Association analyses of East Asian individuals and transindividuals reveal new loci associated with cholesterol

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Citation Report

#	Article	IF	CITATIONS
1	Exome chip meta-analysis identifies novel loci and East Asian–specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	21.4	129
2	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. Diabetes, 2017, 66, 3130-3141.	0.6	17
3	<i>Trans</i> -ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the <i>ANGPTL8</i> HDL-C GWAS Locus. G3: Genes, Genomes, Genetics, 2017, 7, 3217-3227.	1.8	19
4	Penetrance of Polygenic Obesity Susceptibility Loci across the Body Mass Index Distribution. American Journal of Human Genetics, 2017, 101, 925-938.	6.2	103
5	Association of 48 type 2 diabetes susceptibility loci with fasting plasma glucose and lipid levels in Chinese Hans. Diabetes Research and Clinical Practice, 2018, 139, 114-121.	2.8	4
6	Cohort Profile: The Singapore Multi-Ethnic Cohort (MEC) study. International Journal of Epidemiology, 2018, 47, 699-699j.	1.9	67
7	Prediction of cholesterol ratios within a Korean population. Royal Society Open Science, 2018, 5, 171204.	2.4	0
8	WDR11â€mediated Hedgehog signalling defects underlie a new ciliopathy related to Kallmann syndrome. EMBO Reports, 2018, 19, 269-289.	4.5	49
9	Genetic alterations in the NO-cGMP pathway and cardiovascular risk. Nitric Oxide - Biology and Chemistry, 2018, 76, 105-112.	2.7	34
10	The Role of RNA Editing in Cancer Development and Metabolic Disorders. Frontiers in Endocrinology, 2018, 9, 762.	3.5	70
11	Identification of 12 novel loci that confer susceptibility to early-onset dyslipidemia. International Journal of Molecular Medicine, 2018, 43, 57-82.	4.0	5
12	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	12.8	73
13	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	12.8	75
14	Characterization of LncRNA expression profile and identification of novel LncRNA biomarkers to diagnose coronary artery disease. Atherosclerosis, 2018, 275, 359-367.	0.8	99
15	GWAS Reveal Targets in Vessel Wall Pathways to Treat Coronary Artery Disease. Frontiers in Cardiovascular Medicine, 2018, 5, 72.	2.4	16
16	STEPS: an efficient prospective likelihood approach to genetic association analyses of secondary traits in extreme phenotype sequencing. Biostatistics, 2020, 21, 33-49.	1.5	4
17	Angiopoietin-Like 3 (ANGPTL3) and Atherosclerosis: Lipid and Non-Lipid Related Effects. Journal of Cardiovascular Development and Disease, 2018, 5, 39.	1.6	36
18	Integrative genomics identifies new genes associated with severe COPD and emphysema. Respiratory Research, 2018, 19, 46.	3.6	20

#	ARTICLE	IF	CITATIONS
19	Genome-wide association study identifies novel recessive genetic variants for high TGs in an Arab population. Journal of Lipid Research, 2018, 59, 1951-1966.	4.2	24
20	<i>IGF1</i> Gene Is Associated With Triglyceride Levels In Subjects With Family History Of Hypertension From The SAPPHIRe And TWB Projects. International Journal of Medical Sciences, 2018, 15, 1035-1042.	2.5	3
21	ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. Nature Communications, 2019, 10, 3195.	12.8	69
22	Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. Bioinformatics, 2020, 36, 552-557.	4.1	2
23	Contributions of Interactions Between Lifestyle and Genetics on Coronary Artery Disease Risk. Current Cardiology Reports, 2019, 21, 89.	2.9	27
24	Associations with metabolites in Chinese suggest new metabolic roles in Alzheimer's and Parkinson's diseases. Human Molecular Genetics, 2019, 29, 189-201.	2.9	12
25	A genome-wide search for gene-by-obesity interaction loci of dyslipidemia in Koreans shows diverse genetic risk alleles. Journal of Lipid Research, 2019, 60, 2090-2101.	4.2	5
26	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
27	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
28	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
29	Identifying new associated pleiotropic SNPs with lipids by simultaneous test of multiple longitudinal traits: An Iranian family-based study. Gene, 2019, 692, 156-169.	2.2	4
30	Genetic and Epigenetic Fine Mapping of Complex Trait Associated Loci in the Human Liver. American Journal of Human Genetics, 2019, 105, 89-107.	6.2	35
31	Identification of female-specific genetic variants for metabolic syndrome and its component traits to improve the prediction of metabolic syndrome in females. BMC Medical Genetics, 2019, 20, 99.	2.1	16
32	Combined analysis of keratinocyte cancers identifies novel genome-wide loci. Human Molecular Genetics, 2019, 28, 3148-3160.	2.9	46
33	Weighted gene co-expression network analysis to explain the relationship between plasma total carotenoids and lipid profile. Genes and Nutrition, 2019, 14, 16.	2.5	9
34	Allele-specific enhancers mediate associations between LCAT and ABCA1 polymorphisms and HDL metabolism. PLoS ONE, 2019, 14, e0215911.	2.5	3
35	Exome chipâ€driven association study of lipidemia in >14,000 Koreans and evaluation of genetic effect on identified variants between different ethnic groups. Genetic Epidemiology, 2019, 43, 617-628.	1.3	2
36	LncRNA ENST00000602558.1 regulates ABCG1 expression and cholesterol efflux from vascular smooth muscle cells through a p65-dependent pathway. Atherosclerosis, 2019, 285, 31-39.	0.8	26

3

#	Article	IF	CITATIONS
37	Metabolome-based signature of disease pathology in MS. Multiple Sclerosis and Related Disorders, 2019, 31, 12-21.	2.0	41
38	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
39	A Perception on Genome-Wide Genetic Analysis of Metabolic Traits in Arab Populations. Frontiers in Endocrinology, 2019, 10, 8.	3.5	14
40	Enhancer deletion and allelic effects define a regulatory molecular mechanism at the <i>VLDLR</i> cholesterol GWAS locus. Human Molecular Genetics, 2019, 28, 888-895.	2.9	5
41	The Korea Biobank Array: Design and Identification of Coding Variants Associated with Blood Biochemical Traits. Scientific Reports, 2019, 9, 1382.	3.3	179
42	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
43	Generalizability and applicability of results obtained from populations of European descent regarding the effect direction and size of HDL-C level-associated genetic variants to the Hungarian general and Roma populations. Gene, 2019, 686, 187-193.	2.2	12
44	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. Bioinformatics, 2019, 35, 1644-1652.	4.1	36
45	Legacy Data Confound Genomics Studies. Molecular Biology and Evolution, 2020, 37, 2-10.	8.9	23
46	The interaction between ABCA1 polymorphism and physical activity on the HDL-cholesterol levels in a Japanese population. Journal of Lipid Research, 2020, 61, 86-94.	4.2	11
47	Pleiotropy in eye disease and related traits. , 2020, , 315-336.		2
48	Genome-wide association study of metabolic syndrome in Korean populations. PLoS ONE, 2020, 15, e0227357.	2.5	42
49	Integrative Network Analysis of Multi-Omics Data in the Link between Plasma Carotenoid Concentrations and Lipid Profile. Lifestyle Genomics, 2020, 13, 11-19.	1.7	5
50	Progressive effects of single-nucleotide polymorphisms on 16 phenotypic traits based on longitudinal data. Genes and Genomics, 2020, 42, 393-403.	1.4	3
51	Carotid Intima-Media Thickness. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 446-461.	2.4	25
52	TheAPOA5â€rs662799 Polymorphism Is a Determinant of Dyslipidemia in Vietnamese Primary School Children. Lipids, 2020, 55, 683-691.	1.7	2
53	Genetic susceptibility, dietary cholesterol intake, and plasma cholesterol levels in a Chinese population. Journal of Lipid Research, 2020, 61, 1504-1511.	4.2	3
54	ILRUN, a Human Plasma Lipid GWAS Locus, Regulates Lipoprotein Metabolism in Mice. Circulation Research, 2020, 127, 1347-1361.	4.5	11

#	Article	IF	CITATIONS
55	A fast and powerful eQTL weighted method to detect genes associated with complex trait using GWAS summary data. Genetic Epidemiology, 2020, 44, 550-563.	1.3	10
56	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
57	A gene-diet interaction-based score predicts response to dietary fat in the Women's Health Initiative. American Journal of Clinical Nutrition, 2020, 111, 893-902.	4.7	6
58	Characterization and in silico analyses of the BRCA1/2 variants identified in individuals with personal and/or family history of BRCA-related cancers. International Journal of Biological Macromolecules, 2020, 162, 1166-1177.	7.5	5
59	Association Between Genetic Variants in FADS1-FADS2 and ELOVL2 and Obesity, Lipid Traits, and Fatty Acids in Tunisian Population. Clinical and Applied Thrombosis/Hemostasis, 2020, 26, 107602962091528.	1.7	9
60	Candidate Regulators of Dyslipidemia in Chromosome 1 Substitution Lines Using Liver Co-Expression Profiling Analysis. Frontiers in Genetics, 2020, 10, 1258.	2.3	1
61	Biological Role of Unsaturated Fatty Acid Desaturases in Health and Disease. Nutrients, 2020, 12, 356.	4.1	72
62	Genetic variants in the FAM3C gene are associated with lipid traits in Chinese children. Pediatric Research, 2021, 89, 673-678.	2.3	1
63	Network propagation of rare variants in Alzheimer's disease reveals tissue-specific hub genes and communities. PLoS Computational Biology, 2021, 17, e1008517.	3.2	1
64	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. Human Molecular Genetics, 2021, 30, 603-618.	2.9	5
65	Genetic risk scores for cardiometabolic traits in sub-Saharan African populations. International Journal of Epidemiology, 2021, 50, 1283-1296.	1.9	10
66	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	8.8	2
69	Large trans-ethnic meta-analysis identifies AKR1C4 as a novel gene associated with age at menarche. Human Reproduction, 2021, 36, 1999-2010.	0.9	10
70	Comparison of the effectiveness of Martin's equation, Friedewald's equation, and a Novel equation in low-density lipoprotein cholesterol estimation. Scientific Reports, 2021, 11, 13545.	3.3	19
71	The Genetic Basis of Hypertriglyceridemia. Current Atherosclerosis Reports, 2021, 23, 39.	4.8	17
72	Circulating ceramides as biomarkers of cardiovascular disease: Evidence from phenotypic and genomic studies. Atherosclerosis, 2021, 327, 18-30.	0.8	39
74	Evaluating marginal genetic correlation of associated loci for complex diseases and traits between European and East Asian populations. Human Genetics, 2021, 140, 1285-1297.	3.8	12
7 5	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. Communications Biology, 2021, 4, 918.	4.4	11

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76	Both variants of A1CF and BAZ1B genes are associated with gout susceptibility: a replication study and meta-analysis in a Japanese population. Human Cell, 2021, 34, 293-299.	2.7	2
82	Hepatic lipase (LIPC) sequencing in individuals with extremely high and low high-density lipoprotein cholesterol levels. PLoS ONE, 2020, 15, e0243919.	2.5	3
83	Metabolic Syndrome Prediction Using Machine Learning Models with Genetic and Clinical Information from a Nonobese Healthy Population. Genomics and Informatics, 2018, 16, e31.	0.8	27
84	Gene-based association study for lipid traits in diverse cohorts implicates <i>BACE1</i> and <i>SIDT2</i> regulation in triglyceride levels. PeerJ, 2018, 6, e4314.	2.0	14
89	Activity Of Lipoprotein-Associated Paraoxonase-1 Enzymes and Myeloperoxidase in Patients with Chronic Kidney Disease. UkraÃ-nsʹkij žurnal Medicini BìologìÃ- Ta Sportu, 2019, 4, 321-328.	0.2	1
92	Prostaglandin E2 EP receptors in cardiovascular disease: An update. Biochemical Pharmacology, 2022, 195, 114858.	4.4	17
93	A Genome-Wide Association Study of a Korean Population Identifies Genetic Susceptibility to Hypertension Based on Sex-Specific Differences. Genes, 2021, 12, 1804.	2.4	3
94	Phenome-wide association study of the major histocompatibility complex region in the Korean population identifies novel association signals. Human Molecular Genetics, 2022, , .	2.9	1
95	A common variant in $11q23.3$ associated with hyperlipidemia is mediated by the binding and regulation of GATA4. Npj Genomic Medicine, 2022, 7, 4.	3.8	7
97	High-density lipoprotein, low-density lipoprotein and triglyceride levels and upper gastrointestinal cancers risk: a trans-ancestry Mendelian randomization study. European Journal of Clinical Nutrition, 2022, , .	2.9	4
98	Comprehensive Statistical and Bioinformatics Analysis in the Deciphering of Putative Mechanisms by Which Lipid-Associated GWAS Loci Contribute to Coronary Artery Disease. Biomedicines, 2022, 10, 259.	3.2	7
99	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	6.5	3
100	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. Frontiers in Nutrition, 2021, 8, 808054.	3.7	12
101	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
102	Mendelian randomization study of circulating lipids and biliary tract cancer among East Asians. BMC Cancer, 2022, 22, 273.	2.6	3
103	Gene-based association tests using GWAS summary statistics and incorporating eQTL. Scientific Reports, 2022, 12, 3553.	3.3	1
105	Twenty-Five Novel Loci for Carotid Intima-Media Thickness: A Genome-Wide Association Study in >45 000 Individuals and Meta-Analysis of >100 000 Individuals. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 484-501.	2.4	17
109	Organization of gene programs revealed by unsupervised analysis of diverse gene–trait associations. Nucleic Acids Research, 2022, 50, e87-e87.	14.5	5

#	ARTICLE	IF	CITATIONS
110	Meta-analysis of sub-Saharan African studies provides insights into genetic architecture of lipid traits. Nature Communications, 2022, 13, 2578.	12.8	18
111	Longitudinal relationships of polycyclic aromatic hydrocarbons exposure and genetic susceptibility with blood lipid profiles. Environment International, 2022, 164, 107259.	10.0	13
113	The human ATPâ€binding cassette (ABC) transporter superfamily. Human Mutation, 2022, 43, 1162-1182.	2.5	45
114	GWAS of Variant-by-Thiazide Interaction on Lipids Identifies a Novel Low-Density Lipoprotein Cholesterol Locus. Circulation Research, 0, , .	4.5	1
115	GALNT2 rs4846914 SNP Is Associated with Obesity, Atherogenic Lipid Traits, and ANGPTL3 Plasma Level. Genes, 2022, 13, 1201.	2.4	0
116	Genetic evidence for a causal relationship between type 2 diabetes and peripheral artery disease in both Europeans and East Asians. BMC Medicine, 2022, 20, .	5.5	6
118	Detecting associated genes for complex traits shared across East Asian and European populations under the framework of composite null hypothesis testing. Journal of Translational Medicine, 2022, 20, .	4.4	5
119	Coronary artery disease and cancer: a significant resemblance. , 2022, 39, .		O
120	Linear and nonlinear analyses of the association between low–density lipoprotein cholesterol and diabetes: The spurious U–curve in observational study. Frontiers in Endocrinology, 0, 13, .	3.5	0
121	Pleiotropic Effects of APOB Variants on Lipid Profiles, Metabolic Syndrome, and the Risk of Diabetes Mellitus. International Journal of Molecular Sciences, 2022, 23, 14963.	4.1	3
122	Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis. Genome Biology, 2022, 23, .	8.8	17
123	An adaptive test based on principal components for detecting multiple phenotype associations using GWAS summary data. Genetica, 0, , .	1.1	O
124	Lack of GPR180 ameliorates hepatic lipid depot via downregulation of mTORC1 signaling. Scientific Reports, 2023, 13 , .	3.3	1
125	Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics. Nature Communications, 2023, 14, .	12.8	13
126	Age and Genetic Risk Score and Rates of Blood Lipid Changes in China. JAMA Network Open, 2023, 6, e235565.	5.9	2
127	Non-coding and intergenic genetic variants of human arylamine N-acetyltransferase 2 (NAT2) gene are associated with differential plasma lipid and cholesterol levels and cardiometabolic disorders. Frontiers in Pharmacology, 0, 14 , .	3.5	3
128	Hepatic G Protein-Coupled Receptor 180 Deficiency Ameliorates High Fat Diet-Induced Lipid Accumulation via the Gi-PKA-SREBP Pathway. Nutrients, 2023, 15, 1838.	4.1	1
129	Risk factors for anorexia nervosa: A populationâ€based investigation of sex differences in polygenic risk and early life exposures. International Journal of Eating Disorders, 0, , .	4.0	O

#	ARTICLE	IF	CITATIONS
131	Leveraging trans-ethnic genetic risk scores to improve association power for complex traits in underrepresented populations. Briefings in Bioinformatics, 0, , .	6.5	0
132	Similarity and diversity of genetic architecture for complex traits between East Asian and European populations. BMC Genomics, 2023, 24, .	2.8	0
133	Genetically determined circulating resistin concentrations and risk of colorectal cancer: a two-sample Mendelian randomization study. Journal of Cancer Research and Clinical Oncology, 0, , .	2.5	0
135	Hypolipidemic Effect of Rice Bran Oil Extract Tocotrienol in High-Fat Diet-Induced Hyperlipidemia Zebrafish (Danio Rerio) Induced by High-Fat Diet. International Journal of Molecular Sciences, 2024, 25, 2954.	4.1	0