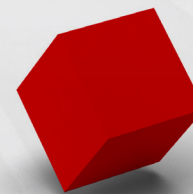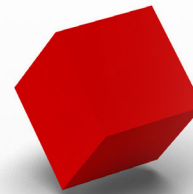# Predictive Genomics Publications

Predictive genomics is already changing the way healthcare will be delivered in the future. The publications summarized here provide just a sampling of the many ways Applied Biosystems™ Axiom™ Genotyping Solutions and other Applied Biosystems microarrays are contributing to population genomics, preemptive pharmacogenomics, and carrier screening research that is revealing meaningful data to help predict disease risk and potential drug response. These studies span the globe, investigate population cohorts from small to very large, and encompass a vast range of health conditions. Read on to explore what is happening in the real world of predictive genomics.

applied biosystems

Contents

Applied Biosystems™ Axiom™ Genotyping Solutions

Applied Biosystems™ Axiom™ Genotyping Solutions: North America region

North America (NA) region

1. Genotyping array design and data quality control in the Million Veteran Program (MVP)

The Million Veteran Program (MVP) was initiated by the United States Department of Veterans Affairs (VA), aiming to create a biobank linking genetic data to clinical records. Using samples of almost half a million participants, the authors designed the **MVP 1.0 custom Axiom Array**. The authors emphasize the ethnic diversity of the participants, concluding that the MVP 1.0 array provides researchers the resources to investigate common and rare genetic variants with the option to link genotype data to the electronic health records of participants.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32243820/	Non-specific Population genomics, biobank, new custom array	Hunter-Zinck H, Shi Y, Li M, et al. (2020) Genotyping Array Design and Data Quality Control in the Million Veteran Program. *Am J Hum Genet* 106(4):535-548. doi: 10.1016/j.ajhg.2020.03.004

2. Measuring genetic variation in the multi-ethnic Million Veteran Program (MVP)

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.biorxiv.org/content/10.1101/2020.01.06.896613v1	Non-specific	Hunter-Zinck H, Shi Y, Li M, et al. (2020) Measuring genetic variation in the multi-ethnic Million Veteran Program (MVP). *bioRxiv* 2020.01.06.896613. doi: 10.1101/2020.01.06.896613

3. Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program (MVP)

This study conducted genotyping of about 313,000 Million Veteran Progarm (MVP) participants using a **customized Affymetrix Axiom Biobank Array,** the **MVP 1.0 Genotyping Array** and linked the genetic data to laboratory and clinical phenotypes extracted from electronic health records. Through a focus on mutations predicted to result in a loss of gene function and a phenome-wide association study, the study yielded novel indications for pharmaceutical inhibitors targeting PCSK9 (abdominal aortic aneurysm), ANGPTL4 (type 2 diabetes) and PDE3B (triglycerides and coronary disease).

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41588-018-0222-9	Blood lipids Predictive genomics, preemptive pharmacogenomics, custom array	Klarin, D., Damrauer, S.M., Cho, K. et al. Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nat Genet 50*, 1514–1523 (2018). doi: 10.1038/s41588-018-0222-9

4. Large-scale genome-wide association study of coronary artery disease in genetically diverse populations

This is a genome-wide association study (GWAS) of coronary artery disease (CAD) incorporating nearly a quarter of a million cases, in which existing studies are integrated with data from cohorts of white, Black and Hispanic individuals from the Million Veteran Program. Approximately 470,000 multi-ethnic participants in MVP were genotypied with a **customized Axiom array**. The study reports near equivalent heritability of CAD across multiple ancestral groups, identifies 95 novel loci, detects eight loci of genome-wide significance in Black and Hispanic individuals, and demonstrates that two common haplotypes at the 9p21 locus are responsible for risk stratification in all populations except those of African origin, in which these haplotypes are virtually absent. A total of 2,822 African American participants were genotyped with the **Affymetrix112 Genome-Wide Human SNP Array 6.0**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35915156/	Coronary artery disease (CAD) Population genomics, predictive genomics, risk stratification	Tcheandjieu C, Zhu X, Hilliard AT, et al. (2022) Large-scale genome-wide association study of coronary artery disease in genetically diverse populations. *Nat Med* 28(8):1679-1692. doi: 10.1038/s41591-022-01891-3

North America (NA) region

5. **Penetrance and pleiotropy of polygenic risk scores for schizophrenia, bipolar disorder, and depression among adults in the US Veterans Affairs Health Care System**

    This study examined whether polygenic risk scores (PRS) for neuropsychiatric conditions developed with civilian data were also associated with risk of those conditions in a Million Veteran Program cohort with a different demographic and disease profile. The results demonstrated that the penetrance of schizophrenia PRS is equivalent across veteran and civilian healthcare systems, despite marked differences in absolute prevalence. The findings suggest that individual-level PRS informed by large-scale genetic studies may have potential for risk stratification across US healthcare systems, albeit with disparate specificity across ancestries. The study also revealed that high PRSs for schizophrenia were also associated with an increased risk of other conditions such as anxiety and respiratory problems and with protective associations with hearing loss and osteoarthritis. MVP participants were genotyped on the **MVP 1.0 Axiom array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36103194/	Psychiatric disorders Predictive genomics, population genomics, polygenic risk score, Million Veteran Program, population diversity	Bigdeli TB, Voloudakis G, Barr PB, et al. (2022) Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia, Bipolar Disorder, and Depression Among Adults in the US Veterans Affairs Health Care System. *JAMA Psych* 79(11):1092-1101. doi: 10.1001/jamapsychiatry.2022.2742

6. **Reproducible Genetic Risk Loci for Anxiety: Results From   200,000 Participants in the Million Veteran Program**

    Using genetic and other data collected from the Million Veteran Program (MVP), investigators from Yale University, the Veterans Affairs Connecticut Healthcare Center, and elsewhere have identified loci that appear to influence susceptibility to anxiety disorder in European American and African American individuals. This is the largest GWAS of anxiety traits to date. Genotyping was done using **Axiom Biobank Genotyping Array** customized for the MVP. The authors identified novel genome-wide significant associations near genes involved with global regulation of gene expression (SATB1) and the estrogen receptor alpha (ESR1). Additionally, the authors identified a locus (MAD1L1) that may have implications for genetic vulnerability across several psychiatric disorders.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/31906708/	Anxiety Population genomics, polygenic risk scoring, Million Veteran Program	Levey DF, Gelernter J, Polimanti R, et al. (2020) Million Veteran Program; Stein MB. Reproducible Genetic Risk Loci for Anxiety: Results From ~200,000 Participants in the Million Veteran Program. *Am J Psychiatry* 177(3):223-232. doi: 10.1176/appi.ajp.2019.19030256

7. **Multi-ancestry, phenome-wide association of complement component 4 variation with psychiatric and brain developmental phenotypes in youth**

    This study is a multi-ancestry phenome-wide association study in children to examine the relationship between genetically regulated expression (GREx) of C4A, childhood brain structure, cognition, and psychiatric symptoms. The data provide a mechanistic, genetic basis for the identication of brainbased biomarkers predictive of psychosis risk. Genotyping was done using the **Affymetrix NIDA Smokescreen Array**, a targeted array for addiction research.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36882872/	Psychiatric disorders Predictive genomics	Hernandez LM, Kim M, Zhang P, et al. (2023) Multi-ancestry phenome-wide association of complement component 4 variation with psychiatric and brain phenotypes in youth. *Genome Biol* 24(1):42. doi: 10.1186/s13059-023-02878-0

For Research Use Only. Not for use in diagnostic procedures.

5

North America (NA) region

8. The socioeconomic gradient in epigenetic ageing clocks: Evidence from the multi-ethnic study of atherosclerosis and the health and retirement study

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC9235889/	Aging	Schmitz LL, Zhao W, Ratliff SM, et al. (2022) The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. *Epigenetics* 17(6):589-611. doi: 10.1080/15592294.2021

9. Race, ancestry, and vitamin D metabolism: The multi-ethnic study of atherosclerosis

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/32869845/	Vitamin D metabolism	Hsu S, Hoofnagle AN, Gupta DK, et al. (2020 Race, Ancestry, and Vitamin D Metabolism: The Multi-Ethnic Study of Atherosclerosis. *J Clin Endocrinol Metab* 105(12):e4337-e4350. doi: 10.1210/clinem/dgaa612

10. Mitochondrial DNA copy number and incident atrial fibrillation

This study includes prospective analyses of approximately 20,000 participants from the Atherosclerosis Risk in Communities Study (ARIC), the Multi-Ethnic Study of Atherosclerosis (MESA), and the Cardiovascular Health Study (CHS). mtDNA-CN from the peripheral blood was calculated from probe intensities on the **Affymetrix Genome-Wide Human SNP Array** in ARIC and MESA and from multiplexed real-time quantitative polymerase chain reaction (qPCR) in CHS. Participants with the lowest quintile of mitochondria DNA copy number had an overall 13% increased risk of incident atrial fibrillation compared to those with the highest quintile.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32933497/	Mitochondria DNA (mtDNA) dysfunction Population genomics, predictive genomics	Zhao D, Bartz TM, Sotoodehnia N, et al. (2020) Mitochondrial DNA copy number and incident atrial fibrillation. *BMC Med* 18:246. doi: 10.1186/s12916-020-01715-6

11. **Multi-Ethnic genome-wide association study of decomposed cardioelectric phenotypes illustrates strategies to identify and characterize evidence of shared genetic effects for complex traits**

    This study investigated how adding ancestrally diverse populations, more precise phenotypic measures, and evidence for shared genetic effects to electrocardiographic trait genome-wide association studies can enhance the detection and characterization of loci. The study examined individual and shared genetic effects underlying six contiguous measures of the electrocardiogram waveform using data from the multi-ethnic PAGE and MESA studies. The authors decomposed electrocardiograms from almost 35,000 multi-ethnic participants and conducted genome-wide association studies using imputed single-nucleotide polymorphisms. Using only one-third as many participants as published electrocardiographic trait genome-wide association studies, the data revealed six novel loci, emphasizing the importance of ancestral diversity and phenotype resolution to maximize efficiency in genome-wide association studies. Genotyping for MESA was performed using the **Affymetrix Genome-Wide Human SNP Array 6.0**.

Link	Medical Condition/Keywords	Citation
www.ahajournals.org/doi/epub/10.1161/ CIRCGEN.119.002680	Electrocardiographic traits Population genomics, population diversity, genome-wide association study	Baldassari AR, Sitlani CM, Highland HM, et al. (2020) Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. *Circ Genom Precis Med* 13(4):e002680. doi: 10.1161/CIRCGEN.119.002680

Applied Biosystems™ Axiom™ Genotyping Solutions: Europe, Middle East, and Africa (EMEA) region

Europe, Middle East, and Africa (EMEA) region

12. Phenome-wide burden of copy-number variation in the UK Biobank

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/31353025/	Acute coronary artery disease, high body mass index	Aguirre M, Rivas MA, Priest J. (2019) Phenome-wide Burden of Copy-Number Variation in the UK Biobank. *Am J Hum Ge*net 105(2):373-383. doi: 10.1016/j.ajhg.2019.07.001

13. Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study

This study used data from approximately 340,000 participants in the UK Biobank to test associations between protein truncation variants and 135 different medical phenotypes. Genotyping of UK Biobank participants was conducted with the **UK Biobank Axiom Array** or **UK Biobank Lung Exome Variant Evaluation (BiLEVE) Axiom Array**. The study identified variants associated with asthma, and eight phenotypes including hypertension and cholesterol. The study concluded that the genetic associations that were identified directly link gene function to the cause of disease and may provide targets for future drug discovery.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/29691392/	Asthma, hypertension, cholesterol Predictive genomics, UK Biobank	DeBoever C, Tanigawa Y, Lindholm ME, et al. (2018) Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. *Nat Commun* 9(1):1612. doi: 10.1038/s41467-018-03910-9

14. Hemochromatosis mutations, brain iron imaging, and dementia in the UK Biobank Cohort

The HFE p.C282Y homozygous mutation in European ancestry populations can lead to iron overload and hemochromatosis, which is common in dementia. This study genotyped over 450,000 European ancestry participants using **Axiom arrays** and **Affymetrix BiLEVE Array**. Male p.C282Y homozygotes had more brain iron deposition, smaller specific gray matter volumes, and increased incidence of dementia compared to those without HFE mutations. The authors used **Axiom microarrays** to estimate p.C282Y associations with brain MRI features plus incident dementia diagnoses during follow-up in a large community cohort. Male p.C282Y homozygotes had more brain iron deposition, smaller specific gray matter volumes, and increased i ncidence of dementia compared to those without HFE mutations. Overall, these results suggest that p.C282Y homozygosity is a significant risk factor for dementia in men with European ancestries.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33427739/	Dementia Population genomics, predictive genomics, UK Biobank	Atkins JL, Pilling LC, Heales CJ, et al. (2021) Hemochromatosis Mutations, Brain Iron Imaging, and Dementia in the UK Biobank Cohort. *J Alzheimers Dis* 79(3):1203-1211. doi: 10.3233/JAD-201080

15. FinnGen Project's role in epilepsy, drug adherence studies showcased at ESHG

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/informatics/finngen-projects-role-epilepsy-drug-adherence-studies-showcased-eshg#.ZAkRUOzMITU	Epilepsy	Petrone, J. (2021) FinnGen Project's Role in Epilepsy, Drug Adherence Studies Showcased at ESHG. *GenomeWeb* April 31, 2021.

16. Molecular screening of familial hypercholesterolemia in the Icelandic population

Familial hypercholesterolemia (FH) is a monogenic disease characterized by a lifelong exposure to high LDL-C levels that can lead to early onset coronary heart disease (CHD). The main causes of FH identified to date include loss-of-function mutations in LDLR or APOB, or gain-of-function mutations in PCSK9. The authors developed a comprehensive next generation sequencing (NGS) panel confirmed using a **custom Phosphorus Affymetrix Axiom array** which they applied on two different resources of FH in the Icelandic population. The study revealed significant diagnostic yields in identifying pathogenic LDLR mutations in both family and population-based genetic testing.

Link	Medical Condition/Keywords	Citation
www.biorxiv.org/content/10.1101/425975v1.abstract	Familial hypercholesterolemia Population genomics, predictive genomics, custom array	Kellogg G, Thorsson B, Cai Y, et al. (2018) Molecular Screening of Familial Hypercholesterolemia in the Icelandic Population. *bioRxiv* 425975. doi: 10.1101/425975

17. Thermo Fisher Scientific, Qatar Genome Program partner to develop microarray for Arab populations

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/business-news/thermo-fisher-scientific-qatar-genome-program-partner-develop-microarray-arab#.ZAkQeOzMITU	General	Staff Writer. (2022) Thermo Fisher Scientific, Qatar Genome Program Partner to Develop Microarray for Arab Populations. *GenomeWeb* May 23, 2022.

18. Genetically predicted telomere length is associated with clonal somatic copy number alterations in peripheral leukocytes

This study sought to better understand the relationship between telomere length and cancer risk by evaluating genetically predicted telomere length (gTL) in relation to the presence of clonal somatic copy number alterations (SCNAs) in peripheral blood leukocytes. Genotyping array data were acquired from ~431,000 participants in the UK Biobank and used to detect SCNAs from intensity information and infer telomere length using a polygenic risk score (PRS) of variants previously associated with leukocyte telomere length. About 3.5% of individuals had a detectable clonal SCNA on an autosomal chromosome. Overall, higher gTL value was positively associated with the presence of an autosomal SCNA. Genotyping was conducted on the **Affymetrix UK BiLEVE Axiom** and **Axiom UK Biobank arrays**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33090998/	Hematologic malignancies Predictive genomics, polygenic risk scoring, UK Biobank	Brown DW, Lin SH, Loh PR, et al. (2022) Genetically predicted telomere length is associated with clonal somatic copy number alterations in peripheral leukocytes. *PLoS Genet* 16(10):e1009078. doi: 10.1371/journal.pgen

19. The effect of blood lipids on the left ventricle: A Mendelian randomization study

This study investigated whether higher low-density lipoprotein (LDL) cholesterol and triglyceride levels and lower high-density lipoprotein cholesterol level are causal risk factors for changes in prognostically important left ventricular (LV) parameters. One-sample Mendelian randomization (MR) of over 17,000 European individuals from the UK Biobank with paired lipid and cardiovascular magnetic resonance data was performed. Genotyping was done using the **UK BiLEVE Axiom Array** and **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33213727/	Ischemic heart disease Polygenic risk scoring, predictive genomics, UK Biobank	Aung N, Sanghvi MM, Piechnik SK, et al. (2020) The Effect of Blood Lipids on the Left Ventricle: A Mendelian Randomization Study. *J Am Coll Cardiol* 76(21):2477-2488. doi: 10.1016/j.jacc.2020.09.583.

20. Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke

Recent genome-wide association studies in stroke have enabled the generation of genomic risk scores (GRS) but their predictive power has been modest compared to established stroke risk factors. This study used a meta-scoring approach to develop a metaGRS for ischaemic stroke (IS) and analyse this score in the UK Biobank. The authors claim this study presents the most powerful IS genomic risk score to date. Genotyping was done on the **UK Biobank Axiom Array**, and imputed to the Haplotype Reference Consortium (HRC) by the UK Biobank.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41467-019-13848-1	Ischemic stroke Polygenic risk score, predictive genomics, UK Biobank	Abraham G, Malik R, Yonova-Doing E, et al. (2019) Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. *Nat Commun* 10:5819. doi: 10.1038/s41467-019-13848-1

21. Clonal myelopoiesis in the UK Biobank cohort: ASXL1 mutations are strongly associated with smoking

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.nature.com/articles/s41375-020-0896-8	Myeloid clonal hematopoiesis (CH)	Dawoud AAZ, Tapper WJ, Cross NCP. (2020) Clonal myelopoiesis in the UK Biobank cohort: ASXL1 mutations are strongly associated with smoking. *Leukemia* 34:2660–2672. doi: 10.1038/s41375-020-0896-8

22. A whole-genome sequence study identifies genetic risk factors for neuromyelitis optica

Neuromyelitis optica (NMO) is a rare autoimmune disease that affects the optic nerve and spinal cord. To elucidate genetic factors driving NMO risk and to clarify the genetic architecture of this disease, This study analyzed up to 6.8 million single-nucleotide polymorphisms (SNPs) and performed copy number variation (CNV) analysis on about 1400 cases and controls. The results revealed two independent significant genetic signals in the major histocompatibility complex (MHC) region associated with NMO. One of these signals may be explained by a common copy number event of the *C4A/C4B* genes. We also provide initial evidence that suggest NMO-IgG+ is genetically more similar to systemic lupus erythematosus (SLE) than to MS. Genotyping during Stage II of the study was done using **Axiom Biobank Arrays**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/29769526/	Neuromyelitis optica Predictive genomics, UK Biobank	Estrada K, Whelan CW, Zhao F, et al. (2018) A whole-genome sequence study identifies genetic risk factors for neuromyelitis optica. *Nat Commun* 9(1):1929. doi: 10.1038/s41467-018-04332-3

Europe, Middle East, and Africa (EMEA) region

23. Finnish Biobank Cooperative launches service to make samples, data available to researchers

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/informatics/finnish-biobank-cooperative-launches-service-make-samples-data-available-researchers#.ZAkdWuzMITU	Non-specific	Petrone J. (2019) Finnish Biobank Cooperative Launches Service to Make Samples, Data Available to Researchers. *GenomeWeb* Dec 20, 2019.

24. FinnGen study demonstrates value of analyzing isolated populations

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/genetic-research/finngen-study-demonstrates-value-analyzing-isolated-populations#.ZAf-9-zMITU	Vision, hearing, fertility	Staff Reporter. (2018) FinnGen Study Demonstrates Value of Analyzing Isolated Populations. *GenomeWeb* Jan 18, 2018.

25. A custom genotyping array reveals population-level heterogeneity for the genetic risks of prostate cancer and other cancers in Africa

To overcome disparities in genomic medicine caused by a preponderance of European study cohorts, the authors developed the **Men of African Descent and Carcinoma of the Prostate (MADCaP) Array** using the **Axiom Genotyping Solution**, creating a custom prostate cancer genotyping array optimized for men of African descent. The authors evaluated the MADCaP Array assessing imputation performance using the African Genome Resource reference panel. To assess the assay's efficacy, genotyping metrics were obtained based on approximately 800 samples from individuals from seven different study sites. The MADCaP pilot dataset also yielded six novel prostate cancer-associated loci with large allele frequency differences across African populations. Demonstrating different genetic profiles for different locations in Sub-Saharan Africa, the authors concluded that the MADCaP Array may enable novel discoveries in historically understudied populations.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32393663/	Prostate cancer Predictive genomics, population genomics, UK Biobank, custom array	Harlemon M, Ajayi O, Kachambwa P, et al. (2020) A Custom Genotyping Array Reveals Population-Level Heterogeneity for the Genetic Risks of Prostate Cancer and Other Cancers in Africa. *Cancer Res* 80(13):2956-2966. doi: 10.1158/0008-5472.CAN-19-2165

26. Gene-based variant analysis of whole-exome sequencing in relation to eosinophil count

Genetic factors have been postulated to contribute to the variation in eosinophil count between individuals. This study explores the effect of rare and common variants combined, in relation to eosinophil count, using whole-exome sequences (WES) from the UK Biobank cohort. 220 genes in 55 distinct genomic regions were found to be associated with eosinophil count, of which seven genes are driven by rare variants, independent of common variants identified in genome-wide association studies. Genotyping was performed using **UK BiLEVE Axiom Arrays** and **UK Biobank Axiom Arrays**.

Link	Medical Condition/Keywords	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC9355086/	Eosinophil count, inflammation Predictive genomics, UK Biobank	Höglund J, Hadizadeh F, Ek WE, et al. (2022) Gene-Based Variant Analysis of Whole-Exome Sequencing in Relation to Eosinophil Count. *Front Immunol* 13:862255. doi: 10.3389/fimmu.2022.862255

27. Characterization of the human ABO genotypes and their association to common inflammatory and cardiovascular diseases in the UK Biobank

This study sought to test for association between blood group ABO genotypes and a large set of common inflammatory and cardiovascular diseases in the UK Biobank participants as well as disease-related protein biomarkers in the Northern Swedish Population Health Study (NSPHS). This study confirmed previous findings of a strong association between ABO and cardiovascular disease, identified associations for both type 1 and type 2 diabetes, and provide additional evidence of significant differences between heterozygous and homozygous allele carriers for pulmonary embolism, deep vein thrombosis, but also for von Willebrand factor levels. Genotyping of UK Biobank participants was performed using **UK BiLEVE Axiom Arrays** and **UK Biobank Axiom Arrays**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34329492/	Blood group, inflammatory disease, cardiovascular disease Population genomics, predictive genomics	Höglund J, Karlsson T, Johansson T, Ek WE, et al. (2021) Characterization of the human ABO genotypes and their association to common inflammatory and cardiovascular diseases in the UK Biobank. *Am J Hematol* 96(11):1350-1362. doi: 10.1002/ajh.26307

28. Genetically raised serum bilirubin levels and lung cancer: a cohort study and Mendelian randomisation using UK Biobank

This study aimed to investigate potential causal relationships between genetically raised serum total bilirubin and lung cancer incidence using one-sample Mendelian randomization and UK Biobank. Genetically raised serum bilirubin, common across human populations, may protect people exposed to high levels of smoke oxidants against lung cancers. Genotyping of UK Biobank participants was done using the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32855344/	Hyperbilirubinaemia, lung cancer Population genomics, polygenic risk score	Horsfall LJ, Burgess S, Hall I, et al. (2020) Genetically raised serum bilirubin levels and lung cancer: a cohort study and Mendelian randomisation using UK Biobank. *Thorax* 75(11):955-964. doi: 10.1136/thoraxjnl-2020-214756

29. Prevalence and cardiometabolic correlates of ketohexokinase gene variants among UK Biobank participants

Loss-of-function variants of the ketohexokinase (KHK) gene cause essential fructosuria (EF), a benign condition characterized by intermittent appearance of fructose in the urine. This study assessed the frequency of KHK variants in participants of the UK Biobank project. UK Biobank participants were genotyped using the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**. As EF is asymptomatic and not considered to require treatment, the study aimed to confirm the benign nature of EF by comparing the cardiometabolic profiles of participants with and without KHK variants. Among the nearly 500,000 UK Biobank participants, the study failed to identify even a single individual with the Gly40Arg/Ala43Thr genotype combination that is present in subjects exhibiting the EF phenotype. The results suggest either that the prevalence of EF is much lower than previously estimated or that there may be important differences in prevalence by race and ethnicity.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33621267/	Essential fructosuria Population genomics, biobank, UK Biobank	Johnston JA, Nelson DR, Bhatnagar P, et al. (2021) Prevalence and cardiometabolic correlates of ketohexokinase gene variants among UK Biobank participants. *PLoS One* 16(2):e0247683. doi: 10.1371/journal.pone.0247683

30. Contribution of genetics to visceral adiposity and its relation to cardiovascular and metabolic disease

The contribution of genetics to the development of visceral adipose tissue (VAT) is under-explored. This study develops sex-stratified, nonlinear prediction models for visceral adipose tissue mass (VAT) using the UK Biobank cohort. A genome-wide association study (GWAS) for predicted VAT mass identified 102 novel visceral adiposity loci. Predicted VAT mass was associated with increased risk of hypertension, heart attack/angina, type 2 diabetes and hyperlipidemia, and Mendelian randomization analysis showed visceral fat to be a causal risk factor for all four diseases. The UK Biobank participants were genotyped using the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/31501611/	Visceral adipose tissue mass Predictive genomics, UK Biobank	Karlsson T, Rask-Andersen M, Pan G, et al. (2019) Contribution of genetics to visceral adiposity and its relation to cardiovascular and metabolic disease. *Nat Med* 25(9):1390-1395. doi: 10.1038/s41591-019-0563-7

31. Molecular screening of familial hypercholesterolemia in Icelanders

Familial hypercholesterolemia (FH) is a monogenic disease characterized by a lifelong exposure to high LDL-C levels that can lead to early onset coronary heart disease (CHD). The main causes of FH identified to date include loss-of-function mutations in LDLR or APOB, or gain-of-function mutations in PCSK9. The authors carried out a comprehensive screening, using a **custom Phosphorus Axiom Array** that was designed based on **Axiom myDesign** custom genotyping array requirements. The study revealed six new mutations in the Icelandic FH families and detected three pathogenic mutations in the general population-based study.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32706999/	Familial hypercholesterolemia Population genomics, predictive genomics, custom array	Kellogg G, Thorsson B, Cai Y, et al. (2020) Molecular screening of familial hypercholesterolemia in Icelanders. *Scand J Clin Lab Invest* 80(6):508-514. doi: 10.1080/00365513.2020.1795919

32. The Longevity-Associated SH2B3 (LNK) genetic variant: Selected aging phenotypes in 379,758 subjects

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/31428775/	Aging	Kuo CL, Joaquim M, Kuchel GA, et al. (2020) The Longevity-Associated SH2B3 (LNK) Genetic Variant: Selected Aging Phenotypes in 379,758 Subjects. *J Gerontol A Biol Sci Med Sci* 75(9):1656-1662. doi: 10.1093/gerona/glz191

33. A polygenic risk score to predict future adult short stature among children

Adult height is highly heritable. This study developed a polygenic risk score (PRS) for adult height as an alternative screening tool to help identify children at risk of developing short stature in adulthood. To create the PRS, the authors obtained height and genotyping data of participants of the UK Biobank study. Combined with sex, the PRS captured 71.1% of the total variance in adult height in the UK Biobank and could also substitute mid-parental height in age-specific Khamis-Roche height predictors to achieve equally strong discriminative power in identifying children with a short stature in adulthood. Participants of the UK Biobank study were genotyped using the **UK Biobank BiLEVE Axiom Array** or **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33788949/	Stature Predictive genomics, polygenic risk score, biobank, UK Biobank	Lu T, Forgetta V, Wu H, et al. (2021) A Polygenic Risk Score to Predict Future Adult Short Stature Among Children. *J Clin Endocrinol Metab* 106(7):1918-1928. doi: 10.1210/clinem/dgab215

34. Novel genotyping algorithms for rare variants significantly improve the accuracy of Applied Biosystems™ Axiom™ array genotyping calls: Retrospective evaluation of UK Biobank array data

This study develops a novel addition to the genotyping algorithm used in the Axiom array analysis of the UK population, which is rare heterozygous adjusted. The algorithm was developed based on a retrospective comparison of genotyping data of the UK Biobank cohort, comparing Axiom array genotyping calls with the corresponding calls from whole exome sequencing. Genotyping of participants in the UK Biobank was done using the **UK Biobank Axiom Array** and **UK Biobank BiLEVE Axiom Array**. The improvement in positive predictive value was roughly equal when comparing to the exome sequencing of approximately 50,000 individuals or more recently of approximately 200,000 individuals, with higher sensitivity in the 200,000 dataset. The improved calling algorithm significantly improved the positive predictive value and the sensitivity of array data, making it suitable for the detection of ultra-rare variants.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36395175/	Non-specific Population genomics, genotyping algorithm	Mizrahi-Man O, Woehrmann MH, Webster TA, et al. (2022) Novel genotyping algorithms for rare variants significantly improve the accuracy of Applied Biosystems™ Axiom™ array genotyping calls: Retrospective evaluation of UK Biobank array data. *PLoS One* 17(11):e0277680. doi: 10.1371/journal.pone.0277680

35. The undiagnosed disease burden associated with alpha-1 antitrypsin deficiency genotypes

Alpha-1 antitrypsin deficiency (AATD) is one of the most common inherited diseases. It is associated with a high disease burden and partially prevented by smoking cessation.This study examined the frequency of homozygous PI*Z (PI*ZZ) genotype in individuals with and without diagnosed AATD from UK Biobank and assessed the associations of the genotypes with clinical outcomes and mortality. A phenome-wide association study (PheWAS) was conducted to reveal disease associations with genotypes. A polygenic risk score (PRS) for expiratory volume and vital capacity (FVC) ratio was used to evaluate variable penetrance of PI*ZZ. Those with PI*ZZ had a substantially higher odds of COPD, asthma, bronchiectasis, pneumonia and cirrhosis diagnoses and a higher hazard of mortality, compared to PI*MM (wildtype). Genotyping of participants in the UK Biobank was done using the **UK Biobank Axiom Array** and **UK Biobank BiLEVE Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32675199/	Alpha-1 antitrypsin deficiency (AATD) undiagnosed diseases Population genomics, predictive genomics, polygenic risk score, UK Biobank	Nakanishi T, Forgetta V, Handa T, et al. (2020) The undiagnosed disease burden associated with alpha-1 antitrypsin deficiency genotypes. *Eur Respir J* 56(6):2001441. doi: 10.1183/13993003.01441-2020

For Research Use Only. Not for use in diagnostic procedures.

15

36. A genome-wide association study of sprint performance in elite youth football players

Sprint speed is an important component of football performance, with teams often placing a high value on sprint and acceleration ability. The aim of this study was to undertake the first genome-wide association study to identify genetic variants associated with sprint test performance in elite youth football players and to further validate the obtained results in additional studies. Genotyping of 1206 subjects using **Axiom 2.0 microarray** data revealed 12 SNPs with suggestive significance.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/31343553/	Athletic performance Population genomics, predictive genomics	Pickering C, Suraci B, Semenova EA, et al. (2019) A Genome-Wide Association Study of Sprint Performance in Elite Youth Football Players. *J Strength Cond Res* 33(9):2344-2351. doi: 10.1519/ JSC.0000000000003259

37. Genetic modifiers of penetrance to liver endpoints in HFE hemochromatosis: Associations in a large community cohort

Iron overload condition hereditary hemochromatosis (HH) can cause liver cirrhosis and cancer, diabetes, and arthritis. Males homozygous for the p.C282Y missense mutation in the Homeostatin Iron Regulator (HFE) gene have greatest risk; yet, only a minority develop these conditions. This study investigates the p.C282Y missense mutation in the homeostatin iron regulator (HFE) gene connected to hereditary hemochromatosis (HH). Homozygote penetrance to clinical disease in a UK Biobank cohort was partly explained by common genetic variants that influence iron and risks of related diagnoses in the general population, including polygenic scores in HH screening and diagnosis. They included UK Biobank HFE p.C282Y homozygous participants of European ancestry. UK Biobank participants were genotyped using **Axiom UK Biobank Axiom Array** and the **UK Biobank BiLEVE Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35567766/	Hereditary hemochromatosis Population genomics, predictive genomics, polygenic risk scoring, UK Biobank	Pilling LC, Atkins JL, Melzer D. (2022) Genetic modifiers of penetrance to liver endpoints in HFE hemochromatosis: Associations in a large community cohort. *Hepatology* 76(6):1735-1745. doi: 10.1002/hep.32575

38. Common conditions associated with hereditary haemochromatosis genetic variants: cohort study in UK Biobank

This study compares prevalent and incident morbidity and mortality between those with the HFE p.C282Y genetic variant (responsible for most hereditary haemochromatosis type 1 and those with no p.C282Y mutations, in a UK Biobank sample of White Europeans. In this study, HFE p.C282Y homozygosity was associated with substantial prevalent and incident clinically diagnosed morbidity in both men and women. UK Biobank participants were genotyped using the **Axiom UK Biobank Axiom Array** and the **UK Biobank BiLEVE Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/30651232/	Hereditary hemochromatosis Population genomics, predictive genomics, UK Biobank	Pilling LC, Tamosauskaite J, Jones G, et al. (2019) Common conditions associated with hereditary haemochromatosis genetic variants: cohort study in UK Biobank. *BMJ* 364:k5222. doi: 10.1136/bmj.k5222

39. Association between migraine prevalence, treatment with proton-pump inhibitors and CYP2C19 phenotypes in UK Biobank

CYP2C19 is the major enzyme involved in clearance of protein pump inhibitors (PPIs). Migraine is a known adverse effect of PPIs. This study of 468,280 participants from the UK Biobank for which both genetic and clinical information was known suggested that treatment with proton-pump inhibitors (PPI) was associated with higher migraine prevalence. However, those with a rapid metabolizer phenotype of CYP2C19 showed a lower migraine prevalence. Genotyping revealed that, in patients treated with PPIs, migraine was more prevalent in participants with specific genetic variations in the gene encoding the CYP2C19 enzyme. These results suggest that individuals with poor CYP2C19 metabolizers may be particularly susceptible to PPI-induced migraines. Genotyping of the UK Biobank cohort was conducted with the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34649359/	Migraine Predictive genomics, preemptive pharmacogenomics, UK Biobank	Pisanu C, Welander NZ, Rukh G, et al. (2021) Association between migraine prevalence, treatment with proton-pump inhibitors and CYP2C19 phenotypes in UK Biobank. *Biomed Pharmacother* 143:112234. doi: 10.1016/j.biopha.2021.112234

40. Identification of TMC1 as a relatively common cause for nonsyndromic hearing loss in the Saudi population

Mutations of the transmembrane channel-like 1 (TMC1) gene cause hearing defects in humans and mice. This study investigates the importance of TMC1 mutations in the Saudi population using a combination of autozygome-guided candidate gene mutation analysis and targeted next generation sequencing in 366 families with HL previously shown to lack mutations in GJB2. The study revealed 12 families that carried five causative TMC1 mutations, including three novel and two reported mutations. Each of the identified recessive mutation was classified as severe, by both age of onset and severity of HL. The **Axiom CEU Human Array** was used in this study.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/31854501/	Hearing loss Population genomics, predictive genomics	Ramzan K, Al-Owain M, Al-Numair NS, et al. (2020) Identification of TMC1 as a relatively common cause for nonsyndromic hearing loss in the Saudi population. *Am J Med Genet B Neuropsychiatr Genet* 183(3):172-180. doi: 10.1002/ajmg.b.32774

41. Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects

In this study, a genome-wide association studies (GWAS) was used to investigate the proportion of body fat distributed to the arms, legs and trunk estimated from segmental bio-electrical impedance analysis (sBIA) for over 362,000 individuals from the UK Biobank using the Axiom array. 98 independent associations with body fat distribution are identified, 29 that have not previously been associated with anthropometric traits. A high degree of sex-heterogeneity was observed and the effects of 37 associated variants are stronger in females compared to males. Genotyping of the UK Biobank cohort was conducted with the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/30664634/	Body fat Population genomics, predictive genomics, UK Biobank	Rask-Andersen M, Karlsson T, Ek WE, et al. (2019) Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects. *Nat Commun* 10(1):339. doi: 10.1038/s41467-018-08000-4

Europe, Middle East, and Africa (EMEA) region

42. Modification of heritability for educational attainment and fluid intelligence by socioeconomic deprivation in the UK Biobank

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/33900812/	Educational attainment and intelligence	Rask-Andersen M, Karlsson T, Ek WE, et al. (2021) Modification of Heritability for Educational Attainment and Fluid Intelligence by Socioeconomic Deprivation in the UK Biobank. *Am J Psychiatry* 178(7):625-634. doi: 10.1176/appi.ajp.2020.20040462

43. KIR gene content imputation from single-nucleotide polymorphisms in the Finnish population

Copy number variations of killer cell immunoglobulin-like receptor (KIR) gene are associated with transplantation outcomes and susceptibility to immune-mediated diseases. Using samples from the Finnish biobank (FinnGen) genotyped for 5900 KIR-region single-nucleotide polymorphisms (SNPs) and analyzed for KIR gene content, the authors created a machine learning model with high overall accuracy for inferring KIR gene content in biobanks and clinical data collections. The samples were genotyped on a **custom Axiom genotyping array** as a part of the FinnGen project.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35036093/	Tumor surveillance, viral infection Predictive genomics, custom array, FinnGen	Ritari J, Hyvärinen K, Partanen J, et al. (2022) KIR gene content imputation from single-nucleotide polymorphisms in the Finnish population. *PeerJ* 10:e12692. doi: 10.7717/peerj.12692

44. The QChip1 knowledgebase and microarray for precision medicine in Qatar

Single-gene disorder (SGD) pathogenic variants found in Greater Middle Eastern populations are under-reported and there are limited screening platforms to assess these variants in the Greater Middle East. The authors developed a **custom microarray called QCHip1 based in the Axiom microarray** that is focused on SNPs prevalent in the Qatari population leading to single gene disorders. Over 108 variants in about 8400 Qatari were identified for inclusion in a genotyping array containing over 165,000 probes for about 83,500 known and potentially pathogenic variants in over 3400 SGDs. The most common pathogenic variants were those causing homocystinuria, and Stargardt disease.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41525-021-00270-0	Single-gene disorders Population genomics, custom array	Rodriguez-Flores JL, Messai-Badji R, Robay A, et al. (2022) The QChip1 knowledgebase and microarray for precision medicine in Qatar. *npj Genom Med* 7:3 (2022). doi: 10.1038/s41525-021-00270-0

45. **Personality, lifestyle and job satisfaction: causal association between neuroticism and job satisfaction using Mendelian randomisation in the UK biobank cohort**

   This study used an analytical method to assess the causal effect of neuroticism, education, and physical activity on job satisfaction. Data were obtained from the UK Biobank cohort. UK Biobank whole-genome genotyping data was derived using the **UK Biobank BiLEVE Axiom Array** and **UK Biobank Axiom Array.** Meta-analyses of genome-wide association studies revealed multiple single nucleotide polymorphisms (SNPs) associated with neuroticism, educational attainment, and habitual physical activity to create a genetic risk score. Mendelian randomization analyses concluded that genetically determined neuroticism was associated with lower job satisfaction, while education and physical activity were not associated with job satisfaction. The outcome emphasized the confounding effect negative personality traits may have on studies assessing job satisfaction.

Link	Medical Condition/Keywords	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC7026032/	Personality, lifestyle and job satisfaction Predictive genomics, population genomics, polygenic risk score, UK Biobank	Rukh G, Dang J, Olivo G, et al. (2020) Personality, lifestyle and job satisfaction: causal association between neuroticism and job satisfaction using Mendelian randomisation in the UK biobank cohort. *Transl Psychiatry* 10(1):11. doi: 10.1038/s41398-020-0691-3

46. **Using Taqman assays to verify eQTL links arising from GWAS studies**

   Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://aacrjournals.org/cancerres/article/79/13_Supplement/5201/636939/Abstract-5201-Using-Taqman-assays-to-verify-eQTL	Cancer	Jackson SM, Veereshlingham H, Varma K. (2019) Abstract 5201: Using Taqman assays to verify eQTL links arising from GWAS studies. *Cancer Res* 79 (13_Supplement):5201.

47. **Hereditary Hemochromatosis Associations with frailty, sarcopenia and chronic pain: Evidence from 200,975 older UK Biobank participants**

   Using over 200,000 UK Biobank volunteers aged 60–70 years, the authors tested associations between C282Y homozygosity with Fried frailty, sarcopenia, and chronic pain using logistic regression adjusted for age and technical genetic covariates. As iron overload is progressive (with menstruation protective), the authors also included specific analyses of older (65–70 years) females and males. Genotyping of the UK Biobank cohort was conducted with the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/30657865/	Hemochromatosis Predictive genomics, UK Biobank	Tamosauskaite J, Atkins JL, Pilling LC, et al. (2019) Hereditary Hemochromatosis Associations with Frailty, Sarcopenia and Chronic Pain: Evidence from 200,975 Older UK Biobank Participants. *J Gerontol A Biol Sci Med Sci* 74(3):337-342. doi: 10.1093/gerona/gly270

48. **Validation of concurrent preimplantation genetic testing for polygenic and monogenic disorders, structural rearrangements, and whole and segmental chromosome aneuploidy with a single universal platform**
Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/31026593/	Polygenic and chromosomal disorders	Treff NR, Zimmerman R, Bechor E, et al. (2019) Validation of concurrent preimplantation genetic testing for polygenic and monogenic disorders, structural rearrangements, and whole and segmental chromosome aneuploidy with a single universal platform. *Eur J Med Genet* 62(8):103647. doi: 10.1016/j.ejmg.2019.04.004

49. **Large copy-number variants in UK Biobank caused by clonal hematopoiesis may confound penetrance estimates**
Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/32574563/	Chromosomal variations	Tuke M, Tyrrell J, Ruth KS, et al. (2020) Large Copy-Number Variants in UK Biobank Caused by Clonal Hematopoiesis May Confound Penetrance Estimates. *Am J Hum Genet* 107(2):325-329. doi: 10.1016/j.ajhg.2020.06.001

50. **A genetic correlation scan identifies blood proteins associated with bone mineral density**
Heredity seems to exert greater influence on human bone mineral density (BMD) and peak body mass (PBM) than environmental factors. This study is a large-scale scan of genetic correlation between BMD and human plasma proteins. Genome-wide association study (GWAS) summary data of the blood proteome and two independent studies of bone mineral density were used to conduct a genetic correlation scan of BMD and the blood proteome. Linkage disequilibrium score regression identified 18 plasma proteins showing genetic correlation signals with BMD. SNP genotyping of UK Biobank participants was conducted via the **UK Biobank Axiom Array** and **UK BiLEVE Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35659283/	Osteoporosis Predictive genomics, UK Biobank, genome-wide association study	Xu J, Zhang S, Si H, et al. (2022) A genetic correlation scan identifies blood proteins associated with bone mineral density. *BMC Musculoskelet Disord* 23(1):530. doi: 10.1186/s12891-022-05453-z

Europe, Middle East, and Africa (EMEA) region

51. Elevated blood pressure increases pneumonia risk: Epidemiological association and mendelian randomization in the UK Biobank

Employing participant data from the UK Biobank study, this study aimed to determine if hypertension increases the risk for pneumonia, and if a genetic predisposition for hypertension is associated with increased risk for pneumonia. The participants in the UK Biobank study were genotyped using the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**. The study revealed that hypertension was independently associated with a risk for respiratory diseases, including pneumonia. The results also indicated that a genetic predisposition to an increase in blood pressure was associated with an increased risk for pneumonia.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33283203/	Hypertension, pneumonia Predictive genomics, UK Biobank	Zekavat SM, Honigberg M, Pirruccello JP, et al. (2020) Elevated Blood Pressure Increases Pneumonia Risk: Epidemiological Association and Mendelian Randomization in the UK Biobank. *Med* 2(2):137-148.e4. doi: 10.1016/j.medj.2020.11.001

52. The QChip1 knowledgebase and microarray for precision medicine in Qatar

Specific causative pathogenic variants for Mendelian (single-gene) disorders (SGD) found in Greater Middle Eastern populations are under-reported. The goal of this project was to develop an inexpensive genotyping microarray based on the Axiom Genotyping S solution to screen Qatari newborns, couples, and patients for SGD risk variants. Over 108 variants in 8445 Qatari were identified for inclusion in a genotyping array containing almost 166,000 probes for approximately 83,500 known and potentially pathogenic variants in more than 3400 SGDs. The majority of Qatari SGD pathogenic variants were not present in other global populations. Given the low cost of sequencing data production, the availability of cloud-based genome analysis infrastructure that does not require large capital investment, and the ease of rapid array design using the **Axiom platform**, a nation or population that currently has no prior knowledge of genetic variation could take the approach presented here and produce a genetic disease screening program in under a year, potentially saving thousands of lives at risk of unknowingly being affected by a genetic disorder.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41525-021-00270-0	Mendelian (single-gene) disorders Population genotyping, custom array, population diversity	Rodriguez-Flores JL, Messai-Badji R, Robay A, et al. (2022) The QChip1 knowledgebase and microarray for precision medicine in Qatar. *npj Genom Med* 7:3. doi: 10.1038/s41525-021-00270-0

53. FinnGen provides genetic insights from a well-phenotyped isolated population

In Finland, a strong founding genetic bottleneck occurred about 120 generations ago followed by rapid population expansion. This bottleneck effect has resulted in numerous strongly deleterious alleles that occur more frequently in Finland compared with other European populations. This study used a **custom Axiom FinnGen1 array** to genotype almost 155,000 individuals. The results yielded 30 new associations, primarily low-frequency variants, that are enriched in the Finnish population. A GWAS of approximately 2000 diseases also identified approximately 2,500 genome-wide significant associations of probable causal coding variants. These findings demonstrate the power of the combination of data from an isolated population and other registers to discover new low-frequency variant associations, even in previously well-studied diseases.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41586-022-05473-8	Non-specific Population genotyping, custom array, founder population, FinnGen	Kurki MI, Karjalainen J, Palta P, et al. (2023) FinnGen provides genetic insights from a well-phenotyped isolated population. *Nature* 613:508–518. doi: 10.1038/s41586-022-05473-8

Europe, Middle East, and Africa (EMEA) region

54. **Genomics PLC to provide polygenic risk scores for UK's Our Future Health Research Program**

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/business-news/genomics-plc-provide-polygenic-risk-scores-uks-our-future-health-research-program#.ZC3uM-zML9F	Non-specific	Staff Reporter. (2022) Genomics PLC to Provide Polygenic Risk Scores for UK's Our Future Health Research Program. *GenomeWeb* Oct 10, 2022.

55. **Genetic risk factors have a substantial impact on healthy life years**

This study introduces an approach using polygenic risk scoring to estimate the effect of genetic risk factors on disability-adjusted life years (DALYs; 'lost healthy life years') using genetic information from approximately 736,000 individuals and considering 80 diseases. To estimate genetic associations, the study used individual-level data from two biobank studies: FinnGen and UK Biobank. The data revealed that rare variants had the highest effect on DALY. In addition, some common variants varied by gender and had effects comparable to modifiable risk factors such as sodium intake and physical activity. The findings indicate that genetic risk factors can explain a sizable number of healthy life years lost both at the individual and population level. Most of the FinnGen participants have been genotyped using a custom Axiom microarray and some UK Biobank participants were genotyped using the **UK BiLEVE Axiom Array** or the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36097220/	Disability-adjusted life years Population genomics, predictive genomics, polygenic risk score, FinnGen	Jukarainen S, Kiiskinen T, Kuitunen S, et al. (2022) Genetic risk factors have a substantial impact on healthy life years. *Nat Med* 9:1893-1901. doi: 10.1038/s41591-022-01957-2

56. **Integrating genome-wide polygenic risk scores and non-genetic risk to predict colorectal cancer diagnosis using UK Biobank data: population based cohort study**

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/36351667/	Colorectal cancer	Briggs SEW, Law P, East JE, et al. (2022) Integrating genome-wide polygenic risk scores and non-genetic risk to predict colorectal cancer diagnosis using UK Biobank data: population based cohort study. *BMJ* 379:e071707. doi: 10.1136/bmj-2022-071707

57. The UK Biobank resource with deep phenotyping and genomic data

The UK Biobank is an open resource containing genetic and phenotypic data on 500,000 participants from across the United Kingdom. Participants were genotyped using the **UK Biobank Lung Exome Variant Evaluation (BiLEVE) Axiom Array** and the **UK Biobank Axiom Array**. In this study, the authors described the genetic dataset provided by UK Biobank, applied quality control procedures, estimated haplotypes, and conducted genotype imputation resulting in approximately 96 million testable variants.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/30305743/	Non-specific Population genomics, predictive genomics, new biobank, UK Biobank	Bycroft C, Freeman C, Petkova D, et al. (2018) The UK Biobank resource with deep phenotyping and genomic data. *Nature* 562(7726):203-209. doi: 10.1038/s41586-018-0579-z

58. German COVID-19 project aims to better understand role of genetics in disease severity

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/covid-19/german-covid-19-project-aims-better-understand-role-genetics-disease-severity#.ZAkZp-zMITU	COVID-19	GenomeWeb, Petrone, Justin. (2021) *GenomeWeb* Mar 30, 2021.

59. Cytox gets CE mark for alzheimer's disease genetic risk test

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/microarrays-multiplexing/cytox-gets-ce-mark-alzheimers-disease-genetic-risk-test#.ZAkdl-zMITU	Alzheimer's disease	Staff Reporter. (2021) Cytox Gets CE Mark for Alzheimer's Disease Genetic Risk Test. *GenomeWeb* Feb 24 2021.

Applied Biosystems™ Axiom™ Genotyping Solutions: Asia Pacific (APAC) region

60. Classification of early age facial growth pattern and identification of the genetic basis in two Korean populations

Genetic features can influence differences of individual growth through the accelerated growth period from childhood to adolescence. This study examined the genetic basis of early age facial growth (EAFG) patterns. They conducted genome-wide association studies (GWAS) for 21 facial feature phenotypes. SNP genotypes were obtained from an **800K SNP Axiom microarray**. Significant associations were found for both horizontal and vertical phenotypes.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35970861/	Facial growth in adolesence Population genomics, predictive genomics, genome-wide association study	Cha MY, Hong YJ, Choi JE, et al. (2022) Classification of early age facial growth pattern and identification of the genetic basis in two Korean populations. *Sci Rep* 2022 12(1):13828. doi: 10.1038/s41598-022-18127-6

61. MedGenome South Asian Research Genotyping Array (SARGAM)

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/resources/new-product/medgenome-south-asian-research-genotyping-array-sargam	Non-specific	Staff Writer. (2019) MedGenome South Asian Research Genotyping Array (SARGAM). *GenomeWeb* Nov. 15, 2019.

62. Taiwan Biobank: A rich biomedical research database of the Taiwanese population

The Taiwan Biobank (TWB) provides one of the largest biobank resources for biomedical and public health research in East Asia. This study presents an overview of TWBs genetic data quality, population structure, and familial relationship, which consists of predominantly Han Chinese ancestry. The TWBv1 array was designed in 2011 based on a customized **Axiom Genome-Wide CHB Array** that contains 650,000 markers on the GRCh37 coordinates, providing a comprehensive coverage of common genetic variation for genome-wide association studies (GWASs). In 2017, the TWBv2 array was designed by Thermo Fisher Scientific with a goal to capture not only GWAS markers but also functional variants by deliberately enriching the content of rare coding risk alleles based on whole-genome sequencing data from TWB samples, including 690,000 markers aligned to the reference build.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36776991/	Non-specific Population genomics, predictive genomics, new biobank, Taiwan Biobank	Feng, YCA Chen CY, Chenet TT, et al. (2022) Taiwan Biobank: A rich biomedical research database of the Taiwanese population. *Cell Genomics* 2:100197. doi: 10.1016/j.xgen.2022.100197

63. MedGenome, Thermo Fisher Array for South Asians to support consumer, MDx test development

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/microarrays-multiplexing/medgenome-thermo-fisher-array-south-asians-support-consumer-mdx-test#.ZApGAuzMITU	Non-specific	Petrone J. (2019) MedGenome, Thermo Fisher Array for South Asians to Support Consumer, MDx Test Development. *GenomeWeb* Dec. 3 2019.

64. Machine learning approaches for the genomic prediction of rheumatoid arthritis and systemic lupus erythematosus

Rheumatoid arthritis (RA) and systemic lupus erythematous (SLE) may share a complex genetic background, including a distinct human leukocyte antigen (HLA) inheritance pattern. Based on genome-wide association data obtained by the Taiwan Precision Medicine Initiative, the authors established machine learning (ML) methods for the genomic prediction of RA and SLE. Genotyping of participants of the Taiwan Precision Medicine Initiative was conducted using the **Taiwan Biobank version 2 (TWBv2) Array** developed with Thermo Fisher Scientific as a **custom Axiom genotyping microarray**. The study identified three genetic variants that may be associated with RA and SLE.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34895289/	Rheumatoid arthritis (RA) and systemic lupus erythematous (SLE) Predictive genomics, custom array, Taiwan Precision Medicine Initiative	Chung CW, Hsiao TH, Huang CJ, et al. (2021) Machine learning approaches for the genomic prediction of rheumatoid arthritis and systemic lupus erythematosus. *BioData Min* 14(1):52. doi: 10.1186/s13040-021-00284-5

65. Thermo Fisher Scientific collaborates with Taiwan Precision Medicine Initiative to genotype 1 million people in Taiwan

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.biospace.com/article/releases/thermo-fisher-scientific-collaborates-with-taiwan-precision-medicine-initiative-to-genotype-1-million-people-in-taiwan/	Serious diseases, e.g., cancer, cardiovascular, neurodegenerative	Thermo Fisher Scientific (Sept 13, 2022) Thermo Fisher Scientific Collaborates with Taiwan Precision Medicine Initiative to Genotype 1 Million People in Taiwan. [Press release].

66. Allelica, SP BioMed partner for breast cancer polygenic risk score study in Taiwan

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.genomeweb.com/molecular-diagnostics/allelica-sp-biomed-partner-breast-cancer-polygenic-risk-score-study-taiwan#.ZAf7xOzMITU	Breast cancer	Staff Reporter. (2023) Allelica, SP BioMed Partner for Breast Cancer Polygenic Risk Score Study in Taiwan. *GenomeWeb* Feb 22 2023.

67. Japonica Array NEO with increased genome-wide coverage and abundant disease risk SNPs

Ethnic-specific SNP arrays are becoming more important to increase the power of genome-wide association studies in diverse population. This study describes the development of a new microarray called **Japonica Array NEO (JPA NEO)** based on the **UK Biobank Axiom Array**. The Japonica Array NEO comprises over 666,000 markers including SNPs of autosomes and the X chromosome selected from an expanded reference panel. Over 28,000 markers were included for the evaluation of previously identified disease risk markers from the literature and databases, and those present in the Japanese population were extracted using the reference panel. JPA NEO is a promising tool for genotyping the Japanese population with genome-wide coverage, contributing to the development of genetic risk scores.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34131746/	Non-specific Population genomics, new custom array, Japonica Array NEO	Sakurai-Yageta M, Kumada K, Gocho C, et al. (2021) Japonica Array NEO with increased genome-wide coverage and abundant disease risk SNPs. *J Biochem* 170(3):399-410. doi: 10.1093/jb/mvab060

68. The Korea Biobank array: Design and identification of coding variants associated with blood biochemical traits

This study introduces the design and implementation of a new array, the **Korea Biobank Array (KoreanChip)** optimized for the Korean population, and demonstrate sfindings from a genome-wide association study (GWAS) of blood biochemical traits. KoreanChip is based on the **Axiom array platform**. To select markers optimized for the Korean genome, the array is especially focused on maximizing genome-wide tagging markers that boosted imputation performance and potentially functional markers influencing disease risk. Screening of validated SNPs was done by referencing the **Axiom Genomic Database (Axiom GD)**, which contains over 26 M validated high-performance markers. De novo variants not in the Axiom GD were experimentally validated using a customized Axiom myDesign genotyping array. KoreanChip comprises more than 833,000 markers including more than 247,000 rare-frequency or functional variants estimated from sequencing data from more than 2,500 Koreans.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/30718733/	Non-specific	Moon S, Kim YJ, Han S, et al. (2019) The Korea Biobank Array: Design and Identification of Coding Variants Associated with Blood Biochemical Traits. *Sci Rep* 9(1):1382. doi: 10.1038/s41598-018-37832-9
	Population genomics, predictive genomics, new custom array, KoreanChip	

69. Preliminary study of genome-wide association identified novel susceptibility genes for hemorheological indexes

in a Chinese Population Hemorheological characteristics play an important role in metabolic disease processes, such as blood and plasma viscosity or erythrocyte rigidity. This study is a genome-wide association study (GWAS) to evaluate the genetic variation associated with hemorheological traits in a cohort of healthy Han Chinese individuals. Participants were genotyped using the **Axiom Precision Medicine Diversity Array** on the **GeneTitan Multi-Channel Instrument**. Genotype clustering was conducted using **Axiom Analysis Suite 6.0 software**. The authors identified 38 single-nucleotide polymorphisms (SNPs) significantly related to hemorheological traits. The study emphasized that the identified SNPs may represent biological candidates for hemorheological indices.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36654975/	Metabolic disease	Sun Y, Cheng Z, Guo Z, et al. (2022) Preliminary Study of Genome-Wide Association Identified Novel Susceptibility Genes for Hemorheological Indexes in a Chinese Population. *Transfus Med Hemother* 49(6):346-357. doi: 10.1159/000524849
	Population genomics, predictive genomics, genome-wide association study	

70. Genetic profiles of 103,106 individuals in the Taiwan Biobank provide insights into the health and history of Han Chinese

Disease-causing genetic mutations are often rare and population specific, requiring the development of biobanks based on diverse cohorts around the world. Aiming to create a large genetic database of individuals with East Asian ancestry, this study combined demographic data, whole-genome sequencing, genotyping data, and HLA allele typing data obtained, among others, from the Taiwan Biobank (TWB). The custom genotyping arrays TWBv1 and TWBv2 were designed using the **Axiom Genotyping Solution**. Highlighting that the Han Chinese population accounts for 19% of the world's population, the study emphasizes the importance of this dataset providing insights into population history, disease burden, and clinical care.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33574314/	Non-specific	Wei CY, Yang JH, Yeh EC, et al. (2021) Genetic profiles of 103,106 individuals in the Taiwan Biobank provide insights into the health and history of Han Chinese. *NPJ Genom Med* 6(1):10. doi: 10.1038/s41525-021-00178-9
	Population genotyping, biobank, custom array, Taiwan Precision Medicine Initiative	

Asia Pacific (APAC) region

71. PKD2 founder mutation is the most common mutation of polycystic kidney disease in Taiwan

To study the disease-causing mutations of autosomal dominant polycystic kidney disease (ADPKD), a total of 920 families were collected and their diagnoses were established via clinical and image studies by Taiwan PKD Consortium investigators. The **Axiom Genome-Wide TWB 2.0 Array** was used for genotyping. The study revealed a unique PKD2 founder mutation that occurred 300 years ago and contributed to the single most common mutation in the Taiwan ADPKD community.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41525-022-00309-w	Polycystic kidney disease Population genomics, predictive genomics	Yu CC, Lee AF, Kohl S. et al. (2022) PKD2 founder mutation is the most common mutation of polycystic kidney disease in Taiwan. *npj Genom. Med* 7:40. doi: 10.1038/s41525-022-00309-w

72. Association of single nucleotide polymorphism rs2228570 with lumbar disc degeneration: A case–control study and meta-analysis

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/34234546/	Lumbar disc degeneration	Zhang H, Chen L, Wang Z, et al. (2021) Association of Single Nucleotide Polymorphism rs2228570 with Lumbar Disc Degeneration: A Case-Control Study and Meta-Analysis. *J Pain Res* 14:2001-2012. doi: 10.2147/JPR.S313790

73. CNVIntegrate: the first multi-ethnic database for identifying copy number variations associated with cancer

This study describes CNVIntegrate, the first web-based system that hosts CNV and CNA data from both healthy populations and cancer patients, respectively, and concomitantly provides statistical comparisons between copy number frequencies of multiple ethnic populations. It further includes, for the first time, well-cataloged CNV and CNA data from Taiwanese healthy individuals and Taiwan Breast Cancer data, respectively, along with imported resources from ExAC, COSMIC and CCLE. CNVIntegrate offers a CNV/CNA-data hub for structured information retrieval for clinicians and scientists towards important drug discoveries and precision treatments.The SNPs were assayed using an **Axiom Genome-Wide TWB Array Plate (TWB array)**, a **custom Axiom array** designed for the Taiwan Biobank.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34259866/	Breast cancer Population genomics, preemptive pharmacogenomics, custom array, copy number variation, database	Chattopadhyay A, Teoh ZH, Wu C-Y, et al. (2021) CNVIntegrate: the first multi-ethnic database for identifying copy number variations associated with cancer, *Database* 2021:baab044. doi: 10.1093/database/baab044

Asia Pacific (APAC) region

74. The ChinaMAP reference panel for the accurate genotype imputation in Chinese populations

Genotype imputation is an efficient approach to estimate unobserved genotypes in genomic data from single nucleotide polymorphism (SNP) genotyping arrays or whole-genome sequencing (WGS). However, European ancestry-dominant reference panels exhibited poor performance in the genotype imputation for Chinese and other East Asian populations. This study describes a high-resolution, population-specific reference panel based on large-scale that was developed to achieve high-quality imputation for Chinese genomic datasets. Compared to the previous reference panels with Chinese samples, the ChinaMAP reference panel showed significant advances in sample size and sequencing depth. Approximately half of the study variants were extracted from the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
www.nature.com/articles/s41422-021-00564-z	Non-specific Population genomics	Li L, Huang P, Sun X, et al. (2021) The ChinaMAP reference panel for the accurate genotype imputation in Chinese populations. *Cell Res* 31:1308–1310. doi: 10.1038/s41422-021-00564-z

75. CAS Array: Design and assessment of a genotyping array for Chinese biobanking

This study describes the design and assessment of a genome-wide SNP array, the **CAS Array**, specifically optimized for cost-effective whole genome genotyping in the Chinese population. The CAS Array is a **custom Axiom array** and is restricted to approximately 650,000 single-nucleotide polymorphism (SNP) markers. SNPs on the **Axiom Asia Precision Medicine Research Array (Axiom APRMA)** were used to achieve adequate coverage of common variants for imputation-based GWAS. The data reveals call rates and concordance rates higher than for commercial arrays. Imputation-based genome coverage reached 98.3% for common SNPs and 63.0% for low-frequency SNPs, both comparable to commercial arrays with larger SNP capacity. The study also yielded a publicly available software tool to facilitate the array utility.

Link	Medical Condition/Keywords	Citation
https://academic.oup.com/pcm/article/6/1/pbad002/7055961	Chronic diseases Population genomics, custom array, genome-wide association study	Zijian Tian, Fei Chen, Jing Wang, Benrui Wu, Jian Shao, Ziqing Liu, Li Zheng, You Wang, Tao Xu, Kaixin Zhou, CAS Array: design and assessment of a genotyping array for Chinese biobanking, *Precision Clinical Medicine*, Volume 6, Issue 1, March 2023, pbad002, doi: 10.1093/pcmedi/pbad002

Applied Biosystems™ Axiom™ Genotyping Solutions: Latin America (LATAM) region

Latin America (LATAM) region

76. LINE-1 and EPAS1 DNA methylation associations with high-altitude exposure

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/30574831/	Adaptive response to high altitude	Childebayeva A, Jones TR, Goodrich JM, et al. (2019) LINE-1 and EPAS1 DNA methylation associations with high-altitude exposure. *Epigenetics* 14(1):1-15. doi: 10.1080/15592294.2018.1561117

77. The association between fasting glucose and sugar sweetened beverages intake is greater in Latin Americans with a high polygenic risk score for type 2 diabetes mellitus

This study investigated the connection of consumption of sugar-sweetened beverages (SSB) in Chile with obesitsy and type-2-diabetes (T2D) to determine whether the effects will mimic those reported in industrialized countries or whether they will be modified by local lifestyle or population genetics. T2D SNPs that met quality criteria were used to calculate a weighted genetic risk score. Genotyping of individuals from a range of Peruvian and Chilean ethnic populations was done using the **Axiom Genome-Wide LAT 1 Array**. The results suggest that the association between SSB intake and fasting glucose in the Chilean population without diabetes is modified by T2D genetic susceptibility. This study provides the first evidence of genotype-by-diet interaction in a Latin American population that modifies the risk for T2D before clinical sings of the disease.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35010944/	Type-2 diabetes Population genomics, predictive genomics, polygenic risk scoring	López-Portillo ML, Huidobro A, Tobar-Calfucoy E, et al. (2021) The Association between Fasting Glucose and Sugar Sweetened Beverages Intake Is Greater in Latin Americans with a High Polygenic Risk Score for Type 2 Diabetes Mellitus. *Nutrients* 14(1):69. doi: 10.3390/nu14010069

78. Fine-scale genomic analyses of admixed individuals reveal unrecognized genetic ancestry components in Argentina

Little is known about the sub-continental origins of the African, European and Native American ancestries of Argentinian populations. This study investigates geographic genetic diversity among Argentinians. Global genotyping was done using the **Axiom Genome-Wide LAT 1 Array**. The study reveals four Native American components segregating in modern Argentinean populations.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32673320/	Ancestry Population genomics, genetic diversity	Luisi P, García A, Berros JM, et al. (2020) Fine-scale genomic analyses of admixed individuals reveal unrecognized genetic ancestry components in Argentina. *PLoS One* 15(7):e0233808. doi: 10.1371/journal.pone.0233808

Latin America (LATAM) region

79. Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components

In this study, a small panel of 150 SNPs was designed to accurately assess ancestry in the largest sampling to date of the Chilean population of mixed ancestry from eight cities. 143 SNPs were included in the **Axiom Genome-Wide LAT 1 World Array**. Genotyping of the participants was also conducted on this array. The developed panel is also able to distinguish between the two main Amerindian components of Chileans: Aymara from the north and Mapuche from the south.

Link

https://pubmed.ncbi.nlm.nih.gov/32299502/

Medical Condition/Keywords

Ancestry

Population genomics, population diversity

Citation

Verdugo RA, Di Genova A, Herrera L, et al. (2020) Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. *Biol Res* 53:15. doi: 10.1186/s40659-020-00284-5

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32

Applied Biosystems™ Axiom™ Genotyping Solutions: Multiple regions

80. Association of habitual alcohol intake with risk of cardiovascular disease

Genetic instruments for habitual alcohol consumption were constructed using single-nucleotide variants (SNVs) associated with alcohol use disorder using data from the UK Biobank. Each instrument using empirical UK Biobank estimates to arrive at population-specific genetic proxies for habitual alcohol consumption. The genetic evidence from this study is suggestive of a causal relationship between alcohol consumption and cardiovascular disease that is consistently risk increasing, with the magnitude of risk rising exponentially at higher levels of intake. Participants in the UK Biobank study were genotyped using the **UK BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC8956974/	Alcohol intake, cardiovascular disease Population genomics	Biddinger KJ, Emdin CA, Haas ME, et al. (2022) Association of Habitual Alcohol Intake With Risk of Cardiovascular Disease. JAMA Netw Open 5(3):e223849. Erratum in: *JAMA Netw Open* 5(4):e2212024. doi: 10.1001/jamanetworkopen.2022.3849

81. A large-scale association study detects novel rare variants, risk genes, functional elements, and polygenic architecture of prostate cancer susceptibility

This is an integrated study of prostate cancer genetic etiology in the large Northern California Kaiser Permanente and UK Biobank population-based cohorts. The study was conducted using a **custom Axiom genotyping array** developed in collaboration with Thermo Fisher Scientific (Affymetrix Inc.) Approximately 12,000 men of European ancestry from Northern California Kaiser Permanente were genotyped and meta-analyzed with almost 200,000 men of European ancestry from the UK Biobank. To improve detection of rare variant associations, our study design prioritized directly genotyping variants of putative functional significance, rare variants from trait-specific whole exome sequencing (WES) cohorts, and rare variants with proximity to trait-associated loci, all on the custom microarray. Three novel loci, including two rare variants, were significant genome-wide in a meta-analysis. Additionally, a polygenic risk score (PRS) was strongly associated with risk.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/33293427/	Prostate cancer Population genomics, genome-wide association study, UK Biobank, Kaiser Permanente	Emami NC, Cavazos TB, Rashkin SR, et al. (2020) A Large-Scale Association Study Detects Novel Rare Variants, Risk Genes, Functional Elements, and Polygenic Architecture of Prostate Cancer Susceptibility. *Cancer Res* 81(7):1695-1703. doi: 10.1158/0008-5472

82. Development and validation of a universal blood donor genotyping platform: a multinational prospective study

This study describes the development of genotype-based universal donor typing platform that could be adopted by blood services worldwide to facilitate a universal extended blood-matching. Validation of the test was performed by genotyping European, South Asian, East Asian, and African blood donors enrolled in the UK Biobank Genotyping was done with the **UK Biobank Axiom Array** with additional donor typing content integrated into a larger **UK BioBank Axiom Array** design. The resulting **UK Biobank version 2 Axiom Array (UKBBv2 array)** includes content for both genome-wide typing and all currently known antigen-coding variants in RBC antigen- and HPA-encoding genes. Genotyping results demonstrated high concordance with clinically validated typing results.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/32750130/	Blood typing Population genomics, UK Biobank, custom array	Gleadall NS, Veldhuisen B, Gollub J, et al. (2020) Development and validation of a universal blood donor genotyping platform: a multinational prospective study. *Blood Adv* 4(15):3495-3506, doi: 10.1182/bloodadvances.2020001894

Multiple regions

83. **A comprehensive evaluation of polygenic score and genotype imputation performances of human SNP arrays in diverse populations**

This study is a comprehensive performance assessment for 23 available human genotyping arrays (including **Axiom UKBiobank Array, JaponicaArray NEO, Axiom Precision Medicine Research Array,** and **Axiom Precision Medicine Diversity Array**) in six ancestry groups using diverse public and in-house datasets. The analyses focus on performance estimation of derived imputation and polygenic scoring in three different traits and diseases. We found that the arrays with a higher number of SNPs are not necessarily the ones with higher imputation performance, but the arrays that are well-optimized for the targeted population could provide very good imputation performance. This study might act as a practical guide for researchers to design their genotyping arrays-based studies.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/36266455/	Non-specific Population genomics, polygenic risk score, population diversity	Nguyen DT, Tran TTH, Tran MH, et al. (2022) A comprehensive evaluation of polygenic score and genotype imputation performances of human SNP arrays in diverse populations. *Sci Rep* 12(1):17556. doi: 10.1038/s41598-022-22215-y

84. **Biobank-driven genomic discovery yields new insight into atrial fibrillation biology**

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/30061737/	Atrial fibrillation	Nielsen JB, Thorolfsdottir RB, Fritsche LG, et al. (2018) Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nat Genet* 50(9):1234-1239. doi: 10.1038/s41588-018-0171-3

85. **Characterization of reference materials with an association for molecular pathology pharmacogenetics working group tier 2 status: YP2C9, CYP2C19, VKORC1, CYP2C cluster variant, and GGCX**

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/34020041/	Warfarin reference standards	Pratt VM, Turner A, Broeckel U, et al. (2021) Characterization of Reference Materials with an Association for Molecular Pathology Pharmacogenetics Working Group Tier 2 Status: CYP2C9, CYP2C19, VKORC1, CYP2C Cluster Variant, and GGCX: A GeT-RM Collaborative Project. *J Mol Diagn* 23(8):952-958. doi: 10.1016/j.jmoldx.2021.04.0128491090

Multiple regions

86. A polygenic risk score predicts mosaic loss of chromosome Y in circulating blood cells

Mosaic loss of Y chromosome (LOY) is the most common somatic change that occurs in circulating white blood cells of older men. LOY in leukocytes is associated with increased risk for all-cause mortality and a range of common disease such as hematological and non-hematological cancer, Alzheimer's disease, and cardiovascular events. This study calculated a PRS for LOY in 5131 men aged 70 years and older. Levels of LOY were estimated using microarrays and validated by whole genome sequencing. They genotyped DNA using the **Axiom Precision Medicine Diversity Research Array (PMDA)**. The results suggest that a PRS for LOY could become a useful tool for risk prediction and targeted intervention for common disease in men.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/34895331/	Mosaic loss of Y chromosome Predictive genomics, polygenic risk scoring	Riaz M, Mattisson J, Polekhina G, et al. (2021) A polygenic risk score predicts mosaic loss of chromosome Y in circulating blood cells. *Cell Biosci* 11(1):205. doi: 10.1186/s13578-021-00716-z

87. Discovery of 318 novel loci for type-2 diabetes and related micro-and macrovascular outcomes among 1.4 million participants in a multi-ethnic meta-analysis

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/32541925/	Type 2 diabetes	Vujkovic M, Keaton JM, Lynch JA, et al. (2020) Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. *Nat Genet* 52(7):680-691. doi: 10.1038/s41588-020-0637-y

88. Polygenic prediction of type 2 diabetes in continental Africa

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC8918234/	Type 2 diabetes	Chikowore T, Ekoru K, Vujkovi M, et al., (2022) Polygenic Prediction of Type 2 Diabetes in Africa. *Diabetes Care* 45(3):717-723. doi: 10.2337/dc21-0365

89. Homeostatic inflammation in the placenta is protective against adult cardiovascular and depressive outcomes

Researchers investigated an expression signature of homeostatic inflammation in the term placenta and use expression quantitative trait loci (eQTLs) to create a polygenic score (PGS) predictive of its expression. Using this PGS in the UK Biobank they carried out a phenome-wide association study. Genotyping of the UK Biobank cohort was conducted with the **UK Biobank BiLEVE Axiom Array** and the **UK Biobank Axiom Array**.

Link	Medical Condition/Keywords	Citation
www.medrxiv.org/content/10.1101/2023.02.20.23286171v1.full-text	Cardiovascular disease, depression, low birth weight Predictive genomics, polygenic risk score, UK Biobank	Fitzgerald E, Shen MJ, Juen Yong HE, et al. (2023) Homeostatic inflammation in the placenta is protective against adult cardiovascular and depressive outcomes. *MedRxiv* doi: 10.1101/2023.02.20.23286171.

90. No Strong Association Between the Apolipoprotein E E4 Allele and Glaucoma: a Multicohort Study

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/37007646/	Glaucoma	Mullany S, Diaz-Torres S, Schmidt JM, et al. (2023) No Strong Association between the Apolipoprotein E E4 Allele and Glaucoma: A Multicohort Study. *Ophthalmol Sci* 3(3):100287. doi: 10.1038/s41398-020-0691-3

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37

Applied Biosystems™ Axiom™ Genotyping Solutions: Region not specified

91. Pharmacogenomics with red cells: a model to study protein variants of drug transporter genes

Variations in the human genome can lead to differences in the efficacy of drugs, ranging from a lack of therapeutic effect to drug-induced toxicity. Many of the membrane proteins of red blood cells are involved in the absorption, distribution, metabolism, and elimination of drugs (ADME). This study evaluated genes expressed in the cell membrane of red blood cells with a drug transport function using the **Axiom PharmacoScan array**. The results identified multiple genes associated with various diseases. Based on the results, the authors propose the use of red blood cells as an easily accessible ex vivo model system to assess the effects of variants of the identified membrane proteins on the pharmacokinetics of drugs.

Link	Medical Condition/Keywords	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC9108996/	Absorption, distribution, metabolism, and elimination of drugs (ADME) Preemptive pharmacogenomics	Flegel WA, Srivastava K, Sissung TM, et al. (2021) Pharmacogenomics with red cells: a model to study protein variants of drug transporter genes. *Vox Sang* 116(2):141-154. doi: 10.1111/vox.12999

92. A cross-disorder dosage sensitivity map of the human genome

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/35917817/	Developmental disorders	Collins RL, Glessner JT, Porcu E. (2022) A cross-disorder dosage sensitivity map of the human genome. *Cell* 185(16):3041-3055.e25. doi: 10.1016/j.cell.2022.06.036

93. Pharmacogenomics in stroke and cardiovascular disease: State of the art

Abstract and keywords excluded due to licensing guidelines. For detailed information and access to the publication, please follow the link provided.

Link	Medical Condition	Citation
https://pubmed.ncbi.nlm.nih.gov/36325912/	Stroke	Ross S, Krebs K, Paré G, et al. (2023) Pharmacogenomics in Stroke and Cardiovascular Disease: State of the Art. *Stroke* 54(1):270-278. doi: 10.1161/STROKEAHA.122.037717

94. Advancing pharmacogenomics from single-gene to preemptive testing

Approximately 90–95% of individuals have an actionable genotype for at least one pharmacogene. For pharmacogenomic testing to have the greatest impact on medication safety and clinical care, genetic information should be made available at the time of prescribing (preemptive testing). However, the use of preemptive pharmacogenomic testing is associated with some logistical concerns, such as consistent reimbursement, processes for reporting preemptive results over an individual's lifetime, and portability of results. Some advocate that pharmacogenomic testing should be reactive and obtained only for certain medications prior to prescribing or after a patient has had an adverse reaction to the medication or is failing therapy. Others advocate for using a preemptive pharmacogenomic testing approach as a prevention and medication safety tool. This review compares and contrasts reactive and preemptive testing and discusses the rationale for implementing pharmacogenomics preemptively along with best practices for using preemptive pharmacogenomics as a preventive tool. The review presents a pharmacogenomics program underway at St. Jude Children's Research Hospital, in which study participants are genotyped using the **Axiom PharmacoScan Array**.

Link	Medical Condition/Keywords	Citation
https://pubmed.ncbi.nlm.nih.gov/35537468/	Non-specific Preemptive pharmacogenomics	Haidar CE, Crews KR, Hoffman JM, et al. (2022) Advancing Pharmacogenomics from Single-Gene to Preemptive Testing. *Annu Rev Genomics Hum Genet* 23:449-473. doi: 10.1146/annurev-genom-111621-102737

95. Pharmacogenomic testing: Clinical evidence and implementation challenges

Technology for identifying individual-specific genetic variants (genotyping) has become more accessible and guidelines for implementation of these data are available from several organizations. Despite the increased interest in genetics in the public sphere, the rate of adoption of pharmacogenomic testing in the clinical setting has been uneven. There is a significant gap in genomic literacy among medical doctors and other health care professionals. Overall, barriers to clinical implementation of pharmacogenomic testing are driven by two primary challenges: 1) availability of evidence and cost-effectiveness to determine whether the testing should be performed at all, and (2) challenges associated with integration into the clinical system and work flow. This review highlights some of the barriers to incorporating pharmacogenomic testing into clinical practice and considers how these barriers could be surmounted. The review presents the Roche AmpliSeq CYP450 array, developed on the **Affymetrix microarray technology**, as an example of an established technology suitable for pharmacogenomics investigations.

Link	Medical Condition/Keywords	Citation
www.ncbi.nlm.nih.gov/pmc/articles/PMC6789586/	Non-specific Preemptive pharmacogenomics	Hippman C, Nislow C. (2019) Pharmacogenomic Testing: Clinical Evidence and Implementation Challenges. *J Pers Med* 9(3):40. doi: 10.3390/jpm9030040

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applied biosystems