	15	80%	3.0×10^{-4}	2.5×10^{-2}	NA	NA
ZNF204P	cross all tissues	25	10	81%	3.0×10^{-4}	2.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs573022400 pval=9×10^{-11} (Klarin, 30275531)
RNF5	cross all tissues	27	11	81%	3.0×10^{-4}	2.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
PIDD	cross all tissues	29	9	81%	3.0×10^{-4}	2.6×10^{-2}	NA	NA
FLG	cross all tissues	39	12	81%	3.1×10^{-4}	2.6×10^{-2}	NA	NA
KCTD14	cross all tissues	11	6	83%	3.1×10^{-4}	2.6×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
AIG1	cross all tissues	11	6	84%	3.1×10^{-4}	2.6×10^{-2}	NA	NA

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
TCTN2	cross all tissues	39	14	80%	3.1×10^{-4}	2.6×10^{-2}	rs1187415 (pval=7.83×10^{-11})	rs7307277 pval=2×10^{-19} (Hoffmann, 29507422)
AC104135.4	cross metabolic tissues	6	3	84%	3.1×10^{-4}	2.6×10^{-2}	NA	NA
CYP21A2	cross all tissues	30	12	81%	3.2×10^{-4}	2.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
RP11-571M6.17	cross all tissues	7	4	90%	3.2×10^{-4}	2.6×10^{-2}	NA	rs61352607 pval=5×10^{-19} (Hoffmann, 29507422)
C20orf112	cross all tissues	14	7	82%	3.2×10^{-4}	2.6×10^{-2}	NA	rs6088793 pval=3×10^{-08} (Klarin, 30275531)
HLA-DRB6	cross metabolic tissues	7	1	81%	3.2×10^{-4}	2.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
YJEFN3	cross all tissues	17	8	84%	3.3×10^{-4}	2.6×10^{-2}	rs72999033 (pval=8.66×10^{-11})	rs10401969 pval=5×10^{-71} (Spracklen, 28334899)
USP36	cross metabolic tissues	3	2	89%	3.3×10^{-4}	2.7×10^{-2}	NA	rs4969145 pval=7×10^{-17} (Klarin, 30275531)
KLRAP1	cross all tissues	32	11	81%	3.3×10^{-4}	2.7×10^{-2}	NA	NA
ZNF285B	cross all tissues	8	4	86%	3.3×10^{-4}	2.7×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
ZNF317	cross all tissues	22	11	81%	3.4×10^{-4}	2.7×10^{-2}	rs116843064 (pval=1.05×10^{-09})	rs116843064 pval=6×10^{-134} (Klarin, 30275531)
MCTP1	cross all tissues	13	4	81%	3.4×10^{-4}	2.7×10^{-2}	NA	NA
MAP1A	cross metabolic tissues	3	2	91%	3.4×10^{-4}	2.7×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)
MAPK1IP1L	cross all tissues	6	3	86%	3.4×10^{-4}	2.7×10^{-2}	NA	NA
RFC2	cross metabolic tissues	5	3	86%	3.4×10^{-4}	2.7×10^{-2}	rs13233571 (pval=2.76×10^{-18})	rs13234131 pval=4×10^{-191} (Klarin, 30275531)
ZNF646	cross all tissues	11	4	85%	3.5×10^{-4}	2.8×10^{-2}	NA	rs2032915 pval=9×10^{-09} (Spracklen, 28334899)
CCNA1	cross metabolic tissues	3	2	83%	3.5×10^{-4}	2.8×10^{-2}	NA	NA
SLC44A4	cross all tissues	6	4	82%	3.6×10^{-4}	2.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
TUBB3	cross all tissues	8	3	82%	3.6×10^{-4}	2.8×10^{-2}	NA	NA
TUBB3	cross all tissues	8	3	82%	3.6×10^{-4}	2.8×10^{-2}	NA	NA
RGS9BP	cross all tissues	7	4	88%	3.6×10^{-4}	2.8×10^{-2}	NA	rs12460070 pval=2×10^{-10} (Klarin, 30275531)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
MPPE1	cross metabolic tissues	8	4	83%	3.6×10^{-4}	2.8×10^{-2}	NA	NA
USP35	cross all tissues	16	6	85%	3.7×10^{-4}	2.8×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
TMEM60	cross all tissues	18	6	81%	3.7×10^{-4}	2.9×10^{-2}	rs13233571 (pval=2.76×10^{-18})	NA
PCNXL3	cross metabolic tissues	5	2	81%	3.7×10^{-4}	2.9×10^{-2}	NA	rs75601653 pval=2×10^{-08} (Klarin, 30275531)
SEC11C	cross all tissues	19	9	82%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
NPC2	cross all tissues	13	6	85%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
KPRP	cross all tissues	5	3	84%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
HLA-DMA	cross all tissues	27	11	81%	3.8×10^{-4}	2.9×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GKAP1	cross metabolic tissues	3	2	89%	3.8×10^{-4}	2.9×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
UBA7	cross metabolic tissues	4	2	94%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
RPLP2	cross all tissues	20	8	82%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
PIDD	cross metabolic tissues	4	2	89%	3.8×10^{-4}	2.9×10^{-2}	NA	NA
CHID1	cross metabolic tissues	4	3	95%	3.9×10^{-4}	2.9×10^{-2}	NA	NA
PKDREJ	cross metabolic tissues	6	2	80%	3.9×10^{-4}	2.9×10^{-2}	NA	NA
SF3A3	cross all tissues	31	8	80%	4.0×10^{-4}	3.0×10^{-2}	NA	NA
CCDC68	cross metabolic tissues	5	3	83%	4.0×10^{-4}	3.0×10^{-2}	NA	NA
SLC26A7	cross all tissues	13	5	82%	4.2×10^{-4}	3.1×10^{-2}	NA	NA
CYP21A1P	cross all tissues	42	19	81%	4.2×10^{-4}	3.1×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
WDR90	cross all tissues	35	14	81%	4.3×10^{-4}	3.2×10^{-2}	NA	NA
IFITM4P	cross all tissues	41	12	82%	4.4×10^{-4}	3.2×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs3118359 pval=3×10^{-13} (Klarin, 30275531)
RHBDL1	cross all tissues	26	9	82%	4.4×10^{-4}	3.2×10^{-2}	NA	NA
SLC38A11	cross metabolic tissues	6	3	84%	4.4×10^{-4}	3.2×10^{-2}	NA	rs10184004 pval=3×10^{-29} (Klarin, 30275531)
KIAA0040	cross all tissues	24	10	81%	4.5×10^{-4}	3.2×10^{-2}	NA	NA
RP11-981G7.6	cross metabolic tissues	5	3	84%	4.5×10^{-4}	3.2×10^{-2}	rs1059611 (pval=4.06×10^{-38})	rs9657541 pval=1×10^{-19} (Klarin, 30275531)

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ACTR3B	cross metabolic tissues	3	2	87%	4.5×10^{-4}	3.2×10^{-2}	NA	NA
RQCD1	cross all tissues	11	5	83%	4.6×10^{-4}	3.3×10^{-2}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
RP11-460N20.4	cross metabolic tissues	7	2	81%	4.6×10^{-4}	3.3×10^{-2}	rs13233571 (pval=2.76×10^{-18})	NA
C1orf159	cross all tissues	40	13	82%	4.6×10^{-4}	3.3×10^{-2}	NA	NA
RASA3	cross metabolic tissues	5	3	84%	4.6×10^{-4}	3.3×10^{-2}	NA	rs6602911 pval=1×10^{-14} (Klarin, 30275531)
FKBPL	cross all tissues	7	4	83%	4.7×10^{-4}	3.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
C4B	cross metabolic tissues	7	4	88%	4.7×10^{-4}	3.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
IPO13	cross metabolic tissues	3	2	84%	4.7×10^{-4}	3.3×10^{-2}	NA	NA
LRGUK	cross all tissues	35	15	82%	4.7×10^{-4}	3.3×10^{-2}	NA	NA
MPHOSPH8	cross metabolic tissues	6	3	85%	4.7×10^{-4}	3.3×10^{-2}	NA	NA
PDCD5	cross all tissues	36	15	81%	4.7×10^{-4}	3.3×10^{-2}	NA	rs12460070 pval=2×10^{-10} (Klarin, 30275531)
HLA-DQA2	cross all tissues	48	12	80%	4.8×10^{-4}	3.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
DPEP1	cross all tissues	6	4	86%	5.0×10^{-4}	3.4×10^{-2}	NA	NA
TNIK	cross all tissues	10	6	83%	5.0×10^{-4}	3.5×10^{-2}	NA	rs11720145 pval=1×10^{-13} (Klarin, 30275531)
CYP21A2	cross metabolic tissues	5	3	90%	5.0×10^{-4}	3.5×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
MYO1C	cross all tissues	6	3	81%	5.1×10^{-4}	3.5×10^{-2}	NA	NA
BRMS1	cross all tissues	11	6	84%	5.1×10^{-4}	3.5×10^{-2}	NA	rs75601653 pval=2×10^{-08} (Klarin, 30275531)
RP3-449M8.9	cross all tissues	23	7	82%	5.2×10^{-4}	3.6×10^{-2}	NA	NA
TCF19	cross all tissues	37	14	81%	5.3×10^{-4}	3.6×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
HINFP	cross all tissues	19	6	80%	5.3×10^{-4}	3.6×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
TEK	cross all tissues	8	3	81%	5.4×10^{-4}	3.6×10^{-2}	NA	NA
C14orf159	cross metabolic tissues	4	3	93%	5.4×10^{-4}	3.7×10^{-2}	NA	NA

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
LST1	cross all tissues	11	7	85%	5.5×10^{-4}	3.7×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs116477171 pval=9×10^{-17} (Hoffmann, 29507422)
ANKRD20A18P	cross all tissues	5	3	93%	5.5×10^{-4}	3.7×10^{-2}	NA	NA
TMEM64	cross metabolic tissues	4	2	88%	5.5×10^{-4}	3.7×10^{-2}	NA	NA
ASCC2	cross all tissues	18	8	80%	5.6×10^{-4}	3.7×10^{-2}	NA	NA
IMPA2	cross all tissues	17	9	82%	5.7×10^{-4}	3.8×10^{-2}	NA	NA
TBK1	cross metabolic tissues	3	2	92%	5.8×10^{-4}	3.8×10^{-2}	NA	NA
RP13-137A17.6	cross all tissues	9	3	84%	5.8×10^{-4}	3.9×10^{-2}	NA	NA
TMPRSS3	cross metabolic tissues	3	2	92%	5.9×10^{-4}	3.9×10^{-2}	NA	NA
MTMR2	cross all tissues	9	4	82%	5.9×10^{-4}	3.9×10^{-2}	NA	NA
ARL14EP	cross all tissues	36	12	81%	5.9×10^{-4}	3.9×10^{-2}	NA	NA
EFHB	cross all tissues	49	11	81%	5.9×10^{-4}	3.9×10^{-2}	NA	NA
PIGH	cross metabolic tissues	5	3	87%	5.9×10^{-4}	3.9×10^{-2}	NA	NA
GMEB2	cross all tissues	18	7	83%	6.0×10^{-4}	3.9×10^{-2}	NA	NA
EPS8L2	cross metabolic tissues	6	3	81%	6.1×10^{-4}	4.0×10^{-2}	NA	NA
NECAB1	cross all tissues	8	5	82%	6.2×10^{-4}	4.0×10^{-2}	NA	NA
OS9	cross all tissues	11	3	83%	6.3×10^{-4}	4.0×10^{-2}	NA	rs61352607 pval=5×10^{-19} (Hoffmann, 29507422)
JMJD8	cross all tissues	28	12	82%	6.3×10^{-4}	4.0×10^{-2}	NA	NA
RPS6KB2	cross all tissues	27	8	82%	6.3×10^{-4}	4.0×10^{-2}	NA	NA
PHLDB2	cross all tissues	9	5	82%	6.3×10^{-4}	4.0×10^{-2}	NA	NA
ZMPSTE24	cross all tissues	8	4	83%	6.3×10^{-4}	4.0×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
FTOP1	cross all tissues	13	6	81%	6.4×10^{-4}	4.1×10^{-2}	NA	rs202032561 pval=1×10^{-10} (Klarin, 30275531)
EGFL7	cross all tissues	7	5	88%	6.5×10^{-4}	4.1×10^{-2}	NA	NA
TSFM	cross all tissues	37	12	82%	6.5×10^{-4}	4.1×10^{-2}	NA	rs61352607 pval=5×10^{-19} (Hoffmann, 29507422)
STX18	cross all tissues	7	3	86%	6.6×10^{-4}	4.2×10^{-2}	rs115335747 (pval=3.10×10^{-08})	rs13108218 pval=1×10^{-16} (Klarin, 30275531)
ELL3	cross all tissues	5	4	92%	6.6×10^{-4}	4.2×10^{-2}	rs139974673 (pval=8.85×10^{-09})	rs150844304 pval=5×10^{-43} (Hoffmann, 29507422)

							Annotation	
Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	GWAS	NHGRI-EBI
GALC	cross metabolic tissues	6	3	87%	6.7×10^{-4}	4.2×10^{-2}	NA	NA
DRD2	cross metabolic tissues	3	2	88%	6.7×10^{-4}	4.2×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs1079596 pval=2×10^{-08} (Klarin, 30275531)
GAB2	cross all tissues	13	5	84%	6.7×10^{-4}	4.2×10^{-2}	NA	rs10793310 pval=3×10^{-11} (Klarin, 30275531)
LGALS3	cross all tissues	13	7	80%	6.7×10^{-4}	4.2×10^{-2}	NA	NA
ZRANB3	cross all tissues	6	3	85%	6.8×10^{-4}	4.2×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA
ACAD8	cross all tissues	13	7	81%	6.8×10^{-4}	4.2×10^{-2}	NA	NA
PPIEL	cross all tissues	11	6	84%	6.8×10^{-4}	4.2×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
PNKD	cross all tissues	21	8	81%	6.8×10^{-4}	4.2×10^{-2}	NA	rs200513066 pval=1×10^{-20} (Klarin, 30275531)
ARL14EP	cross metabolic tissues	5	3	90%	6.9×10^{-4}	4.2×10^{-2}	NA	NA
POGZ	cross all tissues	30	9	82%	6.9×10^{-4}	4.2×10^{-2}	NA	NA
ATP5G1	cross metabolic tissues	3	2	89%	7.0×10^{-4}	4.3×10^{-2}	rs72836561 (pval=1.50×10^{-10})	NA
RP11-110I1.14	cross all tissues	29	11	81%	7.0×10^{-4}	4.3×10^{-2}	rs964184 (pval=1.43×10^{-71})	NA
USP16	cross metabolic tissues	3	2	94%	7.0×10^{-4}	4.3×10^{-2}	NA	NA
MSH5	cross metabolic tissues	3	2	89%	7.1×10^{-4}	4.3×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GSC	cross all tissues	11	5	83%	7.1×10^{-4}	4.3×10^{-2}	NA	NA
SLC12A7	cross all tissues	12	4	84%	7.1×10^{-4}	4.3×10^{-2}	NA	NA
BMP8A	cross metabolic tissues	3	2	89%	7.3×10^{-4}	4.4×10^{-2}	NA	rs72663520 pval=3×10^{-10} (Klarin, 30275531)
HLA-DOB	cross metabolic tissues	8	3	85%	7.3×10^{-4}	4.4×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
EFCAB4A	cross all tissues	20	10	83%	7.4×10^{-4}	4.4×10^{-2}	NA	NA
RMI1	cross metabolic tissues	3	2	86%	7.5×10^{-4}	4.5×10^{-2}	NA	rs1982151 pval=2×10^{-08} (Klarin, 30275531)
ADD1	cross all tissues	8	4	84%	7.5×10^{-4}	4.5×10^{-2}	rs115335747 (pval=3.10×10^{-08})	rs13108218 pval=1×10^{-16} (Klarin, 30275531)
MCM6	cross all tissues	25	11	81%	7.6×10^{-4}	4.5×10^{-2}	rs6704561 (pval=2.46×10^{-08})	NA

Gene	Mode	N tissues	N PCs	Explained variance	P-value	FDR	Annotation	
							GWAS	NHGRI-EBI
ATP6V0B	cross all tissues	5	3	81%	7.6×10^{-4}	4.5×10^{-2}	NA	NA
ZNF234	cross metabolic tissues	3	2	88%	7.6×10^{-4}	4.5×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
GLCCI1	cross metabolic tissues	3	2	84%	7.7×10^{-4}	4.5×10^{-2}	NA	NA
KATNAL2	cross all tissues	20	8	81%	7.7×10^{-4}	4.6×10^{-2}	NA	NA
HSCB	cross all tissues	9	4	82%	7.8×10^{-4}	4.6×10^{-2}	NA	rs5752792 pval=3×10^{-08} (Hoffmann, 29507422)
GSTT2	cross all tissues	48	13	80%	7.8×10^{-4}	4.6×10^{-2}	NA	NA
PRMT1	cross all tissues	9	4	81%	7.8×10^{-4}	4.6×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
GLB1	cross metabolic tissues	3	2	81%	7.8×10^{-4}	4.6×10^{-2}	NA	NA
NUP210L	cross all tissues	14	7	82%	7.9×10^{-4}	4.6×10^{-2}	NA	rs6671166 pval=2×10^{-09} (Hoffmann, 29507422)
FAM57A	cross all tissues	32	12	81%	7.9×10^{-4}	4.6×10^{-2}	NA	NA
GNS	cross all tissues	17	5	80%	7.9×10^{-4}	4.6×10^{-2}	NA	NA
AP006216.11	cross all tissues	14	6	80%	7.9×10^{-4}	4.6×10^{-2}	rs964184 (pval=1.43×10^{-71})	rs7350481 pval=1×10^{-300} (Klarin, 30275531)
LSMEM1	cross all tissues	32	10	81%	7.9×10^{-4}	4.6×10^{-2}	NA	rs2255811 pval=2×10^{-08} (Surakka, 25961943)
ABCC2	cross all tissues	12	6	81%	8.0×10^{-4}	4.6×10^{-2}	NA	NA
CPT1C	cross all tissues	22	8	81%	8.0×10^{-4}	4.6×10^{-2}	rs584007 (pval=2.22×10^{-14})	APOE region
ENTPD7	cross all tissues	10	5	82%	8.1×10^{-4}	4.6×10^{-2}	NA	NA
HLA-DRA	cross all tissues	8	5	84%	8.4×10^{-4}	4.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
C9orf117	cross all tissues	6	3	86%	8.5×10^{-4}	4.8×10^{-2}	NA	NA
GAS8	cross metabolic tissues	8	3	81%	8.5×10^{-4}	4.8×10^{-2}	NA	NA
PFDN6	cross all tissues	5	3	87%	8.5×10^{-4}	4.8×10^{-2}	rs13191810 (pval=1.63×10^{-11})	rs13214992 pval=3×10^{-29} (Klarin, 30275531)
GRK4	cross metabolic tissues	7	2	83%	8.7×10^{-4}	4.9×10^{-2}	rs115335747 (pval=3.10×10^{-08})	rs13108218 pval=1×10^{-16} (Klarin, 30275531)
AP001877.1	cross all tissues	39	10	81%	8.8×10^{-4}	5.0×10^{-2}	NA	NA

Appendix XIII. Summary of identified serum lipid genes

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
CAD	NA	TG	TG	NA	TG	TG
CETP	NA	Dyslipidemia, HDL-C, LDL-C, TC, TG	Dyslipidemia, HDL-C, LDL-C, TC, TG	NA	Dyslipidemia, HDL-C	Dyslipidemia, HDL-C
NRBP1	NA	TC, TG	TC, TG	NA	TG	HDL-C, TG
SNX17	NA	TG	LDL-C, TC, TG	NA	TG	TG
PPM1G	NA	TC, TG	TC, TG	NA	TG	TG
ATRAID	NA	TG	TG	NA	TG	TG
NLRC5	NA	HDL-C, TC	HDL-C, TC	NA	Dyslipidemia, HDL-C	Dyslipidemia, HDL-C
KRTCAP3	NA	TC, TG	TC, TG	NA	TG	TG
ZNF513	NA	LDL-C, TC, TG	TC, TG	NA	TG	TG
LPL	NA	HDL-C, TG	HDL-C, TG	NA	Dyslipidemia	Dyslipidemia, HDL-C
APOB	NA	Dyslipidemia, LDL-C, TC, TG	Dyslipidemia, LDL-C, TC, TG	NA	NA	LDL-C
GCKR	NA	TC, TG	TC, TG	NA	NA	TG
ATP13A1	NA	LDL-C, TC, TG	LDL-C, TC, TG	NA	NA	Dyslipidemia
ZNF259	NA	HDL-C, TC, TG	TG	NA	Dyslipidemia, TG	NA
DOCK7	NA	LDL-C, TC, TG	LDL-C, TC, TG	NA	NA	TG
PSRC1	NA	Dyslipidemia, LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	Dyslipidemia, LDL-C
SORT1	NA	Dyslipidemia, LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	Dyslipidemia, LDL-C
SLC5A6	NA	TG	TG	NA	NA	TG
CELSR2	NA	Dyslipidemia, LDL-C, TC	Dyslipidemia, HDL-C, LDL-C, TC	NA	NA	Dyslipidemia, LDL-C
PCSK7	NA	TG	TG	NA	NA	Dyslipidemia
USP1	NA	LDL-C, TC, TG	LDL-C, TC, TG	NA	NA	TG
PAFAH1B2	NA	TG	Dyslipidemia, TG	NA	NA	Dyslipidemia
CDC42SE1	NA	TG	TG	chr1	NA	NA
GPN1	NA	TC, TG	TC, TG	NA	TG	NA
C2orf16	NA	TG	TG	NA	NA	TG
DNAH10OS	NA	HDL-C, TG	HDL-C, TG	NA	NA	Dyslipidemia

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
RP11-109L13.1	NA	TG	TG	NA	NA	Dyslipidemia
HMBS	NA	TG	TG	NA	NA	TG
RP11-373D23.3	NA	LDL-C, TC, TG	TG	NA	TG	NA
IMPA2	chr18	NA	TG	NA	NA	NA
MPPE1	chr18	NA	TG	NA	NA	NA
WI2-81516×10^{3}.1 (LINC01310)	chr22	NA	LDL-C	NA	NA	NA
FLG	NA	NA	TG	chr1	NA	NA
SEMA3F	NA	HDL-C	HDL-C	NA	NA	NA
RBM6	NA	HDL-C	HDL-C	NA	NA	NA
POLR2J	NA	HDL-C	HDL-C	NA	NA	NA
MARK4	NA	LDL-C, TC	LDL-C	NA	NA	NA
MLXIPL	NA	TG	TG	NA	NA	NA
SYT7	NA	LDL-C, TG	HDL-C, TG	NA	NA	NA
ERCC1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
DEF6	NA	HDL-C, TG	HDL-C	NA	NA	NA
NR1H3	NA	HDL-C	HDL-C	NA	NA	NA
RNASET2	NA	HDL-C	HDL-C, TG	NA	NA	NA
SARS	NA	LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	NA
GAB2	NA	TG	TG	NA	NA	NA
HERPUD1	NA	HDL-C	HDL-C	NA	NA	NA
MPHOSPH9	NA	HDL-C	HDL-C, TG	NA	NA	NA
DGKG	NA	HDL-C	HDL-C	NA	NA	NA
LZTS1	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
ZNF112	NA	LDL-C	LDL-C, TC	NA	NA	NA
ZNF76	NA	HDL-C	HDL-C, TG	NA	NA	NA
OSBPL3	NA	LDL-C	LDL-C	NA	NA	NA
CYP2W1	NA	TC	TC	NA	NA	NA
ACAT1	NA	LDL-C	LDL-C	NA	NA	NA
MKRN2	NA	TC	TC	NA	NA	NA
MCM6	NA	TG	TG	NA	NA	NA
KEAP1	NA	LDL-C	LDL-C	NA	NA	NA
COBLL1	NA	TG	TG	NA	NA	NA
PGS1	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
MT3	NA	HDL-C	HDL-C	NA	NA	NA
OGFOD1	NA	HDL-C	HDL-C	NA	NA	NA
TGDS	NA	LDL-C	LDL-C, TC	NA	NA	NA
P2RX7	NA	HDL-C	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
MLF2	NA	TG	HDL-C, TG	NA	NA	NA
PABPC4	NA	TG	HDL-C, TG	NA	NA	NA
PITPNM2	NA	HDL-C	HDL-C	NA	NA	NA
TTC28	NA	TG	TG	NA	NA	NA
NUP93	NA	HDL-C	HDL-C	NA	NA	NA
TSNAXIP1	NA	HDL-C	HDL-C	NA	NA	NA
ACD	NA	HDL-C	HDL-C	NA	NA	NA
PARD6A	NA	HDL-C	HDL-C	NA	NA	NA
LMF1	NA	TG	TG	NA	NA	NA
BCKDK	NA	TG	TG	NA	NA	NA
KAT8	NA	TG	TG	NA	NA	NA
INTS10	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
CLPTM1	NA	HDL-C, LDL-C	HDL-C, LDL-C	NA	NA	NA
ERCC2	NA	LDL-C, TC	HDL-C, LDL-C	NA	NA	NA
KLC3	NA	LDL-C	LDL-C	NA	NA	NA
DMPK	NA	Dyslipidemia, LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	NA
PDCD5	NA	TG	TG	NA	NA	NA
PLIN3	NA	HDL-C	TC	NA	NA	NA
TYK2	NA	LDL-C	LDL-C, TC	NA	NA	NA
RAB3D	NA	LDL-C	LDL-C	NA	NA	NA
DKFZP761J1410	NA	LDL-C	LDL-C	NA	NA	NA
DNAH11	NA	TC	LDL-C, TC	NA	NA	NA
ABHD11	NA	NA	TG	NA	NA	Dyslipidemia
NSUN5P2	NA	TG	TG	NA	NA	NA
PHF14	NA	HDL-C	HDL-C	NA	NA	NA
BCL7B	NA	TG	TG	NA	NA	NA
SYNGR2	NA	TG	TG	NA	NA	NA
DCPS	NA	LDL-C	LDL-C	NA	NA	NA
ST3GAL4	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
OGFOD2	NA	HDL-C	HDL-C	NA	NA	NA
CDK2AP1	NA	HDL-C	HDL-C	NA	NA	NA
COPS7A	NA	TG	TG	NA	NA	NA
HMGCR	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
HAVCR1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
CLINT1	NA	TC, TG	TC, TG	NA	NA	NA
DARS	NA	TG	HDL-C, TG	NA	NA	NA
TMEM59	NA	LDL-C	LDL-C	NA	NA	NA
IPO13	NA	TG	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ATP6V0B	NA	TG	TG	NA	NA	NA
CD3EAP	NA	HDL-C, LDL-C, TC	HDL-C, LDL-C, TC	NA	NA	NA
APOA1	NA	HDL-C, TG	HDL-C	NA	NA	NA
USP35	NA	TG	HDL-C, TG	NA	NA	NA
CCDC92	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
NPC2	NA	TG	TG	NA	NA	NA
CLCC1	NA	Dyslipidemia, LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	NA
POLK	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
FAM35A	NA	TG	TG	NA	NA	NA
ITPR2	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
SLC12A4	NA	HDL-C	HDL-C	NA	NA	NA
ENKD1	NA	HDL-C	HDL-C	NA	NA	NA
SNRPC	NA	HDL-C	HDL-C	NA	NA	NA
BBS2	NA	HDL-C	HDL-C	NA	NA	NA
MT1G	NA	HDL-C	HDL-C	NA	NA	NA
MT2A	NA	HDL-C	HDL-C, TG	NA	NA	NA
ATG4C	NA	TC, TG	TC, TG	NA	NA	NA
SMARCA4	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
ALDH1A2	NA	HDL-C, TC	HDL-C, TC	NA	NA	NA
SLC44A2	NA	LDL-C	LDL-C, TC	NA	NA	NA
AP1M2	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
CDKN2D	NA	LDL-C	LDL-C	NA	NA	NA
MAU2	NA	LDL-C, TC, TG	LDL-C, TC, TG	NA	NA	NA
DOCK6	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
EXOC3L2	NA	LDL-C	LDL-C	NA	NA	NA
PVRL2	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
APOE	NA	HDL-C, TC, TG	HDL-C, TG	NA	NA	NA
C12orf65	NA	HDL-C	HDL-C	NA	NA	NA
ZNF20	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
RAF1	NA	NA	TC	NA	NA	HDL-C
GSTM1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
MYBPC3	NA	HDL-C	HDL-C	NA	NA	NA
DDB2	NA	HDL-C	HDL-C	NA	NA	NA
ACP2	NA	HDL-C	HDL-C	NA	NA	NA
FADS2	NA	LDL-C, TG	LDL-C, TC, TG	NA	NA	NA
TMEM258	NA	LDL-C, TC, TG	LDL-C, TC, TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
COQ10A	NA	HDL-C	HDL-C	NA	NA	NA
TCF19	NA	TG	TG	NA	NA	NA
NARS2	NA	TG	HDL-C, TG	NA	NA	NA
TUBGCP4	NA	TG	TG	NA	NA	NA
IFT172	NA	TG	TG	NA	NA	NA
KHK	NA	NA	TG	NA	NA	TG
EMILIN1	NA	TC, TG	TC, TG	NA	NA	NA
TRIM54	NA	TC, TG	NA	NA	TG	NA
GALNT6	NA	TC	LDL-C, TC	NA	NA	NA
WDFY2	NA	LDL-C, TG	LDL-C, TC, TG	NA	NA	NA
TXNL4B	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
CPNE2	NA	HDL-C	HDL-C	NA	NA	NA
CTRL	NA	HDL-C	HDL-C	NA	NA	NA
DPEP3	NA	HDL-C	HDL-C	NA	NA	NA
GFOD2	NA	HDL-C	HDL-C	NA	NA	NA
NPEPPS	NA	TC	LDL-C, TC	NA	NA	NA
CCDC40	NA	TG	TG	NA	NA	NA
NTN5	NA	LDL-C	LDL-C, TC	NA	NA	NA
GEMIN7	NA	LDL-C, TC	HDL-C, LDL-C, TC	NA	NA	NA
MYO1F	NA	TG	HDL-C	NA	NA	NA
C19orf52	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
CARM1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
RERE	NA	NA	HDL-C, TG	NA	NA	LDL-C
SYPL2	NA	LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	NA
RXRG	NA	HDL-C	HDL-C	NA	NA	NA
POGZ	NA	NA	TG	chr1	NA	NA
ITPRIP	NA	TC	TC	NA	NA	NA
ABHD1	NA	NA	TG	NA	NA	TG
PPP1R18	NA	HDL-C	HDL-C, TG	NA	NA	NA
WTAP	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
SLC22A3	NA	LDL-C	Dyslipidemia, LDL-C, TC	NA	NA	NA
TRIM50	NA	TG	TG	NA	NA	NA
CSGALNACT1	NA	TG	HDL-C, TG	NA	NA	NA
NRBF2	NA	TG	TG	NA	NA	NA
FER	NA	TG	TG	NA	NA	NA
FADS1	NA	LDL-C, TG	LDL-C, TC, TG	NA	NA	NA
SIDT2	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ABCB9	NA	HDL-C	HDL-C	NA	NA	NA
RILPL2	NA	HDL-C	HDL-C	NA	NA	NA
ARL14EP	NA	TG	TG	NA	NA	NA
POC5	NA	TC	LDL-C, TC	NA	NA	NA
ABCA6	NA	TC	LDL-C, TC	NA	NA	NA
TNIK	NA	TG	TG	NA	NA	NA
N6AMT1	NA	HDL-C	HDL-C	NA	NA	NA
PSD3	NA	TG	TG	NA	NA	NA
RWDD2B	NA	HDL-C	HDL-C	NA	NA	NA
PKN3	NA	LDL-C	LDL-C, TC	NA	NA	NA
BRE	NA	TC, TG	TG	NA	NA	NA
RSPRY1	NA	HDL-C	HDL-C	NA	NA	NA
ZNF233	NA	LDL-C	TG	NA	NA	NA
ZNF235	NA	LDL-C	LDL-C, TC	NA	NA	NA
EFHB	NA	TG	TG	NA	NA	NA
SPC24	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
ATXN7L2	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
LYSMD1	NA	TG	NA	chr1	NA	NA
C1orf106	NA	LDL-C	TC	NA	NA	NA
SPDYE6	NA	HDL-C	HDL-C	NA	NA	NA
UCN	NA	TG	NA	NA	TG	NA
PLB1	NA	TG	TG	NA	NA	NA
RNF123	NA	HDL-C	HDL-C	NA	NA	NA
MST1R	NA	HDL-C	HDL-C	NA	NA	NA
CTSB	NA	TG	TG	NA	NA	NA
ABCA1	NA	TC	HDL-C, TC	NA	NA	NA
GKAP1	NA	TG	TG	NA	NA	NA
SLC39A13	NA	HDL-C	HDL-C	NA	NA	NA
PSMC3	NA	HDL-C	HDL-C, TC	NA	NA	NA
LIPC	NA	HDL-C, TC	HDL-C, TC, TG	NA	NA	NA
KATNAL2	NA	TG	TG	NA	NA	NA
AP1G1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
NUDT21	NA	HDL-C	HDL-C	NA	NA	NA
FBXO22	NA	TG	TG	NA	NA	NA
EFNA1	NA	TG	TG	NA	NA	NA
DUS2	NA	HDL-C	HDL-C	NA	NA	NA
ZNF180	NA	TG	TG	NA	NA	NA
GATAD2A	NA	TC, TG	TC, TG	NA	NA	NA
ZNF283	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
FTH1	NA	LDL-C	LDL-C, TC	NA	NA	NA
PPIP5K1	NA	TG	TG	NA	NA	NA
ADAL	NA	TG	TG	NA	NA	NA
IRS1	NA	HDL-C	HDL-C	NA	NA	NA
PCSK9	NA	LDL-C	LDL-C, TC	NA	NA	NA
ACYP2	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
SLC38A11	NA	TG	TG	NA	NA	NA
SEZ6L2	NA	TC	TC	NA	NA	NA
LILRA3	NA	HDL-C	HDL-C, TC	NA	NA	NA
UGT2B7	NA	TC	TC	NA	NA	NA
KCNK3	NA	TG	TG	NA	NA	NA
TTC40	NA	TG	TG	NA	NA	NA
HINFP	NA	TG	TG	NA	NA	NA
RNASEH2C	NA	HDL-C	HDL-C	NA	NA	NA
PARP15	NA	HDL-C	HDL-C, TG	NA	NA	NA
C2orf70	NA	TG	NA	NA	TG	NA
CYB561D1	NA	LDL-C	HDL-C	NA	NA	NA
STAG3L3	NA	TG	TG	NA	NA	NA
AP006621.1	NA	TG	TG	NA	NA	NA
SLC22A1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
DOK7	NA	TC	LDL-C, TC	NA	NA	NA
ZNF404	NA	LDL-C	LDL-C, TC	NA	NA	NA
SPRYD4	NA	HDL-C	TC	NA	NA	NA
VPS37D	NA	TG	TG	NA	NA	NA
ZNF285B	NA	LDL-C, TC	HDL-C, LDL-C, TC, TG	NA	NA	NA
MAMSTR	NA	LDL-C	LDL-C	NA	NA	NA
FUT2	NA	LDL-C, TC	LDL-C	NA	NA	NA
PIDD	NA	TG	TG	NA	NA	NA
C18orf32	NA	TC	TC	NA	NA	NA
RPLP2	NA	TG	TG	NA	NA	NA
ZNF491	NA	LDL-C	LDL-C	NA	NA	NA
PNPLA2	NA	TG	TG	NA	NA	NA
TMEM64	NA	TG	TG	NA	NA	NA
PLEC	NA	LDL-C	LDL-C	NA	NA	NA
RMI1	NA	TG	TG	NA	NA	NA
ZNF664	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
F2	NA	HDL-C	HDL-C	NA	NA	NA
GNB1L	NA	LDL-C	TC	NA	NA	NA
AMIGO1	NA	LDL-C	LDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ARL6IP4	NA	HDL-C	HDL-C, TG	NA	NA	NA
CCDC159	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
BMP8A	NA	TG	TG	NA	NA	NA
SETD8	NA	HDL-C	HDL-C	NA	NA	NA
NIPSNAP1	NA	TG	TG	NA	NA	NA
MROH2A	NA	LDL-C, TC	TC	NA	NA	NA
STMN3	NA	TG	TG	NA	NA	NA
RASA3	NA	TG	TG	NA	NA	NA
ZNF284	NA	LDL-C	LDL-C	NA	NA	NA
BACE1	NA	TG	TG	NA	NA	NA
CEACAM19	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
MT1X	NA	HDL-C	HDL-C	NA	NA	NA
BCAM	NA	LDL-C, TC	LDL-C	NA	NA	NA
NRN1L	NA	HDL-C	HDL-C	NA	NA	NA
ANKDD1B	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
HLA-DRB1	NA	TG	TG	NA	NA	NA
HLA-DRB9	NA	TG	TG	NA	NA	NA
ZNF781	NA	TC	TC	NA	NA	NA
IGF2R	NA	LDL-C	LDL-C, TC	NA	NA	NA
AL133458.1	NA	HDL-C	HDL-C	NA	NA	NA
PIWIL2	NA	HDL-C	HDL-C	NA	NA	NA
C20orf112	NA	TG	TG	NA	NA	NA
KANK2	NA	LDL-C, TC	Dyslipidemia, LDL-C, TC	NA	NA	NA
DNAH10	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
MYO1C	NA	TG	TG	NA	NA	NA
HLA-DRB5	NA	TG	TG	NA	NA	NA
TBKBP1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
DAXX	NA	TG	TG	NA	NA	NA
TAP2	NA	TG	TG	NA	NA	NA
HLA-DRA	NA	TG	TG	NA	NA	NA
NOTCH4	NA	TG	TG	NA	NA	NA
PBX2	NA	TG	TG	NA	NA	NA
AGER	NA	TG	TG	NA	NA	NA
PRRT1	NA	TG	TG	NA	NA	NA
FKBPL	NA	TG	TG	NA	NA	NA
DXO	NA	TG	TG	NA	NA	NA
SLC44A4	NA	TG	TG	NA	NA	NA
CSNK2B	NA	TG	TG	NA	NA	NA
GPANK1	NA	TG	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
POU5F1	NA	TG	TG	NA	NA	NA
PSORS1C2	NA	TG	TG	NA	NA	NA
PSORS1C1	NA	TG	TG	NA	NA	NA
ZNF155	NA	TC	LDL-C, TC	NA	NA	NA
MT1DP	NA	HDL-C	HDL-C	NA	NA	NA
MT1A	NA	HDL-C	HDL-C	NA	NA	NA
ATP5O	NA	Dyslipidemia	Dyslipidemia	NA	NA	NA
CDPF1	NA	TC, TG	TC, TG	NA	NA	NA
HCG27	NA	HDL-C, TG	HDL-C	NA	NA	NA
NUP62	NA	TG	TG	NA	NA	NA
FGFR1OP	NA	HDL-C	HDL-C	NA	NA	NA
RP11-288H12.3	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
GSTM2	NA	LDL-C	LDL-C, TC	NA	NA	NA
LCAT	NA	HDL-C	HDL-C	NA	NA	NA
ATF6B	NA	TG	TG	NA	NA	NA
MYBPHL	NA	LDL-C	LDL-C	NA	NA	NA
VPS52	NA	TG	TG	NA	NA	NA
C2CD4D	NA	TG	NA	chr1	NA	NA
MRPL45P2	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
HMGN2P19	NA	TC	LDL-C, TC	NA	NA	NA
LINC00452	NA	TG	TG	NA	NA	NA
HLA-DRB6	NA	TG	TG	NA	NA	NA
AP006216.11	NA	HDL-C, TG	TG	NA	NA	NA
TAPBP	NA	TG	TG	NA	NA	NA
MRPL35P2	NA	TG	TG	NA	NA	NA
HLA-DQB2	NA	TG	TG	NA	NA	NA
SEC1P	NA	LDL-C	LDL-C	NA	NA	NA
AC067959.1	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
EBAG9P1	NA	TG	TG	NA	NA	NA
PINLYP	NA	HDL-C	HDL-C, TC	NA	NA	NA
RP11-166B2.1	NA	HDL-C	HDL-C, TG	NA	NA	NA
HLA-B	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
AC074117.13	NA	TC, TG	NA	NA	TG	NA
IFITM4P	NA	HDL-C	HDL-C, TG	NA	NA	NA
ZBTB22	NA	TG	TG	NA	NA	NA
OXCT2P1	NA	TG	HDL-C, TG	NA	NA	NA
RP11-295M18.2	NA	LDL-C	LDL-C, TC	NA	NA	NA
AP006621.5	NA	TG	TG	NA	NA	NA
HYPK	NA	TG	TG	NA	NA	NA
MRPL33	NA	TC, TG	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
PPIEL	NA	TG	TG	NA	NA	NA
GSTA2	NA	TG	TG	NA	NA	NA
P2RY11	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
C4A	NA	TG	HDL-C, TG	NA	NA	NA
TNXA	NA	TG	TG	NA	NA	NA
TAP2	NA	TG	TG	NA	NA	NA
RP11-452H21.4	NA	TG	TG	NA	NA	NA
CHMP4A	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
PABPC1P4	NA	HDL-C	HDL-C	NA	NA	NA
KLRAP1	NA	TG	TG	NA	NA	NA
HP	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
AC012065.7	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
HPR	NA	LDL-C, TC	LDL-C, TC	NA	NA	NA
ZNF234	NA	TG	TG	NA	NA	NA
XXbac-BPG248L24.12	NA	HDL-C, TG	HDL-C, TG	NA	NA	NA
RP11-110I1.14	NA	TG	TG	NA	NA	NA
XXbac-BPG299F13.14	NA	TG	TG	NA	NA	NA
RP11-295M18.6	NA	LDL-C	LDL-C	NA	NA	NA
M6PR	NA	NA	TC	NA	NA	NA
DBNDD1	NA	NA	TG	NA	NA	NA
GDE1	NA	NA	HDL-C	NA	NA	NA
CX3CL1	NA	HDL-C	NA	NA	NA	NA
GTF2IRD1	NA	TG	NA	NA	NA	NA
SPAG9	NA	TG	NA	NA	NA	NA
QPCTL	NA	LDL-C	NA	NA	NA	NA
PPP5C	NA	NA	TC	NA	NA	NA
ZBTB32	NA	NA	LDL-C	NA	NA	NA
MVP	NA	TC	NA	NA	NA	NA
MTMR11	NA	NA	NA	chr1	NA	NA
DPEP1	NA	NA	TG	NA	NA	NA
NUDCD3	NA	NA	LDL-C	NA	NA	NA
MRE11A	NA	NA	TG	NA	NA	NA
ABCC2	NA	NA	TG	NA	NA	NA
PLEKHO1	NA	NA	NA	chr1	NA	NA
AGPAT4	NA	NA	LDL-C	NA	NA	NA
CENPQ	NA	NA	HDL-C	NA	NA	NA
RPL26L1	chr5	NA	NA	NA	NA	NA
SPDL1	chr5	NA	NA	NA	NA	NA
LCP2	chr5	NA	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
RFC2	NA	NA	TG	NA	NA	NA
HOMER3	NA	LDL-C, TC, TG	NA	NA	NA	NA
THOC3	NA	NA	TG	NA	NA	NA
PLEKHA5	NA	TG	NA	NA	NA	NA
GALC	NA	NA	TG	NA	NA	NA
USP36	NA	NA	TG	NA	NA	NA
TBXAS1	NA	NA	TG	NA	NA	NA
WAPL	chr10	NA	NA	NA	NA	NA
UHRF1BP1	NA	NA	HDL-C	NA	NA	NA
PTPN21	NA	TG	NA	NA	NA	NA
SLC12A3	NA	HDL-C	NA	NA	NA	NA
TRIB2	NA	NA	TC	NA	NA	NA
STK10	chr5	NA	NA	NA	NA	NA
FBXW11	chr5	NA	NA	NA	NA	NA
MOV10L1	chr22	NA	NA	NA	NA	NA
PVR	NA	LDL-C	NA	NA	NA	NA
PANX2	chr22	NA	NA	NA	NA	NA
SELENOO	chr22	NA	NA	NA	NA	NA
ADCYAP1R1	NA	NA	HDL-C	NA	NA	NA
ADD2	NA	NA	Dyslipidemia	NA	NA	NA
SIRT6	NA	NA	LDL-C, TC	NA	NA	NA
MTMR2	NA	NA	TG	NA	NA	NA
ZMPSTE24	NA	NA	TG	NA	NA	NA
MAPRE3	NA	NA	NA	NA	NA	TG
GSTT2	NA	NA	TG	NA	NA	NA
GNAO1	NA	NA	HDL-C	NA	NA	NA
ADD1	NA	NA	TG	NA	NA	NA
COQ9	NA	HDL-C	NA	NA	NA	NA
BIRC5	NA	NA	NA	NA	NA	LDL-C
WDR76	NA	NA	TG	NA	NA	NA
GABRP	chr5	NA	NA	NA	NA	NA
CWF19L1	NA	NA	HDL-C	NA	NA	NA
C19orf77	NA	NA	NA	NA	NA	Dyslipidemia
TMED1	NA	LDL-C, TC	NA	NA	NA	NA
UPB1	NA	NA	HDL-C	NA	NA	NA
BRD1	chr22	NA	NA	NA	NA	NA
HSCB	NA	NA	TG	NA	NA	NA
APOBEC3H	NA	NA	TC	NA	NA	NA
ASCC2	NA	NA	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ZBED4	chr22	NA	NA	NA	NA	NA
MLC1	chr22	NA	NA	NA	NA	NA
HDAC10	chr22	NA	NA	NA	NA	NA
PIGH	NA	NA	TG	NA	NA	NA
CTSG	NA	NA	LDL-C, TC	NA	NA	NA
PRPF6	NA	NA	TG	NA	NA	NA
GMEB2	NA	NA	TG	NA	NA	NA
NOP56	NA	NA	HDL-C	NA	NA	NA
RHBDL1	NA	NA	TG	NA	NA	NA
VAPA	chr18	NA	NA	NA	NA	NA
LIPG	NA	HDL-C	NA	NA	NA	NA
ACP5	NA	NA	LDL-C	NA	NA	NA
KPNA3	NA	TC	NA	NA	NA	NA
DHODH	NA	NA	TC	NA	NA	NA
CDIPT	NA	NA	TC	NA	NA	NA
RASL12	NA	NA	TC	NA	NA	NA
RNF40	NA	TG	NA	NA	NA	NA
DECR1	NA	TG	NA	NA	NA	NA
EHD4	NA	NA	Dyslipidemia	NA	NA	NA
OIP5	NA	NA	HDL-C	NA	NA	NA
SFRP1	NA	TG	NA	NA	NA	NA
GLCCI1	NA	NA	TG	NA	NA	NA
SH2D4A	NA	NA	HDL-C	NA	NA	NA
NFKBIB	NA	NA	TC	NA	NA	NA
RELB	NA	LDL-C, TC	NA	NA	NA	NA
CKM	NA	LDL-C, TC	NA	NA	NA	NA
RASIP1	NA	LDL-C	NA	NA	NA	NA
SUGP1	NA	TC, TG	NA	NA	NA	NA
ETHE1	NA	NA	HDL-C	NA	NA	NA
SMG9	NA	NA	Dyslipidemia	NA	NA	NA
IMPDH1	NA	NA	HDL-C	NA	NA	NA
CCSER2	chr10	NA	NA	NA	NA	NA
TMEM106B	NA	NA	TG	NA	NA	NA
TBL2	NA	NA	TG	NA	NA	NA
TFAM	NA	TG	NA	NA	NA	NA
SH3D19	NA	LDL-C	NA	NA	NA	NA
KPNB1	NA	LDL-C	NA	NA	NA	NA
DUSP3	NA	NA	TG	NA	NA	NA
TRIM2	NA	NA	TG	NA	NA	NA
MAGOHB	NA	NA	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
HGFAC	NA	NA	TC	NA	NA	NA
MTCH2	NA	TC	NA	NA	NA	NA
MAK	NA	NA	HDL-C	NA	NA	NA
DDX55	NA	NA	HDL-C	NA	NA	NA
SOBP	NA	NA	TC	NA	NA	NA
DAP	NA	NA	HDL-C	NA	NA	NA
NME5	NA	NA	TG	NA	NA	NA
PRSS16	NA	NA	HDL-C	NA	NA	NA
SLC12A7	NA	NA	TG	NA	NA	NA
ERGIC1	chr5	NA	NA	NA	NA	NA
COL4A3BP	NA	LDL-C, TC	NA	NA	NA	NA
ATP6V0E1	chr5	NA	NA	NA	NA	NA
STAM2	NA	NA	TG	NA	NA	NA
GALNT3	NA	NA	LDL-C	NA	NA	NA
IGFBP2	NA	NA	HDL-C	NA	NA	NA
MPV17	NA	TC, TG	NA	NA	NA	NA
EIF2B4	NA	TG	NA	NA	NA	NA
FNDC4	NA	TC, TG	NA	NA	NA	NA
PRDM2	NA	TC	NA	NA	NA	NA
ADPRHL2	NA	TC	NA	NA	NA	NA
KIAA1324	NA	LDL-C	NA	NA	NA	NA
B4GALT2	NA	NA	HDL-C	NA	NA	NA
GTF3C3	NA	NA	LDL-C, TC	NA	NA	NA
PRPF3	NA	NA	NA	chr1	NA	NA
APH1A	NA	NA	NA	chr1	NA	NA
PTBP3	NA	NA	LDL-C	NA	NA	NA
C1orf54	NA	NA	NA	chr1	NA	NA
CA14	NA	NA	NA	chr1	NA	NA
C2orf43	NA	NA	LDL-C, TC	NA	NA	NA
GPR75	NA	HDL-C	NA	NA	NA	NA
DUSP1	chr5	NA	NA	NA	NA	NA
LCN1P1	NA	NA	TG	NA	NA	NA
LTBP2	NA	NA	HDL-C	NA	NA	NA
TEK	NA	NA	TG	NA	NA	NA
SUPT7L	NA	TG	NA	NA	NA	NA
KCNIP2	NA	NA	HDL-C	NA	NA	NA
NECAB1	NA	NA	TG	NA	NA	NA
TTC21B	NA	LDL-C	NA	NA	NA	NA
SSUH2	NA	TG	NA	NA	NA	NA
ZRANB3	NA	NA	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
PPDPF	NA	NA	TG	NA	NA	NA
EGR2	NA	TG	NA	NA	NA	NA
ACADS	NA	NA	HDL-C	NA	NA	NA
TUBGCP6	chr22	NA	NA	NA	NA	NA
TSFM	NA	NA	TG	NA	NA	NA
IKZF4	NA	NA	HDL-C	NA	NA	NA
HOXD1	NA	NA	HDL-C	NA	NA	NA
POMT1	NA	NA	HDL-C	NA	NA	NA
C1orf159	NA	NA	TG	NA	NA	NA
DOK4	NA	HDL-C	NA	NA	NA	NA
GRK4	NA	NA	TG	NA	NA	NA
GTF3C4	NA	NA	TG	NA	NA	NA
LGALS3	NA	NA	TG	NA	NA	NA
FOSB	NA	LDL-C	NA	NA	NA	NA
SNRPD2	NA	NA	Dyslipidemia	NA	NA	NA
VASP	NA	LDL-C	NA	NA	NA	NA
SYMPK	NA	NA	LDL-C	NA	NA	NA
IGFLR1	NA	LDL-C	NA	NA	NA	NA
PRMT1	NA	NA	TG	NA	NA	NA
MACF1	NA	TG	NA	NA	NA	NA
PNKD	NA	NA	TG	NA	NA	NA
MTL5	NA	NA	HDL-C	NA	NA	NA
POMP	NA	NA	LDL-C, TC	NA	NA	NA
ELL3	NA	NA	TG	NA	NA	NA
KRI1	NA	NA	LDL-C, TC	NA	NA	NA
TOMM40	NA	LDL-C	NA	NA	NA	NA
APOC1	NA	HDL-C, TC, TG	NA	NA	NA	NA
NSUN5	NA	TG	NA	NA	NA	NA
CEP85	NA	LDL-C	NA	NA	NA	NA
CCNA1	NA	NA	TG	NA	NA	NA
YIPF2	NA	LDL-C, TC	NA	NA	NA	NA
ATG4D	NA	LDL-C, TC	NA	NA	NA	NA
ZNF317	NA	NA	TG	NA	NA	NA
PKDREJ	NA	NA	TG	NA	NA	NA
ACTR3B	NA	NA	TG	NA	NA	NA
C14orf159	NA	NA	TG	NA	NA	NA
TRIM5	NA	NA	TG	NA	NA	NA
ELP2	NA	NA	HDL-C	NA	NA	NA
ANGPTL3	NA	TC	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
TMEM60	NA	NA	TG	NA	NA	NA
ORC3	NA	HDL-C	NA	NA	NA	NA
GNS	NA	NA	TG	NA	NA	NA
GSC	NA	NA	TG	NA	NA	NA
AOAH	NA	NA	HDL-C	NA	NA	NA
GSTM5	NA	NA	LDL-C	NA	NA	NA
GSTM3	NA	NA	Dyslipidemia, LDL-C, TC	NA	NA	NA
NAPG	chr18	NA	NA	NA	NA	NA
DOCK2	chr5	NA	NA	NA	NA	NA
LRP4	NA	HDL-C	NA	NA	NA	NA
AP1AR	NA	NA	TC	NA	NA	NA
MSI1	NA	NA	Dyslipidemia	NA	NA	NA
G3BP2	NA	NA	TG	NA	NA	NA
USO1	NA	TG	NA	NA	NA	NA
OS9	NA	NA	TG	NA	NA	NA
ETNK1	NA	TG	NA	NA	NA	NA
FAM129A	NA	NA	HDL-C	NA	NA	NA
TMBIM1	NA	NA	TG	NA	NA	NA
PHF11	NA	NA	TC	NA	NA	NA
GAS8	NA	NA	TG	NA	NA	NA
SCN2A	NA	TG	NA	NA	NA	NA
VPS45	NA	NA	NA	chr1	NA	NA
DSCC1	NA	NA	TG	NA	NA	NA
BUD13	NA	TG	NA	NA	NA	NA
ADAM10	NA	NA	HDL-C	NA	NA	NA
GNAL	chr18	NA	NA	NA	NA	NA
NBPF3	NA	NA	HDL-C	NA	NA	NA
KIAA1715	NA	NA	HDL-C	NA	NA	NA
PHLDB2	NA	NA	TG	NA	NA	NA
SBNO1	NA	HDL-C	NA	NA	NA	NA
VPS37B	NA	NA	HDL-C	NA	NA	NA
CDAN1	NA	NA	NA	NA	NA	Dyslipidemia
PCSK6	NA	NA	TC	NA	NA	NA
FEM1C	NA	TG	NA	NA	NA	NA
AIG1	NA	NA	TG	NA	NA	NA
NPC1	NA	NA	HDL-C	NA	NA	NA
TMC6	NA	NA	TG	NA	NA	NA
NFIC	NA	NA	Dyslipidemia	NA	NA	NA
CBLC	NA	LDL-C	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ZNF593	NA	LDL-C, TC	NA	NA	NA	NA
CCDC25	NA	NA	HDL-C	NA	NA	NA
PSMA5	NA	Dyslipidemia, LDL-C, TC	NA	NA	NA	NA
SLC26A7	NA	NA	TG	NA	NA	NA
PRUNE1	NA	NA	NA	chr1	NA	NA
RORC	NA	NA	NA	chr1	NA	NA
TUFT1	NA	NA	NA	chr1	NA	NA
SF3B4	NA	NA	NA	chr1	NA	NA
ECM1	NA	NA	NA	chr1	NA	NA
ZNF687	NA	NA	NA	chr1	NA	NA
TARS2	NA	NA	NA	chr1	NA	NA
CGN	NA	NA	NA	chr1	NA	NA
SNX27	NA	NA	NA	chr1	NA	NA
SETDB1	NA	NA	NA	chr1	NA	NA
ADAMTSL4	NA	NA	NA	chr1	NA	NA
MCL1	NA	NA	NA	chr1	NA	NA
CTSK	NA	NA	NA	chr1	NA	NA
RFX5	NA	NA	NA	chr1	NA	NA
PI4KB	NA	NA	NA	chr1	NA	NA
PIP5K1A	NA	NA	NA	chr1	NA	NA
ANP32E	NA	NA	NA	chr1	NA	NA
MINDY1	NA	NA	NA	chr1	NA	NA
ANXA9	NA	NA	NA	chr1	NA	NA
SELENBP1	NA	NA	NA	chr1	NA	NA
CERS2	NA	NA	NA	chr1	NA	NA
ENSA	NA	NA	NA	chr1	NA	NA
SEMA6C	NA	NA	NA	chr1	NA	NA
MRPL9	NA	NA	NA	chr1	NA	NA
ARNT	NA	NA	NA	chr1	NA	NA
C1orf56	NA	NA	NA	chr1	NA	NA
OAZ3	NA	NA	NA	chr1	NA	NA
HORMAD1	NA	NA	NA	chr1	NA	NA
GOLPH3L	NA	NA	NA	chr1	NA	NA
GABPB2	NA	NA	NA	chr1	NA	NA
NUP210L	NA	NA	TG	NA	NA	NA
GDF7	NA	LDL-C, TC	NA	NA	NA	NA
ABCG8	NA	LDL-C, TC	NA	NA	NA	NA
UBXN4	NA	TG	NA	NA	NA	NA
LCN2	NA	LDL-C	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
RQCD1	NA	NA	TG	NA	NA	NA
FAM171A1	NA	TG	NA	NA	NA	NA
PDGFC	NA	NA	NA	NA	Dyslipidemia	NA
CDHR1	chr10	NA	NA	NA	NA	NA
KCNMB1	chr5	NA	NA	NA	NA	NA
LRIT1	chr10	NA	NA	NA	NA	NA
PNLDC1	NA	NA	LDL-C	NA	NA	NA
C7orf50	NA	NA	HDL-C	NA	NA	NA
ATP6V1B2	NA	HDL-C, TG	NA	NA	NA	NA
RGR	chr10	NA	NA	NA	NA	NA
ACAD8	NA	NA	TG	NA	NA	NA
GUF1	NA	NA	TG	NA	NA	NA
TMEM56	NA	NA	TC	NA	NA	NA
STK32B	NA	TG	NA	NA	NA	NA
CENPH	NA	NA	HDL-C	NA	NA	NA
PIEZO2	chr18	NA	NA	NA	NA	NA
ARFGAP2	NA	HDL-C	NA	NA	NA	NA
SERPINH1	NA	NA	HDL-C, TG	NA	NA	NA
DRD2	NA	NA	TG	NA	NA	NA
EML3	NA	NA	LDL-C	NA	NA	NA
INCENP	NA	NA	TG	NA	NA	NA
FCGR1A	NA	NA	NA	chr1	NA	NA
TIRAP	NA	LDL-C	NA	NA	NA	NA
KCTD14	NA	NA	TG	NA	NA	NA
LRGUK	NA	NA	TG	NA	NA	NA
USP16	NA	NA	TG	NA	NA	NA
SH3RF2	NA	NA	Dyslipidemia	NA	NA	NA
PDE6D	NA	NA	HDL-C	NA	NA	NA
KCNJ6	NA	NA	HDL-C	NA	NA	NA
SCN3A	NA	NA	TG	NA	NA	NA
FRMD1	NA	HDL-C	NA	NA	NA	NA
ABCA9	NA	NA	TC	NA	NA	NA
ABCA5	NA	NA	LDL-C	NA	NA	NA
PPP4R1	chr18	NA	NA	NA	NA	NA
APCDD1	chr18	NA	NA	NA	NA	NA
ATP5G1	NA	NA	HDL-C, TG	NA	NA	NA
TRIM74	NA	TG	NA	NA	NA	NA
UBE2Z	NA	NA	HDL-C	NA	NA	NA
ELMSAN1	NA	HDL-C	NA	NA	NA	NA
TMPRSS3	NA	NA	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
FGF18	chr5	NA	NA	NA	NA	NA
C9orf117	NA	NA	TG	NA	NA	NA
LRWD1	NA	NA	HDL-C	NA	NA	NA
DHRS4	NA	NA	TG	NA	NA	NA
PLCD3	NA	HDL-C	NA	NA	NA	NA
DPYSL5	NA	NA	NA	NA	NA	TG
C12orf43	NA	NA	HDL-C	NA	NA	NA
SV2A	NA	NA	NA	chr1	NA	NA
WDR90	NA	NA	TG	NA	NA	NA
JMJD8	NA	NA	TG	NA	NA	NA
CIART	NA	NA	NA	chr1	NA	NA
PSMD4	NA	NA	NA	chr1	NA	NA
PSMB4	NA	NA	NA	chr1	NA	NA
CELF3	NA	NA	NA	chr1	NA	NA
THEM4	NA	NA	NA	chr1	NA	NA
GNPDA2	NA	NA	TG	NA	NA	NA
AMFR	NA	NA	HDL-C	NA	NA	NA
RGS12	NA	NA	HDL-C	NA	NA	NA
PSKH1	NA	HDL-C	NA	NA	NA	NA
ZNF230	NA	NA	LDL-C	NA	NA	NA
ZNF221	NA	LDL-C, TC	NA	NA	NA	NA
INTU	NA	NA	TG	NA	NA	NA
ICOSLG	NA	NA	HDL-C	NA	NA	NA
MAD2L1	NA	NA	HDL-C	NA	NA	NA
SIK3	NA	HDL-C, TG	NA	NA	NA	NA
STAG3L2	NA	NA	TG	NA	NA	NA
CREBRF	chr5	NA	NA	NA	NA	NA
BRI3	NA	NA	TG	NA	NA	NA
ZNF653	NA	LDL-C, TC	NA	NA	NA	NA
NUDT5	NA	NA	TG	NA	NA	NA
GHITM	chr10	NA	NA	NA	NA	NA
CYB561A3	NA	LDL-C	NA	NA	NA	NA
RPS6KA4	NA	NA	HDL-C	NA	NA	NA
ACOT11	NA	NA	TC	NA	NA	NA
OTUD7B	NA	NA	NA	chr1	NA	NA
RPRD2	NA	NA	NA	chr1	NA	NA
CTSS	NA	NA	NA	chr1	NA	NA
BNIPL	NA	NA	NA	chr1	NA	NA
TNFAIP8L2	NA	NA	NA	chr1	NA	NA
SCNM1	NA	NA	NA	chr1	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
TMOD4	NA	NA	NA	chr1	NA	NA
VPS72	NA	NA	NA	chr1	NA	NA
ARL5B	NA	LDL-C	NA	NA	NA	NA
CCDC68	NA	NA	TG	NA	NA	NA
DCST2	NA	TG	NA	NA	NA	NA
SLC4A1AP	NA	NA	TG	NA	NA	NA
COQ7	NA	NA	HDL-C	NA	NA	NA
CAMKV	NA	HDL-C	NA	NA	NA	NA
RAB8A	NA	NA	LDL-C, TC	NA	NA	NA
TLX3	chr5	NA	NA	NA	NA	NA
KRT80	NA	NA	TC	NA	NA	NA
STK17A	NA	NA	TC	NA	NA	NA
MAPK1IP1L	NA	NA	TG	NA	NA	NA
GPER1	NA	NA	HDL-C, TC	NA	NA	NA
FREM1	NA	LDL-C	NA	NA	NA	NA
WBSCR27	NA	NA	TG	NA	NA	NA
REEP3	NA	TG	NA	NA	NA	NA
UBTD2	chr5	NA	NA	NA	NA	NA
RNASE6	NA	NA	LDL-C	NA	NA	NA
ISCA2	NA	NA	LDL-C, TG	NA	NA	NA
GYLTL1B	NA	NA	LDL-C	NA	NA	NA
PACSIN3	NA	NA	HDL-C	NA	NA	NA
RAPSN	NA	HDL-C	NA	NA	NA	NA
RFNG	NA	NA	HDL-C	NA	NA	NA
TM4SF4	NA	LDL-C	NA	NA	NA	NA
SEC11C	NA	NA	TG	NA	NA	NA
TMPRSS5	NA	NA	HDL-C	NA	NA	NA
STRCP1	NA	TG	NA	NA	NA	NA
YWHAB	NA	NA	HDL-C	NA	NA	NA
MAP1A	NA	NA	TG	NA	NA	NA
TRABD	chr22	NA	NA	NA	NA	NA
POP5	NA	TC	NA	NA	NA	NA
IRGQ	NA	NA	NA	NA	NA	Dyslipidemia
ZNF229	NA	TG	NA	NA	NA	NA
ZNF646	NA	NA	TG	NA	NA	NA
RASA4B	NA	NA	HDL-C	NA	NA	NA
TMC4	NA	NA	HDL-C	NA	NA	NA
FAM57A	NA	NA	TG	NA	NA	NA
DNAI2	NA	LDL-C	NA	NA	NA	NA
CD320	NA	NA	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
MGAT5B	NA	NA	NA	NA	NA	Dyslipidemia
RAB3IL1	NA	LDL-C	NA	NA	NA	NA
BATF2	NA	NA	Dyslipidemia	NA	NA	NA
PAH	NA	NA	Dyslipidemia	NA	NA	NA
SPATA5L1	NA	NA	HDL-C	NA	NA	NA
FOXI1	chr5	NA	NA	NA	NA	NA
TXNDC2	chr18	NA	NA	NA	NA	NA
RAB31	chr18	NA	NA	NA	NA	NA
TNXB	NA	TG	NA	NA	NA	NA
GSTM4	NA	NA	LDL-C, TC	NA	NA	NA
TCTN2	NA	NA	HDL-C, TG	NA	NA	NA
STX18	NA	NA	TG	NA	NA	NA
CEP120	NA	HDL-C	NA	NA	NA	NA
CPT1C	NA	NA	TG	NA	NA	NA
BPGM	NA	TC	NA	NA	NA	NA
EGFL7	NA	NA	TG	NA	NA	NA
GALNTL6	NA	TG	NA	NA	NA	NA
GLB1	NA	NA	TG	NA	NA	NA
IRF2BP1	NA	LDL-C	NA	NA	NA	NA
SH3PXD2B	chr5	NA	NA	NA	NA	NA
CCNE2	NA	TG	NA	NA	NA	NA
GIMAP8	NA	TG	NA	NA	NA	NA
MCTP1	NA	NA	TG	NA	NA	NA
ENC1	NA	NA	TC	NA	NA	NA
RPS6KB2	NA	NA	TG	NA	NA	NA
RPL23P2	NA	NA	HDL-C	NA	NA	NA
EXOSC10	NA	TG	NA	NA	NA	NA
TRAPPC12	NA	NA	LDL-C, TC	NA	NA	NA
C1QTNF4	NA	NA	HDL-C	NA	NA	NA
EPS8L2	NA	NA	TG	NA	NA	NA
EFCAB4A	NA	NA	TG	NA	NA	NA
MUS81	NA	LDL-C	NA	NA	NA	NA
CD151	NA	NA	TG	NA	NA	NA
CHID1	NA	NA	TG	NA	NA	NA
VEGFB	NA	NA	HDL-C	NA	NA	NA
GMPPB	NA	HDL-C	NA	NA	NA	NA
C2orf73	NA	NA	LDL-C	NA	NA	NA
DENND4A	NA	NA	NA	NA	NA	HDL-C
NPAS4	NA	LDL-C	NA	NA	NA	NA
MRFAP1	NA	NA	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
BRMS1	NA	NA	TG	NA	NA	NA
RPL15	NA	TG	NA	NA	NA	NA
ZNF408	NA	NA	NA	NA	NA	HDL-C
CKAP5	NA	HDL-C	NA	NA	NA	NA
SOCS4	NA	TG	NA	NA	NA	NA
ANKRD62	chr18	NA	NA	NA	NA	NA
LRRC25	NA	NA	LDL-C	NA	NA	NA
CCDC85B	NA	NA	HDL-C	NA	NA	NA
TMEM252	NA	NA	HDL-C	NA	NA	NA
GRID1	chr10	NA	NA	NA	NA	NA
AIM1L	NA	NA	TC	NA	NA	NA
CRLF3	NA	TG	NA	NA	NA	NA
DNAJC30	NA	NA	TG	NA	NA	NA
GCNT4	NA	TC	NA	NA	NA	NA
ALG12	chr22	NA	NA	NA	NA	NA
PPFIA3	NA	NA	LDL-C	NA	NA	NA
CADM1	NA	NA	TG	NA	NA	NA
C2CD4C	NA	NA	Dyslipidemia	NA	NA	NA
SF3A3	NA	NA	TG	NA	NA	NA
TBK1	NA	NA	TG	NA	NA	NA
BOLA1	NA	NA	NA	chr1	NA	NA
WDR6	NA	NA	HDL-C	NA	NA	NA
ERBB4	NA	NA	HDL-C	NA	NA	NA
RIIAD1	NA	NA	NA	chr1	NA	NA
EFCAB13	NA	LDL-C, TC	NA	NA	NA	NA
FAM101A	NA	HDL-C	NA	NA	NA	NA
CRELD2	chr22	NA	NA	NA	NA	NA
WSCD1	NA	TG	NA	NA	NA	NA
HLA-DQB1	NA	NA	TG	NA	NA	NA
ZBTB42	NA	NA	HDL-C	NA	NA	NA
CEND1	NA	TG	NA	NA	NA	NA
C1orf194	NA	NA	LDL-C	NA	NA	NA
GPBAR1	NA	NA	TG	NA	NA	NA
MAPK11	NA	TG	NA	NA	NA	NA
ZNF571	NA	NA	LDL-C, TC	NA	NA	NA
ZNF572	NA	HDL-C, TG	NA	NA	NA	NA
LRRC57	NA	NA	TC	NA	NA	NA
MRPL14	NA	LDL-C	NA	NA	NA	NA
LSMEM1	NA	NA	TG	NA	NA	NA
NPM1	chr5	NA	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
CD300LF	NA	NA	TG	NA	NA	NA
HKR1	NA	NA	TC	NA	NA	NA
CYP4F12	NA	NA	TC	NA	NA	NA
KCNIP1	chr5	NA	NA	NA	NA	NA
TDRKH	NA	NA	NA	chr1	NA	NA
UBA7	NA	NA	HDL-C, TG	NA	NA	NA
NBPF12	NA	NA	TC	NA	NA	NA
MAPK12	chr22	NA	NA	NA	NA	NA
IL17REL	chr22	NA	NA	NA	NA	NA
PLSCR1	NA	NA	HDL-C	NA	NA	NA
C10orf99	chr10	NA	NA	NA	NA	NA
TMEM89	NA	NA	HDL-C	NA	NA	NA
H3F3C	NA	LDL-C	NA	NA	NA	NA
HIST2H3D	NA	NA	NA	chr1	NA	NA
TMEM50A	NA	NA	LDL-C	NA	NA	NA
C22orf34	chr22	NA	NA	NA	NA	NA
BTBD9	NA	NA	TG	NA	NA	NA
MPHOSPH8	NA	NA	TG	NA	NA	NA
HIST2H2AC	NA	NA	NA	chr1	NA	NA
HIST2H2AB	NA	NA	NA	chr1	NA	NA
NTNG2	NA	NA	TG	NA	NA	NA
HIST2H2BE	NA	NA	NA	chr1	NA	NA
SERINC4	NA	TG	NA	NA	NA	NA
TPK1	NA	NA	HDL-C	NA	NA	NA
UBE2L3	NA	NA	TC	NA	NA	NA
CACNA1H	NA	NA	HDL-C, TG	NA	NA	NA
ZNF782	NA	TG	NA	NA	NA	NA
ZNF512B	NA	TG	NA	NA	NA	NA
RGS9BP	NA	NA	TG	NA	NA	NA
SPATC1	NA	NA	LDL-C	NA	NA	NA
MRPS21	NA	NA	NA	chr1	NA	NA
EPOR	NA	LDL-C, TC	NA	NA	NA	NA
HAPLN4	NA	NA	TC	NA	NA	NA
DNAH17	NA	NA	TG	NA	NA	NA
OR7D2	NA	NA	TC	NA	NA	NA
PGAP1	NA	NA	LDL-C, TC	NA	NA	NA
MRPL21	NA	NA	TC	NA	NA	NA
SMTNL2	NA	NA	HDL-C	NA	NA	NA
TUBB3	NA	NA	TG	NA	NA	NA
UCKL1	NA	TG	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
PIM3	chr22	NA	NA	NA	NA	NA
LTN1	NA	NA	HDL-C	NA	NA	NA
RASGEF1A	NA	NA	TG	NA	NA	NA
RHCE	NA	NA	LDL-C, TC	NA	NA	NA
MSANTD1	NA	NA	TG	NA	NA	NA
BLOC1S3	NA	LDL-C	NA	NA	NA	NA
MIR346	chr10	NA	NA	NA	NA	NA
POM121	NA	NA	TG	NA	NA	NA
COX20	NA	NA	TG	NA	NA	NA
THEM5	NA	NA	NA	chr1	NA	NA
KPRP	NA	NA	TG	NA	NA	NA
LRIT2	chr10	NA	NA	NA	NA	NA
FAM153C	NA	TG	NA	NA	NA	NA
UGT2B15	NA	TC	NA	NA	NA	NA
LOC100268168	chr5	NA	NA	NA	NA	NA
NF1	NA	NA	TC	NA	NA	NA
AC104135.3	NA	NA	TG	NA	NA	NA
PCNXL3	NA	NA	HDL-C, TG	NA	NA	NA
SNORA74B	chr5	NA	NA	NA	NA	NA
S100A10	NA	NA	NA	chr1	NA	NA
TAF13	NA	NA	LDL-C	NA	NA	NA
UGT2B17	NA	NA	TC	NA	NA	NA
HIST1H2BK	NA	NA	HDL-C	NA	NA	NA
AC005003.1	NA	NA	HDL-C	NA	NA	NA
NEURL1B	chr5	NA	NA	NA	NA	NA
CCDC151	NA	LDL-C	NA	NA	NA	NA
ENTPD7	NA	NA	TG	NA	NA	NA
ZNF334	NA	NA	HDL-C	NA	NA	NA
EFCAB9	chr5	NA	NA	NA	NA	NA
CPEB1	NA	LDL-C	NA	NA	NA	NA
RP11-495P10.3	NA	NA	LDL-C, TC	NA	NA	NA
ZNF69	NA	LDL-C, TC	NA	NA	NA	NA
LPA	NA	LDL-C, TC	NA	NA	NA	NA
SMOC1	NA	LDL-C	NA	NA	NA	NA
CTA-217C2.1	NA	TG	NA	NA	NA	NA
PRMT6	NA	NA	Dyslipidemia	NA	NA	NA
LINC00161	NA	HDL-C	NA	NA	NA	NA
RP11-460N20.4	NA	NA	TG	NA	NA	NA
POLR2J2	NA	NA	HDL-C	NA	NA	NA
NUTM2E	NA	NA	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
HIST2H2BF	NA	NA	NA	chr1	NA	NA
HIST2H2BC	NA	NA	NA	chr1	NA	NA
LINC00858	chr10	NA	NA	NA	NA	NA
RP4-794H19.4	NA	NA	TG	NA	NA	NA
TMEM57	NA	NA	LDL-C, TC	NA	NA	NA
BMPR2	NA	NA	TC	NA	NA	NA
PFDN6	NA	NA	TG	NA	NA	NA
RXRB	NA	TG	NA	NA	NA	NA
HLA-DMA	NA	NA	TG	NA	NA	NA
RNF5	NA	NA	TG	NA	NA	NA
CYP21A1P	NA	NA	TG	NA	NA	NA
STK19	NA	NA	NA	NA	NA	LDL-C
MSH5	NA	NA	TG	NA	NA	NA
C6orf25	NA	NA	HDL-C	NA	NA	NA
LY6G6C	NA	NA	TG	NA	NA	NA
LY6G5C	NA	NA	TG	NA	NA	NA
BAG6	NA	NA	TG	NA	NA	NA
LST1	NA	NA	HDL-C, TG	NA	NA	NA
HLA-C	NA	NA	HDL-C	NA	NA	NA
CCHCR1	NA	TG	NA	NA	NA	NA
CDSN	NA	TG	NA	NA	NA	NA
C6orf15	NA	TG	NA	NA	NA	NA
HLA-E	NA	TG	NA	NA	NA	NA
HCG9	NA	NA	TC	NA	NA	NA
AC104135.4	NA	NA	TG	NA	NA	NA
DOC2GP	NA	NA	TG	NA	NA	NA
RANBP17	chr5	NA	NA	NA	NA	NA
ZNF204P	NA	NA	TG	NA	NA	NA
RP11-458D21.1	NA	NA	TC	NA	NA	NA
FAM205A	NA	NA	HDL-C, TG	NA	NA	NA
GPR56	NA	HDL-C	NA	NA	NA	NA
RGL3	NA	NA	LDL-C	NA	NA	NA
NYNRIN	NA	NA	LDL-C, TC	NA	NA	NA
MIR554	NA	NA	NA	chr1	NA	NA
GRID1-AS1	chr10	NA	NA	NA	NA	NA
LPAL2	NA	LDL-C	NA	NA	NA	NA
KIAA0040	NA	NA	TG	NA	NA	NA
YWHAZP4	NA	HDL-C, TG	NA	NA	NA	NA
LINGO4	NA	NA	NA	chr1	NA	NA
MLLT11	NA	NA	NA	chr1	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
ZBTB9	NA	NA	TG	NA	NA	NA
ATP6V1G2	NA	TG	NA	NA	NA	NA
AC104135.2	NA	NA	TG	NA	NA	NA
PPM1N	NA	NA	LDL-C	NA	NA	NA
RPS17P1	NA	HDL-C	NA	NA	NA	NA
ZNF90	NA	NA	LDL-C	NA	NA	NA
RP11-384F7.2	NA	NA	HDL-C	NA	NA	NA
PISD	NA	NA	Dyslipidemia	NA	NA	NA
ARHGDIG	NA	NA	TG	NA	NA	NA
METTL12	NA	LDL-C, TG	NA	NA	NA	NA
APOC1P1	NA	TG	NA	NA	NA	NA
USP8P1	NA	TG	NA	NA	NA	NA
PGBD3	NA	HDL-C	NA	NA	NA	NA
ERVFRD-1	NA	NA	HDL-C	NA	NA	NA
ANKRD20A18P	NA	NA	TG	NA	NA	NA
RP11-426L16.8	NA	TG	NA	NA	NA	NA
RP11-420K8.2	NA	TG	NA	NA	NA	NA
LOC284933	chr22	NA	NA	NA	NA	NA
TAFA5	chr22	NA	NA	NA	NA	NA
VIMP1	NA	HDL-C	NA	NA	NA	NA
FADS3	NA	NA	LDL-C	NA	NA	NA
HLA-DPB1	NA	TG	NA	NA	NA	NA
C4B	NA	NA	TG	NA	NA	NA
RP11-37B2.1	NA	NA	TG	NA	NA	NA
SBDSP1	NA	NA	TG	NA	NA	NA
LINC00869	NA	NA	NA	chr1	NA	NA
RP11-119D9.1	NA	NA	HDL-C	NA	NA	NA
FTOP1	NA	NA	TG	NA	NA	NA
AC114814.4	NA	TG	NA	NA	NA	NA
AC012309.5	NA	NA	LDL-C, TC	NA	NA	NA
ATXN7L3B	NA	NA	TG	NA	NA	NA
WDR46	NA	TG	NA	NA	NA	NA
LINC01030	NA	TG	NA	NA	NA	NA
AC019172.2	NA	NA	TG	NA	NA	NA
CTD-2330K9.3	NA	HDL-C	NA	NA	NA	NA
CHMP1B	chr18	NA	NA	NA	NA	NA
FALEC	NA	NA	NA	chr1	NA	NA
RP13-631K18.5	NA	NA	LDL-C	NA	NA	NA
HCG22	NA	NA	TG	NA	NA	NA
RP11-766N7.3	NA	NA	HDL-C	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
PATL2	NA	TG	NA	NA	NA	NA
AC011242.5	NA	LDL-C	NA	NA	NA	NA
TAS2R31	NA	NA	Dyslipidemia	NA	NA	NA
CEACAM22P	NA	LDL-C	NA	NA	NA	NA
AP001877.1	NA	NA	TG	NA	NA	NA
TUBB3	NA	NA	TG	NA	NA	NA
RP11-426C22.6	NA	NA	LDL-C	NA	NA	NA
RPS18	NA	NA	TG	NA	NA	NA
RP11-243A14.1	NA	NA	LDL-C	NA	NA	NA
CYP21A2	NA	NA	TG	NA	NA	NA
MIR378E	chr5	NA	NA	NA	NA	NA
AC109829.1	NA	TG	NA	NA	NA	NA
C5orf58	chr5	NA	NA	NA	NA	NA
ACTBP13	NA	HDL-C	NA	NA	NA	NA
APOC2	NA	HDL-C, LDL-C, TC	NA	NA	NA	NA
C18orf61	chr18	NA	NA	NA	NA	NA
LINC01366	chr5	NA	NA	NA	NA	NA
FAM103A2P	NA	HDL-C	NA	NA	NA	NA
POLR2J2	NA	NA	HDL-C	NA	NA	NA
B3GALT4	NA	NA	TG	NA	NA	NA
SNHG8	NA	NA	TC	NA	NA	NA
B3GNT9	NA	HDL-C	NA	NA	NA	NA
HLA-DQA2	NA	NA	TG	NA	NA	NA
RP11-777F6.3	NA	LDL-C	NA	NA	NA	NA
RP11-175I17.2	NA	NA	HDL-C	NA	NA	NA
RPL39P36	NA	LDL-C	NA	NA	NA	NA
LY6G5B	NA	NA	TG	NA	NA	NA
COX19	NA	NA	TC	NA	NA	NA
RP13-137A17.6	NA	NA	TG	NA	NA	NA
HLA-DOB	NA	NA	TG	NA	NA	NA
RP1-111B22.3	NA	NA	LDL-C	NA	NA	NA
RP11-137H2.6	NA	NA	Dyslipidemia	NA	NA	NA
HLA-DMB	NA	NA	TG	NA	NA	NA
CTC-498M16.4	NA	NA	HDL-C	NA	NA	NA
RP11-439M11.1	NA	NA	TC	NA	NA	NA
ZNF512	NA	TC, TG	NA	NA	NA	NA
GSTA1	NA	NA	TG	NA	NA	NA
RP11-425L10.1	NA	HDL-C	NA	NA	NA	NA
ETV5	NA	HDL-C	NA	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
RP11-421M1.8	NA	NA	LDL-C	NA	NA	NA
AC144652.1	NA	LDL-C, TC	NA	NA	NA	NA
RP11-20D14.6	NA	NA	TC	NA	NA	NA
YJEFN3	NA	NA	LDL-C, TC, TG	NA	NA	NA
UGT2B29P	NA	TC	NA	NA	NA	NA
CRMP1	NA	NA	NA	NA	NA	Dyslipidemia
PRKAB1	NA	NA	NA	NA	NA	LDL-C
RP11-1105O14.1	NA	TG	NA	NA	NA	NA
GJA8	NA	NA	NA	chr1	NA	NA
NBPF14	NA	NA	NA	chr1	NA	NA
ALG1L10P	NA	NA	TC	NA	NA	NA
RP11-56A10.1	NA	NA	TG	NA	NA	NA
RUNX2	NA	NA	NA	NA	NA	HDL-C
HCAR3	NA	NA	HDL-C	NA	NA	NA
GJA5	NA	NA	NA	chr1	NA	NA
POLR2M	NA	NA	HDL-C	NA	NA	NA
TCHH	NA	NA	NA	chr1	NA	NA
hsa-mir-8072	NA	NA	HDL-C	NA	NA	NA
ZNF225	NA	LDL-C, TC	NA	NA	NA	NA
S100A11	NA	NA	NA	chr1	NA	NA
BSG	NA	NA	NA	NA	NA	Dyslipidemia
NADSYN1	NA	NA	NA	NA	NA	Dyslipidemia
GATC	NA	NA	HDL-C	NA	NA	NA
ZNF625	NA	LDL-C, TC	NA	NA	NA	NA
RP11-7F17.3	NA	NA	TG	NA	NA	NA
RP11-991C1.1	NA	NA	LDL-C	NA	NA	NA
LACC1	NA	NA	NA	NA	NA	Dyslipidemia
RP3-449M8.6	NA	TG	NA	NA	NA	NA
THTPA	NA	TG	NA	NA	NA	NA
RP11-66B24.1	NA	NA	TG	NA	NA	NA
LINC00565	NA	NA	TG	NA	NA	NA
TCHHL1	NA	NA	NA	chr1	NA	NA
GPR89B	NA	NA	NA	chr1	NA	NA
LINC02591	NA	NA	NA	chr1	NA	NA
HRNR	NA	NA	NA	chr1	NA	NA
MIR3912	chr5	NA	NA	NA	NA	NA
MIR4257	NA	NA	NA	chr1	NA	NA
MBP	NA	NA	NA	NA	NA	Dyslipidemia
RP11-271K11.5	NA	NA	TG	NA	NA	NA

Gene	BioVU			HCHS/SOL		
	IBD mapping	PrediXcan		IBD mapping	PrediXcan	
		Tissue specific	Cross tissue		Tissue specific	Cross tissue
MIR3201	chr22	NA	NA	NA	NA	NA
LIME1	NA	NA	NA	NA	NA	LDL-C
MIR4535	chr22	NA	NA	NA	NA	NA
LINC00663	NA	NA	NA	NA	NA	LDL-C
AC006126.4	NA	LDL-C, TC	NA	NA	NA	NA
RP11-15A1.3	NA	LDL-C	NA	NA	NA	NA
ILF3-AS1	NA	LDL-C	NA	NA	NA	NA
AC069278.4	NA	LDL-C, TC	NA	NA	NA	NA
CTD-2162K18.4	NA	NA	TC	NA	NA	NA
LOC100421166	NA	TC	NA	NA	NA	NA
APOC4	NA	Dyslipidemia, HDL-C, TG	NA	NA	NA	NA
ZNF285	NA	LDL-C	NA	NA	NA	NA
TCTEX1D2	NA	NA	NA	NA	NA	TG
FDX1L	NA	LDL-C, TC	NA	NA	NA	NA
RP11-813F20.2	NA	HDL-C	NA	NA	NA	NA
LIN37	NA	NA	LDL-C	NA	NA	NA
C14orf182	NA	NA	NA	NA	NA	TG
RP3-449M8.9	NA	NA	LDL-C, TG	NA	NA	NA
RP11-571M6.17	NA	NA	TG	NA	NA	NA
RPTN	NA	NA	NA	chr1	NA	NA
RP11-288H12.4	NA	NA	LDL-C	NA	NA	NA
LINC01138	NA	NA	NA	chr1	NA	NA
RP11-85G21.3	NA	NA	TG	NA	NA	NA
PPIAL4F	NA	NA	NA	chr1	NA	NA
CTD-2235C13.3	NA	LDL-C, TC	NA	NA	NA	NA
PPIAL4E	NA	NA	NA	chr1	NA	NA
NBPF15	NA	NA	NA	chr1	NA	NA
CTC-366B18.4	NA	TC	NA	NA	NA	NA
PPIAL4D	NA	NA	NA	chr1	NA	NA
RP11-981G7.6	NA	NA	TG	NA	NA	NA
RP11-395N3.2	NA	HDL-C	NA	NA	NA	NA
FCGR1CP	NA	NA	NA	chr1	NA	NA
MIR5087	NA	NA	NA	chr1	NA	NA
INSYN2B	chr5	NA	NA	NA	NA	NA
LSP1P5	NA	NA	NA	chr1	NA	NA