# BENJAMIN F. VOIGHT
# CURRICULUM VITAE

Associate Professor
Department of Systems Pharmacology and Translational Therapeutics
and Department of Genetics
University of Pennsylvania – Perelman School of Medicine
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CV last updated: October 2023

## EMPLOYMENT HISTORY

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| 2017–Present | Associate Professor (with tenure),<br>Department of Systems Pharmacology and Translational Therapeutics<br>Department of Genetics<br>University of Philadelphia - Perelman School of Medicine<br>Philadelphia, PA |
| 2012–2017 | Assistant Professor, Department of Genetics<br>University of Philadelphia - Perelman School of Medicine |
| 2011–2017 | Assistant Professor, Department of Systems Pharmacology and Translational Therapeutics, University of Pennsylvania |
| 2006–2011 | Postdoctoral Research Fellow (2006-2009)<br>Research Scientist (2009-2011)<br>Advised by Drs. Mark Daly and David Altshuler<br>Massachusetts General Hospital and<br>The Broad Institute of Harvard and MIT, Cambridge, MA |

## EDUCATION

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|---|---|
| 2006 | Ph.D., Advised by Drs. Jonathan Pritchard and Nancy Cox<br>Human Genetics, University of Chicago |
| 2001 | B.S. in Biology and B.A. Mathematics<br>University of Washington, Seattle<br>[Transferred from Gonzaga University, Spokane, WA, in 1999] |

## CURRENT RESEARCH SUPPORT

***As PI:***

2020–2025 UM1 DK126193. *"Functional interrogation of T2D-associated genes in human stem-cell derived models and mice*" (MPIs: P. Seale, **B. Voight**, D. Rader, S. Grant, K. Kaestner, W. Yang)
**Objective: Using human genetics data and computational prioritization tools, identify and functionally validate candidate genes underlying susceptibility to type 2 diabetes.**

2022–2023 Institute of Translational Medicine and Therapeutics Pilot Grant. *"Interplay of obesity and volumetric breast density with respect to breast cancer risk"* (PIs: A.M. McCarthy, D. Kontos, **B. Voight**)
**Objective: Perform genome-wide association for volumetric breast density and use human genetics to perform causal inference between volumetric breast density and risk to cancer.**

***Additional:***

2022–2027 VA BX006159: "*Leveraging the genetics of carotid stenosis for identifying novel risk factors and therapeutic opportunities"* (PI: S. Damrauer). Role: Co-I.
**Objective: Use human genetics data to identify and characterize causal risk factors underlying carotid stenosis.**

2020–2024 U01 DK123594: "*The human pancreas analysis program for type 2 diabetes.*" (PIs: K. Kaestner, A. Naji). Role: Co-I.
**Objective: Obtain primary pancreatic islet specimens from deceased donors, perform multi-omics profiling and in-vivo functional characterization of islet function, and release all data to the research community.**

2020–2024 R01 DK087635: *"Epigenetic Landscape of Chronic Kidney Disease.*" (PI: K. Susztak). Role: Co-I
**Objective: Perform large-scale association studies for measures of kidney function (eGFR) and perform multi-omics profiling to identify variants and genes underlying susceptibility to chronic kidney disease.**

2016–2026 UL1 TR001878: Institutional Clinical and Translational Science Award. Role: Key personnel.
**Objective: This provides modest support for my training role as Associate Director for the Bioinformatics concentration in the Masters in Translational Research program. In this role, I serve as a bioinformatics mentor for clinicians who aim to develop bioinformatics training towards developing independence as translational researchers.**

2021–2024 R01 AI146026: "*Promoter interactome-aided mapping of unexplored CVID genetic landscapes*." (PI: N. Romberg). Role: Co-I
**Objective: To identify causal genets underlying CVID, our contribution is to create maps of variation associated with change in gene expression (eQTLs) in primary pediatric immune tissues (obtained from tonsils).**

2023–2024 I21 HX003714: "*Precision Pharmacogenomic Perioperative Prediction"* (PI: T. Barrett). Role: Co-I
**Objective: The goal of this pilot study is to improve the VA Surgical Quality Improvement Program by incorporating pharmacogenetic information into prediction.**

2021–2023 T01 BX003362: "*Genetics of Cardiometabolic Diseases in the VA Population*." (PI: P. Tsao, K-M. Chang). Role: Co-I
**Objective: Using human genetics data from the Million Veteran Program to identify and characterize risk factors for complex metabolic disease, including type 2 diabetes, cardiovascular disease, and liver disease.**

## COMPLETED SUPPORT

***As PI:***

2020–2022 Penn Chronobiology and Sleep Institute Pilot Project. "*Discovery and analysis of human genetic variation associated with circadian gene expression levels*" (PIs: **B. Voight**, C. Brown, no award number)
**Objective: A pilot project to develop computational tools to identify variation associated with gene expression over circadian (24 hour) time.**

2014–2021 NIH R01/R56 DK101478: *"Algorithms to identify non-coding mutational burden and disease-relevant pathways"*
**Objective: The goal of this proposal was to develop computational approaches to understand the role of non-coding mutational burden in type 2 diabetes.**

2019–2020 T2D Accelerating Medicine Partnerships (PIs: K. Susztak, B. Voight, M. Lazar, C. Brown), *"Prioritizing causal genes and variants for diabetic kidney disease"*
**Objective: The goal of this proposal was to identify genetic variation associated with change in gene expression in primary kidneys of patients with diabetic kidney disease.**

2019–2020 Linda Pechenik Montague Investigator Award (no award number)
**Objective: This (non-project) award supported human genetics and causal inference studies across hematopoietic and anthropometric traits.**

2018–2019 NIH R01 DK101478 S1, Supplemental support to applying developed methods to Alzheimer's disease and related traits
**Objective: The purpose of this supplement was to perform multi-trait association studies between Alzheimer's disease and neurocognitive traits and cardiometabolic traits.**

2016–2019 ITMAT Maturational Human Biology Pilot Grant: *"Characterizing the genetic determinants of pubertal timing and body weight regulation"*
**Objective: The goal of this pilot study was to perform association studies for puberty and obesity during pediatric development.**

2012–2016 AHA 13SDG14330006: "*Human genetics of high-density lipoprotein to elucidate the etiology of heart disease*"
**Objective: The goal of this study was to further explore the role of variants linked to lipid levels and heart disease risk, and develop new tools for polygenic risk score prediction.**

2013–2014 H1201 W.W. Smith Charitable Trust: "*Identifying the etiological basis for heightened risk of cardiovascular disease in the context of glycemic disorder*"
**Objective: The goal of this study was to perform multi-trait association and causal inference studies between type 2 diabetes and heart disease.**

2012–2014 Alfred P. Sloan Foundation Fellowship (No award number)
**Objective: This fellowship supported computational methods to identify balancing selection and characterize the frequency of polymorphism levels in human populations**

***Additional:***

2021–2022 MVP-DOE2: "*Phenotypic and Genomic Architecture of Cardiovascular Disease Sub*types." (PI: S. Damrauer). Role: Co-I
**Objective: Use human genetics data to characterize the basis of peripheral artery disease and perform causal inference studies.**

2019-2020 NIH R01 HG010067: "*Network-based algorithms for target identification and drug repositioning from genetic associations,"* Role: Co-I (PI: C. Greene)
**Objective: Apply tools from network-based approaches with human genetics to identify leads for drug repurposing.**

2018–2021 MVP-DOE2, "*Phenotypic and Genomic Architecture of Cardiovascular Disease Subtypes*" Role: Co-I (PIs: S. Damrauer)
**Objective: Use human genetics data to characterize the basis of peripheral artery disease and perform causal inference studies.**

2015–2016 March of Dimes Preterm Birth Research Center Grant. (Role: Co-Investigator).

**Objective: To characterize the genetics of pre-term birth and causal genes.**

## PENDING SUPPORT

***As PI:***

2023–2028 R01 DK136823. *"Systematic target validation for non-alcoholic fatty liver disease using computational approaches and in vivo deep phenotyping*" (MPIs: M. den Hoed, **B. Voight (contact)**)
**Objective: To characterize causal variants and genes for non-alcoholic fatty liver disease and perform medium-throughput functionally validation of candidates using the zebrafish model system using high dimension imaging analysis.**

2023-2028 U24 DK138512. "*An interactive resource to generate and provide integrated knowledge of the human pancreas"* (MPIs: K. Gaulton, J. Flannick, N. Burtt, A. Gloyn, **B. Voight**)
**Objective: To develop a platform for investigation for type 1 diabetes, which hosts aggregated data, providing an analytics library and computational workflows for analysis, with collaborative outreach efforts to the diabetes community.**

2024-2029 R01 HG013499. *"Methods for inference of mutation rate and functional constraint with applications in human health".* (MPIs: Z. Gao, I. Mathieson, **B. Voight (contact))**
**Objective: Using a novel computational method we recently developed this proposal will create best-in-class models that capture variability in mutation rates across species, quantifying functional constraint in across the human genome, applying that knowledge to prioritize variants at non-coding complex disease associated signals likely to be causal.**

2024-2029 R01 NIDDK # pending. *"Mapping the gene regulatory architecture of pancreatic islet-specific cell types to diabetes".* (MPIs: K. Gaulton, **B. Voight (contact)**)
**Objective: Use single-cell genomics data generated from pancreatic islets to map variation associated with expression and chromatin accessibility and to characterize cis-regulatory elements across all islet-specific cell types.**

## AWARDS AND HONORS

2019 Recipient of the Linda Pechenik Montague Investigator Award (see also Grants)
2017 Penn Medicine Award of Excellence Recipient: The Michael S. Brown New Investigator Research Award
2017 Recipient of the 2014 Presidential Early Career Award for Scientist and Engineers (PECASE), Department of Health and Human Services
2012 Selected Alfred P. Sloan Research Fellow (see also Grants)

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| 2009 | Semi-finalist, Trainee Research Award, 59th Meeting of the American Society of Human Genetics |
| 2007 | Team Award for Outstanding Research, Clinical Research Day, Massachusetts General Hospital |
| 2006 | PhD Dissertation Award, Best in the Biological Sciences Division, University of Chicago |
| 2006 | New York Times Front Page News article, “Still evolving, human genes tell new story” (Voight et al, see Ref #3) |
| 2000-2006 | Numerous travel awards and scholarships (MSRI/PMMB, Keystone Symposium, NHGRI, etc.) |
| 1998-1999 | McDonald’s Fellowship for Biological Studies, Gonzaga University |
| 1997-1999 | Academic Merit Scholarship and Academic Debate Scholarship, Gonzaga University |

## PROFESSIONAL ACTIVITIES

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|---|---|
| 2018–Present | Chair, Genomics and Computational Biology Graduate Group, University of Pennsylvania |
| 2018–Present | Statistical Reviewer, *JAMA Network Open* |
| 2018–Present | Associate Director (Bioinformatics Concentration) of the Master of Science in Translational Research program, University of Pennsylvania |
| 2017–Present | Associate Editor, *Circulation: Genomic and Precision Medicine* |
| 2012–Present | Member: The American Diabetes Association<br>Member: The American Heart Association |
| 2011–Present | Member of numerous Penn internal committees (e.g. Curriculum Committee for GCB and GGR, task force for graduate biostatistics, CTSA KL2/ITMAT fellowship reviewer, IBI Faculty Search, Genetics Faculty Search, PennOmics Governance, ITMAT Junior Investigator Symposium, etc.). |
| 2002–Present | External referee for numerous journals (*Nature*, *Nature Genetics, Cell, Lancet, JAMA, PLoS Medicine, Science Advances*, *Bioinformatics, ATVB, JACC, AJHG,* many others.) |
| 2001–Present | Member: American Society of Human Genetics |
| 2022 | Reviewer, VA 2023/01 ZRD1 GAST-L (01) 1, BL/CS Merit Review |
| 2022 | Reviewer, NIH 2022/10 GHD |
| 2022 | Reviewer, NIH ZRG1 2022/05 ZRG1 GGG-S(55) R (PAR-20-117) |
| 2020 | Reviewer, NIH ZRG1 PSE-C(90) Special Emphasis Panel, |
| 2020 | Reviewer, NIH RFA-DK19-014, “Catalyst Award in Diabetes, Endocrinology and Metabolic Diseases” |
| 2018–2020 | Associate Editor, *bioverlay.org* |
| 2015–2018 | Vice Chair, Genomics and Computational Biology Graduate Group, University of Pennsylvania |
| 2012–2018 | Co-organizer of the Penn Bioinformatics Forum (with Yoseph Barash) |
| 2012–2018 | Editorial Review Board, *Frontiers* (Pop Gen, Stat Gen) |
| 2015–2017 | Editorial Board Member, *Circulation: Cardiovascular Genetics* |
| 2016–2017 | Member, American Heart Association’s Institute for Precision Cardiovascular Medicine Data Science and Technology Committee |
| 2016 | Reviewer, NIH Special Emphasis Panel for RFA-DK-15-025, NIH/NIDDK |

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| 2016-17, 2019 | Program Committee, RECOMB Satellite Meeting on Computational Methods in Genetics |
| 2013-14, 2017 | Reviewer for American Heart Association GTOE Study Section |
| 2013–2014 | Associate Scientific Advisor, *Science Translational Medicine* |
| 2013 | Ad hoc reviewer, NIH Special Emphasis Panel for K23/K99 Career Awards, NIH/NIEHS |

## INVITED LECTURES (OUTSIDE PHILADELPHIA, SINCE 2017 PROMOTION TO ASSOCIATE)

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| 2023 | SugarScience Webinar Series |
| 2023 | Festival of Genomics and Biodata, Boston, MA |
| 2023 | Accelerating Medicines Partnerships Common Metabolic Disease Parliament Meeting, Boston, MA |
| 2022 | Invited Seminar, Rutgers Institute for Translational Medicine and Science (RITMS), Rutgers University, New Brunswick, NJ |
| 2020 | 70th Annual Meeting of the American Society of Human Genetics (held virtually) |
| 2020 | European Society of Human Genetics, Berlin Germany (held virtually) |
| 2019 | Invited Seminar, Regeneron Pharmaceuticals, Tarrytown, NY |
| 2019 | Big Data Institute Seminar Series, University of Oxford, Oxford, UK |
| 2019 | Special Seminar, University of Exeter, Exeter UK |
| 2019 | 4th International Conference on Mendelian Randomization, University of Bristol, Bristol, UK |
| 2019 | Special Seminar, Glaxo-Smith-Kline, Cambridge UK |
| 2019 | MRC Epidemiology Unit Special Seminar, University of Cambridge, Cambridge UK |
| 2019 | Department of Human Genetics Seminar Series Alumni Speaker, University of Chicago, IL |
| 2019 | Research Seminar Series, Brigham Young University, Provo, UT |
| 2018 | Research Seminar Series, HudsonAlpha Institute for Biotechnology, Huntsville, AL |
| 2018 | Integrated Biosciences Seminar Series, University of Akron, Akron, OH |
| 2018 | Million Veteran's Program Science Conference, Nashville, TN |
| 2017 | Center for Computational Medicine and Bioinformatics Seminar Series, University of Michigan, Ann Arbor, MI |
| 2017 | 5 Points Seminar Series, New York Genome Center, New York, NY |
| 2017 | Bioinformatics Seminar Series, GlaxoSmithKline, King of Prussia, PA |
| 2017 | 67th Annual Meeting of the American Society of Human Genetics (Invited Session Organizer), Orlando, FL |
| 2017 | Five Points Lecture Series, New York Genome Center, New York, NY |
| 2017 | Genetics and Bioinformatics Seminar Series, Glaxo-Smith-Kline, King of Prussia, PA |

## INVITED LECTURES (OUTSIDE PHILADELPHIA, 2011-2017)

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| 2017 | American Diabetes Association's 77th Annual Meeting, San Diego, CA |
| 2017 | Genome Sciences Seminar Series, Center for Public Health Genomics, University of Virginia, Charlottesville, VA |

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| 2016 | Program in Quantitative Genomics Seminar Series, Harvard School of Public Health, Boston, MA |
| 2016 | Frontiers in Bioinformatics and Systems Biology Seminar Series, University of California, San Diego, CA |
| 2016 | Genetics Institute Seminar Series, Vanderbilt University, TN |
| 2016 | Institute for Personalized Medicine seminar Series, Icahn School of Medicine, Mount Sinai, NY |
| 2016 | Seminar Series, University of California at Los Angeles, CA |
| 2016 | CIHR – Strategic Training for Advanced Genetic Epidemiology International Speaker Seminar Series, University of Toronto, Canada |
| 2016 | New York Area Population Genomics Workshop, Princeton University |
| 2015 | Department of Genetics Seminar Series, Yale University, NH |
| 2013 | Bioscience Conference on Genomics in Medicine, Copenhagen, Denmark |
| 2013 | Keynote Lecture, American Heart Association Epi\|NPAM Council's Spring Conference, New Orleans, LA |
| 2013 | 73rd Meeting of the American Diabetes Association, Chicago, IL |
| 2012 | 62nd Annual Meeting of the American Society of Human Genetics (Invited Session Organizer), San Francisco, CA |
| 2012 | Medical Population Genetics Seminar Series, The Broad Institute of Harvard and MIT, Cambridge, MA |
| 2012 | Department of Biology Seminar Series, University of Vermont, Burlington, VT |
| 2012 | Session Co-Chair, 25th Annual Cold Spring Harbor Meeting, Biology of Genomes, Cold Spring Harbor, NY |
| 2011 | 1st Annual Illumina America's Scientific Summit, Clearwater Beach, FL |
| 2011 | Botnia 20th Anniversary Symposium, Lund University, Vaasa, Finland |
| 2011 | The 2011 European Human Genetics Conference, Amsterdam RAI, The Netherlands |
| 2011 | National Institute of Genomic Medicine in Mexico, Ciudad de México, Mexico |

## TEACHING ACTIVITIES

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|---|---|
| 2013–2019, 2021-Present | Co-Director, *Introduction to Bioinformatics* (CIS/MTR/GCB5350)<br>Undergrad/grad/post-doc/MD/MD+PhD, ~90 students<br>Includes lectures and administrative responsibilities.<br>100+ hours total, 50+ direct contact |
| 2019–Present | Guest Lecturer, *Statistics for Genomics and Biomedical Informatics* (GCB533) |
| 2019–Present | Guest Lecturer, *Professional Development Series,* MSTR Program |
| 2015–Present | Guest Lecturer, CTSA Summer Internship Seminar |
| 2022 | Director, *Introduction to Bioinformatics* - Independent Study (GCB999) |
| 2014 | Guest Lecturer, *Biology of Human Disease* (BIOL015) |
| 2013 | Guest Lecturer, *Advanced Computational Biology* (GCB537) |
| 2012 | Guest Lecturer, *Introduction to Genome Sciences* (GCB534) |
| 2012-2013 | Lecturer, Medical School Module One, *Genetic Foundations of Disease* |
| 2006–2011 | Organizer of several workshops in statistical genetic analysis |

## STUDENT AND POSTDOCTORAL MENTORSHIP

### *CURRENT MENTEES*

2023–Present Brandon Wenz (PhD Student, GE)

2021–Present Da (Mia) Lee (PhD Student, PGG)
- Selected for Genomics T32 (2023)

2021–Present Mitch Conery (PhD Student, GCB, joint with Struan Grant)
- Selected for Genomics T32 (2022)
- Reviewer's Choice Abstract, ASHG (2023)

2021–Present Mary Ann Hazuga (PhD Student, GCB, joint with Struan Grant)

### *PREVIOUS MENTEES*

#### POST-DOCTORAL FELLOWS

2020–2022 Louise Wang (Post-doc, MD Gastroenterology Fellow)
- *VA CDA Award (2022)*
- *Now: Assistant Professor of Medicine, Yale School of Medicine, Section of Digestive Diseases*

2015–2021 Chris Thom (Post-doc, MD/PhD Neonatology Resident)
- *CHOP Senior Resident Research Award (2017)*
- *Selected for Pediatrics T32 (2017)*
- *Foerderer Research Award (2018)*
- *Marshall Klaus Neonatal-Perinatal Research Award (2019)*
- *Philadelphia Perinatal Society Thomas Boggs Research Award (2019)*
- *61st American Society of Hematology Annual Meeting Abstract Achievement Award (2019)*
- *CHOP K-readiness Award (2019)*
- *Eastern Society of Pediatric Research Trainee Young Investigator Award Finalist (2020)*
- *CHOP Distinguished Research Trainee Award (2020)*
- *SPR Fellows' Basic Science Award (2020)*
- *K99 Award Recipient (2021)*
- *Now: Assistant Professor of Pediatrics, Children's Hospital of Philadelphia*

2015–2020 Diana Cousminer (Post-doc, joint with Struan Grant)
- *Young Investigator Travel award, ASBMR Bone-omics Symp. (2016)*
- *ADA Postdoc Fellowship Award Recipient (2016-2018)*
- *ASBMR Young Investigator Award (2018)*
- *CHOP Distinguished Research Trainee Award (2019)*
- *K99 Award recipient (2019-2021)*
- *ASHG Charles J. Epstein Post-doc Award Recipient (2019)*
- *Now: Scientific Leader, GSK*

2012–2017 Paul Babb (Post-doc)
- *Post-doc Symposium Poster Award (2014)*
- *Now, Research Scientist, Karius Inc.*

2015–2017 Kim Lorenz (Post-doc)
- *Selected for a Diabetes/Endocrine Post-doc T32 (2015-2016)*
- *Now: Bioinformatician in my group*

## PHD CANDIDATES

2018–2023 Chris Adams (PhD Student, GCB)
- *Now: Quantitative Analyst, Philadelphia Phillies*

2018–2023 Will Bone (PhD Student, GCB, joint with Marylyn Ritchie)
- *AHA Predoctoral Fellowship (2020-2022)*
- *2020 ASHG Abstract Reviewer's Choice Award*
- *Travel Award, 2021 CHARGE Consortium Meeting (Virtual)*
- *2023 Recipient - Saul Winegrad Award for Best Dissertation (GCB)*
- *Now: Computational Biologist, Recursion, Inc.*

2016–2021 Katerina Gawronski (PhD Student, GE, joint with Casey Brown)
- *Selected for Genetics T32 (2016-2018)*
- *American Polish Cultural Society Scholarship (2016-2019)*
- *SAGES Poster Award (2018)*
- *AHA Predoctoral Fellowship (2019-2021)*
- *ASHG Charles J. Epstein Pre-doc Award Semi-Finalist (2019)*
- *Now: Senior Consultant, ClearView (Newton, MA)*

2014–2019 Kelsey Johnson (PhD Student, GE)
- *Selected for Genetics T32 (2014-2016)*
- *Now: Post-doc, Blehkman and Albert Labs (U. of Minnesota)*

2014–2018 Katie Siewert (PhD Student, GCB)
- *Selected for Genomics and Computational Biology T32 (2015-2017)*
- *2019 Recipient - Saul Winegrad Award for Best Dissertation (GCB)*
- *Now: Senior Research Scientist in Computational Genomics, Vertex*

2012–2016 Varun Aggarwala (PhD Student, GCB)
- *Semi-finalist for the ASHG Charles J. Epstein Trainee Award (2015)*
- *Penn Genetics Retreat Poster Award (2015)*
- *Post-doc, Faith Lab, Mt. Sinai*
- *Now: Asst. Professor, JIO Institute, Navi Mumbai, India*

## MASTER'S CANDIDATES

2018–2021 Zhuoran Ding (Masters in Biostatistics, GGEB)
- *Now: PhD Student, GGEB, Univ. of Pennsylvania*

2018 Kaushik Visvanathan (Master's student, CS)

2016–2018 Onur Yörük (Masters in Genomics and Computational Biology, GCB)

## UNDERGRADUATE / POST-BACS

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|---|---|
| 2022 | Sanjana Akula (Undergraduate, SAS) |
| 2020–2022 | Brian Chen (Undergraduate, SAS) |
| 2018–2020 | Sanjana Adurty (Undergraduate, SAS) |
| | *- Now: Medical School, Univ. of Pittsburgh* |
| 2015–2017 | Rachael ("Rocky") Aikens (Swarthmore Undergrad) |
| | *- Penn Summer Undergrad Internship Program (2016)* |
| | *- Penn CTSA Summer Internship (2015)* |
| | *- Now: Statistician, Mathematica (Policy Research)* |
| 2015–2016 | David Nicholson (Post-Bac) |
| | *- Selected for the Penn Summer Undergrad Intership Program (2014)* |
| | *- Selected for the PennPrep Program (2015)* |
| | *- Now: Data Scientist at Digital Science and Research Solutions Ltd.* |
| 2013–2015 | Peter Yin (Undergrad) |
| | *- Undergraduate Research and Fellowship Recipient (2015)* |
| | *- Now: Automation Engineer, Zymogen, Emeryville CA* |

## PUBLICATIONS (FROM 161 PAPERS, H-INDEX=83, CITATIONS=75,461)

### LINK TO FULL PUBLICATION LIST:

**https://www.ncbi.nlm.nih.gov/myncbi/benjamin.voight.1/bibliography/public/**

### *PREPRINTS*

[1] Hui D, Thom CS, Lorenz K, Damrauer SM, Assimes TL, **Voight BF**. Mendelian randomization analyses reveal mediating factors of the causal effect of height on coronary artery disease. medRxiv. 2023 May 5:2021.12.16.21267869. doi: 10.1101/2021.12.16.21267869. [r]

[2] Suzuki K, Hatzikotoulas K, Southam L, Taylor HJ, Yin X, Lorenz KM, …, VA Million Veteran Program, …, McCarthy MI*, Meigs JB*, Boehnke M*, Rotter JI*, Vujkovic M*, **Voight BF***, Morris AP*, Zeggini E*. Multi-ancestry genome-wide study in >2.5 million individuals reveals heterogeneity in mechanistic pathways of type 2 diabetes and complications. medRxiv. 2023 Mar 31:2023.03.31.23287839. doi: 10.1101/2023.03.31.23287839. [r]

[3] Tsao NL, Judy R, Levin MG, Shakt G; Regeneron Genetics Center; Penn Medicine BioBank; **Voight BF**, Chen J, Damrauer SM. Evaluation of the Performance of the RECODe Equation with the Addition of Polygenic Risk Scores for Adverse Cardiovascular Outcomes in Individuals with Type II Diabetes. medRxiv. 2023 May 5:2023.05.03.23289457. doi: 10.1101/2023.05.03.23289457.

[4] Verma A, Huffman JE, Rodriguez A, Conery M, Liu M, Ho YL, Kim Y, Heise DA, Guare L, Panickan VA, Garcon H, Linares F, Costa L, Goethert I, Tipton R, Honerlaw J, Davies L, Whitbourne S, Cohen J, Posner DC, Sangar R, Murray M, Wang X, Dochtermann DR, Devineni P, Shi Y, Nandi TN, Assimes TL, Brunette CA, Carroll RJ, Clifford R, Duvall S, Gelernter J, Hung A, Iyengar SK, Joseph J, Kember R, Kranzler H, Levey D, Luoh SW,

Merritt VC, Overstreet C, Deak JD, Grant SFA, Polimanti R, Roussos P, Sun YV, Venkatesh S, Voloudakis G, Justice A, Begoli E, Ramoni R, Tourassi G, Pyarajan S, Tsao PS, O'Donnell CJ, Muralidhar S, Moser J, Casas JP, Bick AG, Zhou W, Cai T, **Voight BF**, Cho K, Gaziano MJ, Madduri RK, Damrauer SM, Liao KP. Diversity and Scale: Genetic Architecture of 2,068 Traits in the VA Million Veteran Program. medRxiv. 2023 Jun 29:2023.06.28.23291975. doi: 10.1101/2023.06.28.23291975. [r]

[5] Lee DSM, DePaolo JS, Aragam KG, Biddinger K, Conery M, Dilitikas O, Hoffman-Andrews L, Judy RL, Khan A, Kulo I, Puckelwartz MJ, Reza N, Satterfield BA, Singhal P; Regeneron Genetics Center; Arany ZP, Cappola TP, Carruth E, Day SM, Do R, Haggarty CM, Joseph J, McNally E, Nadkarni G, Owens AT, Rader DJ, Ritchie MD, Sun Y, **Voight BF**, Levin MG, Damrauer SM. Common- and rare-variant genetic architecture of heart failure across the allele frequency spectrum. medRxiv. 2023 Jul 19:2023.07.16.23292724. doi: 10.1101/2023.07.16.23292724.

[6] Yuan S, Li Y, Wang L, Xu F, Chen J, Levin MG, Xiong Y, Voight BF, Damrauer SM, Gill D, Burgess S, Åkesson A, Michaëlsson K, Li X, Shen X, Larsson SC. Deciphering the genetic architecture of atrial fibrillation offers insights into disease prediction, pathophysiology and downstream sequelae. medRxiv. 2023 Jul 25:2023.07.20.23292938. doi: 10.1101/2023.07.20.23292938.

## ***SELECTED KEY PUBLICATIONS* [FROM >150 PAPERS]**

*: DENOTES EQUAL CONTRIBUTION

[1] **Voight BF**, Pritchard JK. (2005). Confounding from cryptic relatedness in case-control association studies. *PLoS Genet.* 1(3): e32.

[2] **Voight BF***, Adams AA*, Frisse L, Quan Y, Hudson RR, Di Rienzo A. (2005). Interrogating multiple aspects of variation in a full resequencing data set to infer human population size changes. *Proc Natl Acad Sci USA* 102(51):18508-18513.

[3] **Voight BF***, Kudaravalli S*, Wen X, Pritchard JK. (2006). A map of recent positive selection in the human genome. *PLoS Biol.* 4(3): e72. PMCID: PMC1382018

[4] Tishkoff SA, Reed FA, Ranciaro A, **Voight BF**, Babbitt CC, Silverman JS, Powell K, Mortensen HM, Hirbo JB, Osman M, Ibrahim M, Omar SA, Lema G, Nyambo TB, Ghori J, Bumpstead S, Pritchard JK, Wray GA, Deloukas P. (2007) Convergent adaptation of human lactase persistence in Africa and Europe. *Nat. Genet.* 39(1): 31-40.

[5] Saxena R, **Voight BF**, Lyssenko V, Burtt NP, …, Ricke D, Purcell S. (2007) Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science* 316(5829): 1331-1336.

[6] de Bakker PIW, Ferreira MA, Jia X, Neale BM, Raychaudhuri S, **Voight BF**. (2008). Practical aspects of imputation-driven meta-analysis of genome-wide association studies. *Hum Mol Genet*. 17(R2): R122-R128.

[7] Zeggini E*, Scott LJ*, Saxena R*, **Voight BF*** on behalf of the DIAGRAM Consortium. (2008). Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nat. Genet. 40(5): 638-645.

[8] Kathiresan S, Melander O, Guiducci C, Surti A, Burtt NP, Rieder MJ, Cooper GM, Roos C, **Voight BF**, Havulinna AS, Wahlstrand B, Hedner T, Corella D, Tai ES, Ordovas JM, Berglund G, Vartiainen E, Jousilahti P, Hedblad B, Taskinen MR, Newton-Cheh C, Salomaa V, Peltonen L, Groop L, Altshuler DM, Orho-Melander M. (2008) Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. Nat Genet. 2008 Feb;40(2):189-97.

[9] Kathiresan S, **Voight BF**, Purcell S, Musunuru K, …, Salomaa V, Schwartz SM. (2009) Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nat Genet*. 41(3): 334-341.

[10] **Voight BF***, Scott LJ*, Steinthorsdottir V*, Morris AP*, Dina C* on behalf of the DIAbetes Genome-wide Replication and Meta-Analysis (DIAGRAM) Consortium. (2010). Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nat Genet*. 42(7): 579-589.

[11] Pulit SL, **Voight BF**, de Bakker PI. (2010). Multiethnic genetic association studies improve power for locus discovery. *PLoS ONE* 5(9): e12600.

[12] Guey LT, Kravic J, Melander O, Burtt NP, Laramie JM, Lyssenko V, Jonsson A, Lindholm E, Tuomi T, Isomaa B, Nilsson P, Almgren P, Kathiresan S, Groop L, Seymour AB, Altshuler D, **Voight BF**. (2011). Power in the phenotypic extremes: A simulation study of power in discovery and replication of rare variants. *Gen Epidemiol*. 35(4): 236-246.

[13] Neale BM, Rivas MA, **Voight BF**, Altshuler D, Devlin B, Orho-Melander M, Kathiresan S, Purcell SM, Roeder K, Daly MJ. (2011). Testing for an unusual distribution of rare variants. *PLoS Genet*. 7(3): e1001322.

[14] Cotsapas C*, **Voight BF***, Rossin E, Lage K, Neale BM, Wallace C, Abecasis GR, Barrett JC, Behrens T, Cho J, De Jager PL, Elder JT, Graham RR, Gregersen P, Klareskog L, Siminovitch KA, van Heel DA, Wijmenga C, Worthington J, Todd JA, Hafler DA, Rich SS, Daly MJ; on behalf of the FOCiS Network of Consortia. (2011). Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genet*. 7(8): e1002254.

[15] Bumgarner SL, Neuert G, **Voight BF**, Symbor-Nagrabska A, Grisafi P, van Oudenaarden A, Fink GR. (2012) Single-Cell Analysis Reveals that Noncoding RNAs Contribute to Clonal Heterogeneity by Modulating Transcription Factor Recruitment. *Mol. Cell* Feb 24; 45(4):470-82.

[16] Stahl EA, Wegmann D, Trynka G, Gutierrez-Achury J, Do R, **Voight BF**, Kraft P, Chen R, Kallberg HJ, Kurreeman FA; Diabetes Genetics Replication and Meta-analysis Consortium; Myocardial Infarction Genetics Consortium, Kathiresan S, Wijmenga C, Gregersen PK, Alfredsson L, Siminovitch KA, Worthington J, de Bakker PI, Raychaudhuri S, Plenge RM. (2012). Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. *Nat Genet*. Mar 25;44(5):483-9.

[17] Neale BM, Kou Y, Liu L, Ma'ayan A, Samocha KE, Sabo A, Lin CF, Stevens C, Wang LS, Makarov V, Polak P, Yoon S, Maguire J, Crawford EL, Campbell NG, Geller ET, Valladares O, Schafer C, Liu H, Zhao T, Cai G, Lihm J, Dannenfelser R, Jabado O, Peralta Z, Nagaswamy U, Muzny D, Reid JG, Newsham I, Wu Y, Lewis L, Han Y, **Voight BF**, …, Gibbs RA, Roeder K, Schellenberg GD, Sutcliffe JS, Daly MJ. (2012) Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature* Apr 4;485(7397):242-5.

[18] **Voight BF***, Peloso GM*, Orho-Melander M, Frikke-Schmidt R, Barbalic M, Jensen MK, …, O'Donnell CJ, Salomaa V, Rader DJ, Peltonen L, Schwartz SM, Altshuler D, Kathiresan S. Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet* Aug 11;380(9841):572-802.

[19] Perry JR, **Voight BF**, Yengo L, Amin N, Dupuis J, …, Frayling TM, Cauchi S. (2012). Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genet*. May;8(5):e1002741.

[20] **Voight BF***, Kang HM*, Ding J, Palmer CD, Sidore C, Chines PS, Burtt NP, Fuchsberger C, Li Y, Erdmann J, et al. (2012). The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genet*. Aug;8(8):e1002793.

[21] Morris AP*, **Voight BF***, Teslovich TM*, Ferreira T*, Segrè AV*, Steinthorsdottir V, Strawbridge RJ, Khan H, Grallert H, Mahajan A, et al. (2012). Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat. Genet*. Aug 12;44(9):981-990.

[22] **Voight BF**, Cotsapas C (2012). Human genetics offers an emerging picture of common pathways and mechanisms in autoimmunity. *Curr Opin Immunol*. Oct;24(5):552-7.

[23] Georgi B, **Voight BF**, Bućan M (2013). From mouse to human: evolutionary genomics analysis of human orthologs of essential genes. *PLoS Genet*. May;9(5):e1003484.

[24] Flannick J, Thorleifsson G, Beer NL, Jacobs SB, Grarup N, Burtt NP, Mahajan A, Fuchsberger C, Atzmon G, Benediktsson R, …, **Voight BF**, Wilson JG, Boehnke M, McCarthy MI, Njølstad PR, Pedersen O, Groop L, Cox DR, Stefansson K, Altshuler D. (2014). Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genet.* Apr 4;46(4):357-363.

[25] Prokopenko I, Poon W, Mägi R, Prasad B R, Salehi SA, Almgren P, Osmark P, Bouatia-Naji N, Wierup N, Fall T, …, **Voight BF**, et al. (2014). A central role for GRB10 in regulation of islet function in man. *PLoS Genet* Apr 3;10(4):e1004235.

[26] MacArthur DG, Manolio TA, Dimmock DP, Rehm HL, Shendure J, Abecasis GR, Adams DR, Altman RB, Antonarakis SE, Ashley EA, Barrett JC, Biesecker LG, Conrad DF, Cooper GM, Cox NJ, Daly MJ, Gerstein MB, Goldstein DB, Hirschhorn JN, Leal SM, Pennacchio LA, Stamatoyannopoulos JA, Sunyaev SR, Valle D, **Voight BF**, Winckler W, Gunter C (2014). Guidelines for investigating causality of sequence variants in human disease. *Nature* Apr 24;508:469-476.

[27] **Voight, BF** (2014). MR_predictor: a simulation engine for Mendelian Randomization studies. *Bioinformatics.* Dec 1; 30(23):3432-4.

[28] Yin, P and **Voight, BF** (2015). MeRP: a high-throughput pipeline for Mendelian Randomization Analysis. *Bioinformatics.* Mar 15;31(6):957-9.

[29] Jansen H, Loley C, Lieb W, Pencina MJ, Nelson CP, Kathiresan S, Peloso GM, **Voight BF**, Reilly MP, Assimes TL, Boerwinkle E, Hengstenberg C, Laaksonen R, McPherson R, Roberts R, Thorsteinsdottir U, Peters A, Gieger C, Rawal R, Thompson JR, König IR; CARDIoGRAM consortium, Vasan RS, Erdmann J, Samani NJ, Schunkert H.

(2015) Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis* Jun 3;241(2):419-426.

[30] Soccio RE, Chen ER, Rajapurkar SR, Safabakhsh P, Marinis JM, Dispirito JR, Emmett MJ, Briggs ER, Fang B, Everett LJ, Lim HW, Won KJ, Steger DJ, Wu Y, Civelek M, **Voight BF**, Lazar MA. (2015) Genetic Variation Determines PPARγ Function and Anti-diabetic Drug Response in Vivo. *Cell* Jul 2;162(1):33-44.

[31] Gaulton KJ, Ferreira T, Lee Y, Raimondo A, Mägi R, …, **Voight BF**, et al. (2015) Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nat Genet.* 2015 Dec;47(12):1415-25.

[32] Keenan T, Zhao W, Rasheed A, Ho WK, Malik R, …, Rader DJ, **Voight BF***, Saleheen D*. Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. J Am Coll Cardiol. 2016 Feb 2;67(4):407-16.

[33] Aggarwala V, and **Voight BF**. An expanded sequence context model broadly explains variability in polymorphism levels across the human genome. *Nat Genet*. 2016 Apr;48(4):349-55.

[34] Cousminer DL, Arkader A, **Voight BF**, Pacifici M, Grant SF. Assessing the general population frequency of rare coding variants in the EXT1 and EXT2 genes previously implicated in hereditary multiple exostoses. Bone. 2016 Sep 9;92:196-200.

[35] Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, …, **Voight BF** et al. The genetic architecture of type 2 diabetes. *Nature*. 2016 Aug 4;536(7614):41-7.

[36] Cousminer DL, Arkader A, **Voight BF**, Pacifici M, Grant SF. Assessing the general population frequency of rare coding variants in the EXT1 and EXT2 genes previously implicated in hereditary multiple exostoses. Bone. 2016 Nov;92:196-200.

[37] Aikens RC, Zhao W, Saleheen D, Reilly MP, Epstein SE, Tikkanen E, Salomaa V, **Voight BF**. Systolic Blood Pressure and Risk of Type 2 Diabetes: a Mendelian Randomization Study. Diabetes. 2017 Feb;66(2):543-550.

[38] Yin P, Anttila V, Siewert KM, Palotie A, Smith GD, **Voight BF**. Serum calcium and risk of migraine: a Mendelian randomization study. Hum Mol Genet. 2017 Feb 15;26(4):820-828

[39] Aggarawala V, Ganguly A, **Voight BF**. *De novo* mutational profile in RB1 clarified using a mutation rate modeling algorithm. *BMC Genomics.* 2017 Feb 14;18(1):155.

[40] Brynedal B, Choi J, Raj T, Bjornson R, Stranger BE, Neale BM, **Voight BF**, Cotsapas C. Large-Scale trans-eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. Am J Hum Genet. 2017 100(4):481-591.

[41] Mishra R, Chesi A, Cousminer DL, Hawa MI, Bradfield JP, Hodge KM, Guy VC, Hakonarson H, Bone Mineral Density in Childhood Study, Mauricio D, Schloot NC, Yderstræde KB, **Voight BF**, Schwartz S, Boehm BO, Leslie RD, Grant SFA. Relative contribution of type 1 and type 2 diabetes loci to the genetic etiology of adult-onset, non-insulin-requiring autoimmune diabetes. BMC Med. 2017 Apr 25;15(1):88.

[42] Babb PL, Lahens NF, Correa-Garhwal SM, Nicholson DN, Kim EJ, Hogenesch JB, Kuntner M, Higgins L, Hayashi CY, Agnarsson I, **Voight BF**. The *Nephila clavipes* genome

highlights the diversity of spider silk genes and their complex expression. Nat. Genet. 2017 Jun;49(6):895-903.

[43] Scott RA, Scott LJ, Mägi R, Marullo L, Gaulton KJ, …, **Voight BF**, Morris AP, Boehnke M, McCarthy MI, Prokopenko I. An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*. 2017 Nov;66(11):2888-2902

[44] Zhao W, Rasheed A, Tikkanen E, Lee JJ, …, **Voight BF***, Saleheen D*. Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nat. Genet. 2017 Oct;49(10):1450-1457.

[45] Siewert KM and **Voight BF**. Detecting Long-term Balancing Selection Using Allele Frequency Correlation. Mol. Biol. Evol. 2017 Nov;1;34(11):2996-3005.

[46] Tragante V, Gho JMIH, Felix JF, Vasan RS, Smith NL, **Voight BF**; CHARGE Heart Failure Working Group, Palmer C, van der Harst P, Moore JH, Asselbergs FW. Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Min. 2017 May 26;10:18.

[47] Cousminer DL, Mitchell JA, Chesi A, Roy SM, Kalkwarf HJ, Lappe JM, Gilsanz V, Oberfield SE, Shepherd JA, Kelly A, McCormack SE, **Voight BF**, Zemel BS, Grant SF. Genetically Determined Later Puberty Impacts Lowered Bone Mineral Density in Childhood and Adulthood. *J Bone Miner Res*. 2018 Mar;33(3):430-436.

[48] Johnson KE and **Voight BF**. Patterns of shared signatures of recent positive selection across human populations. *Nat Ecol Evol*. 2018 Apr;2(4):713-720.

[49] Khetarpal SA, Babb PL, Zhao W, Hancock-Cerutti WF, Brown CD, Rader DJ, **Voight BF**. Multiplexed Targeted Resequencing Identifies Coding and Regulatory Variation Underlying Phenotypic Extremes of High-Density Lipoprotein Cholesterol in Humans. *Circ Genom Precis Med*. 2018 Jul;11(7):e002070.

[50] Cousminer DL, Ahlqvist E, Mishra R, Andersen MK, Chesi A, Hawa MI, Davis A, Hodge KM, Bradfield JP, Zhou K, Guy VC, Åkerlund M, Wod M, Fritsche LG, Vestergaard H, Snyder J, Højlund K, Linneberg A, Käräjämäki A, Brandslund I, Kim CE, Witte D, Sørgjerd EP, Brillon DJ, Pedersen O, Beck-Nielsen H, Grarup N, Pratley RE, Rickels MR, Vella A, Ovalle F, Melander O, Harris RI, Varvel S, Grill VER; Bone Mineral Density in Childhood Study, Hakonarson H, Froguel P, Lonsdale JT, Mauricio D, Schloot NC, Khunti K, Greenbaum CJ, Åsvold BO, Yderstræde KB, Pearson ER, Schwartz S, **Voight BF**, Hansen T, Tuomi T, Boehm BO, Groop L, Leslie RD, Grant SFA. First Genome-Wide Association Study of Latent Autoimmune Diabetes in Adults Reveals Novel Insights Linking Immune and Metabolic Diabetes. *Diabetes Care*. 2018 Nov;41(11):2396-2403.

[51] Siewert KM and **Voight BF**. Bivariate Genome-Wide Association Scan Identifies 6 Novel Loci Associated With Lipid Levels and Coronary Artery Disease. *Circ Genom Precis Med.* 2018 Dec;11(12):e002239.

[52] Cousminer DL, McCormack SE, Mitchell JA, Chesi A, Kindler JM, Kelly A, **Voight BF**, Kalkwarf HJ, Lappe JM, Shepherd JA, Oberfield SE, Gilsanz V, Zemel BS, Grant SFA. Postmenopausal osteoporotic fracture-associated COLIA1 variant impacts bone accretion in girls. *Bone*. 2019 Apr;121:221-226.

[53] Aikens RC, Johnson KE, **Voight BF**. Signals of variation in human mutation rate at multiple levels of sequence context. Mol Biol Evol. 2019 May 1;36(5):955-965.

[54] Chanfreau-Coffinier C, Hull LE, Lynch JA, DuVall SL, Damrauer SM, Cunningham FE, **Voight BF**, Matheny ME, Oslin DW, Icardi MS, Tuteja S. Projected Prevalence of Actionable Pharmacogenetic Variants and Level A Drugs Prescribed Among US Veterans Health Administration Pharmacy Users. JAMA Netw Open. 2019 Jun 5;2(6):e195345.

[55] Benson KK, Hu W, Weller AH, Bennett AH, Chen ER, Khetarpal SA, Yoshino S, Bone WP, Wang L, Rabinowitz JD, **Voight BF**, Soccio RE. Natural human genetic variation determines basal and inducible expression of PM20D1, an obesity-associated gene. Proc Natl Acad Sci U S A. 2019 Nov 12;116(46):23232-23242.

[56] Siewert KM, **Voight BF**. BetaScan2: Standardized Statistics to Detect Balancing Selection Utilizing Substitution Data. Genome Biol Evol. 2020 Feb 1;12(2):3873-3877.

[57] Mishra R, Åkerlund M, Cousminer DL, Ahlqvist E, Bradfield JP, Chesi A, Hodge KM, Guy VC, Brillon DJ, Pratley RE, Rickels MR, Vella A, Ovalle F, Harris RI, Melander O, Varvel S, Hakonarson H, Froguel P, Lonsdale JT, Mauricio D, Schloot NC, Khunti K, Greenbaum CJ, Yderstræde KB, Tuomi T, **Voight BF**, Schwartz S, Boehm BO, Groop L, Leslie RD, Grant SFA. Genetic Discrimination Between LADA and Childhood-Onset Type 1 Diabetes Within the MHC. Diabetes Care. 2020 Feb;43(2):418-425.

[58] Emdin CA, Haas ME, Khera AV, Aragam K, Chaffin M, Klarin D, Hindy G, Jiang L, Wei WQ, Feng Q, Karjalainen J, Havulinna A, Kiiskinen T, Bick A, Ardissino D, Wilson JG, Schunkert H, McPherson R, Watkins H, Elosua R, Bown MJ, Samani NJ, Baber U, Erdmann J, Gupta N, Danesh J, Saleheen D, Chang KM, Vujkovic M, **Voight B**, Damrauer S, Lynch J, Kaplan D, Serper M, Tsao P, Mercader J, Hanis C, Daly M, Denny J, Gabriel S, Kathiresan S. A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genet. 2020 Apr;16(4):e1008629.

[59] Thom CS, Jobaliya CD, Lorenz K, Maguire JA, Gagne A, Gadue P, French DL, **Voight BF**. Tropomyosin 1 genetically constrains in vitro hematopoiesis. BMC Biol. 2020 May 14;18(1):52.

[60] Siewert KM, Klarin D, Damrauer SM, Chang KM, Tsao PS, Assimes TL, Davey Smith G, **Voight BF**. Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. Int J Epidemiol. 2020 Jun 1;49(3):1022-1031.

[61] Kember RL, Levin MG, Cousminer DL, Tsao N, Judy R, Schur GM, Lubitz SA, Ellinor PT, McCormack SE, Grant SFA, Rader DJ, **Voight BF**, Damrauer SM. Genetically Determined Birthweight Associates With Atrial Fibrillation: A Mendelian Randomization Study. Circ Genom Precis Med. 2020 Jun;13(3):e002553.

[62] Thom CS, **Voight BF**. Genetic colocalization atlas points to common regulatory sites and genes for hematopoietic traits and hematopoietic contributions to disease phenotypes. BMC Med Genomics. 2020 Jun 29;13(1):89.

[63] Vujkovic M, Keaton JM, Lynch JA, Miller DR, Zhou J, Tcheandjieu C, Huffman JE, Assimes TL, Lorenz K, Zhu X, Hilliard AT, Judy RL, Huang J, Lee KM, Klarin D, Pyarajan S, Danesh J, Melander O, Rasheed A, Mallick NH, Hameed S, Qureshi IH, Afzal MN, Malik U, Jalal A, Abbas S, Sheng X, Gao L, Kaestner KH, Susztak K, Sun YV, DuVall SL, Cho K, Lee JS, Gaziano JM, Phillips LS, Meigs JB, Reaven PD, Wilson PW, Edwards TL, Rader DJ, Damrauer SM, O'Donnell CJ, Tsao PS, Chang KM, **Voight BF***, Saleheen D*. 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. 2020 Jul;52(7):680-691.

[64] Serper M, Vujkovic M, Kaplan DE, Carr RM, Lee KM, Shao Q, Miller DR, Reaven PD, Phillips LS, O'Donnell CJ, Meigs JB, Wilson PWF, Vickers-Smith R, Kranzler HR, Justice AC, Gaziano JM, Muralidhar S, Pyarajan S, DuVall SL, Assimes TL, Lee JS, Tsao PS, Rader DJ, Damrauer SM, Lynch JA, Saleheen D*, **Voight BF***, Chang KM*. Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. PLoS One. 2020;15(8):e0237430.

[65] Johnson KE, Siewert KM, Klarin D, Damrauer SM, Chang KM, Tsao PS, Assimes TL, Maxwell KN, **Voight BF**. The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. PLoS Med. 2020 Sep;17(9):e1003302.

[66] Balcha SA, Demisse AG, Mishra R, Vartak T, Cousminer DL, Hodge KM, **Voight BF**, Lorenz K, Schwartz S, Jerram ST, Gamper A, Holmes A, Wilson HF, Williams AJK, Grant SFA, Leslie RD, Phillips DIW, Trimble ER. Type 1 diabetes in Africa: an immunogenetic study in the Amhara of North-West Ethiopia. Diabetologia. 2020 Oct;63(10):2158-2168.

[67] Levin MG, Judy R, Gill D, Vujkovic M, Verma SS, Bradford Y, Ritchie MD, Hyman MC, Nazarian S, Rader DJ, **Voight BF**, Damrauer SM. Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. PLoS Med. 2020 Oct;17(10):e1003288.

[68] Thom CS, Ding Z, Levin MG, Damrauer SM, Lee KM, Lynch J, Chang KM, Tsao PS, Cho K, Wilson PWF, Assimes TL, Sun YV, O'Donnell CJ, Vujkovic M*, **Voight BF***. Genetic determinants of increased body mass index mediate the effect of smoking on increased risk for type 2 diabetes but not coronary artery disease. Hum Mol Genet. 2020 Nov 25;29(19):3327-3337.

[69] Levin MG, Klarin D, Assimes TL, Freiberg MS, Ingelsson E, Lynch J, Natarajan P, O'Donnell C, Rader DJ, Tsao PS, Chang KM, **Voight BF**, Damrauer SM. Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases: A Mendelian Randomization Study. JAMA Netw Open. 2021 Jan 4;4(1):e2034461.

[70] Correa-Garhwal SM, Babb PL, **Voight BF**, Hayashi CY. Golden orb-weaving spider (Trichonephila clavipes) silk genes with sex-biased expression and atypical architectures. G3 (Bethesda). 2021 Jan 18;11(1).

[71] Bone WP, Siewert KM, Jha A, Klarin D, Damrauer SM, Chang KM, Tsao PS, Assimes TL, Ritchie MD, **Voight BF**. Multi-trait association studies discover pleiotropic loci between Alzheimer's disease and cardiometabolic traits. Alzheimers Res Ther. 2021. Feb 4;13(1):34.

[72] Pazoki R, Vujkovic M, Elliott J, Evangelou E, Gill D, Ghanbari M, van der Most PJ, Pinto RC, Wielscher M, Farlik M, Zuber V, de Knegt RJ, Snieder H, Uitterlinden AG, Lynch JA, Jiang X, Said S, Kaplan DE, Lee KM, Serper M, Carr RM, Tsao PS, Atkinson SR, Dehghan A, Tzoulaki I, Ikram MA, Herzig KH, Järvelin MR, Alizadeh BZ, O'Donnell CJ, Saleheen D, **Voight BF***, Chang KM*, Thursz MR*, Elliott P*. Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nat Commun. 2021 May 10;12(1):2579.

[73] Levin MG, Klarin D, Walker VM, Gill D, Lynch J, Hellwege JN, Keaton JM, Lee KM, Assimes TL, Natarajan P, Hung AM, Edwards TL, Rader DJ, Gaziano JM, Davies NM, Tsao PS, Chang KM, **Voight BF**, Damrauer SM. Association Between Genetic Variation in

Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. Arterioscler Thromb Vasc Biol. 2021 Jun;41(6):2027-2034.

[74] Veturi Y, Lucas A, Bradford Y, Hui D, Dudek S, Theusch E, Verma A, Miller JE, Kullo I, Hakonarson H, Sleiman P, Schaid D, Stein CM, Edwards DRV, Feng Q, Wei WQ, Medina MW, Krauss RM, Hoffmann TJ, Risch N, **Voight BF**, Rader DJ, Ritchie MD. A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nat Genet. 2021 Jul;53(7):972-981.

[75] Guan Y, Liang X, Ma Z, Hu H, Liu H, Miao Z, Linkermann A, Hellwege JN, **Voight BF**, Susztak K. A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis. Nat Commun. 2021 Aug 23;12(1):5078.

[76] Sheng X, Guan Y, Ma Z, Wu J, Liu H, Qiu C, Vitale S, Miao Z, Seasock MJ, Palmer M, Shin MK, Duffin KL, Pullen SS, Edwards TL, Hellwege JN, Hung AM, Li M, **Voight BF**, Coffman TM, Brown CD, Susztak K. Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. Nat Genet. 2021 Sep;53(9):1322-1333.

[76] Levin MG, Klarin D, Georgakis MK, Lynch J, Liao KP, **Voight BF**, O'Donnell CJ, Chang KM, Assimes TL, Tsao PS, Damrauer SM. A Missense Variant in the IL-6 Receptor and Protection From Peripheral Artery Disease. Circ Res. 2021 Oct 29;129(10):968-970.

[77] Bellomo TR, Bone WP, Chen BY, Gawronski KAB, Zhang D, Park J, Levin M, Tsao N, Klarin D, Lynch J, Assimes TL, Gaziano JM, Wilson PW, Cho K, Vujkovic M, O'Donnell CJ, Chang KM, Tsao PS, Rader DJ, Ritchie MD, Damrauer SM, **Voight BF**. Multi-Trait Genome-Wide Association Study of Atherosclerosis Detects Novel Pleiotropic Loci. Front Genet. 2021;12:787545. doi: 10.3389/fgene.2021.787545.

[78] Thom CS, Wilken MB, Chou ST, **Voight BF**. Body mass index and adipose distribution have opposing genetic impacts on human blood traits. Elife. 2022 Feb 15;11. doi: 10.7554/eLife.75317.

[79] Walker VM, Vujkovic M, Carter AR, Davies NM, Udler MS, Levin MG, Davey Smith G, **Voight BF**, Gaunt TR, Damrauer SM. Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes. Diabetologia. 2022 May;65(5):790-799.

[80] Vujkovic M, Ramdas S, Lorenz KM, Guo X, Darlay R, Cordell HJ, He J, Gindin Y, Chung C, Myers RP, Schneider CV, Park J, Lee KM, Serper M, Carr RM, Kaplan DE, Haas ME, MacLean MT, Witschey WR, Zhu X, Tcheandjieu C, Kember RL, Kranzler HR, Verma A, Giri A, Klarin DM, Sun YV, Huang J, Huffman JE, Townsend Creasy K, Hand NJ, Liu CT, Long MT, Yao J, Budoff M, Tan J, Li X, Lin HJ, Chen YI, Taylor KD, Chang RK, Krauss RM, Vilarinho S, Brancale J, Nielsen JB, Locke AE, Jones MB, Verweij N, Baras A, Reddy KR, Neuschwander-Tetri BA, Schwimmer JB, Sanyal AJ, Chalasani N, Ryan KA, Mitchell BD, Gill D, Wells AD, Manduchi E, Saiman Y, Mahmud N, Miller DR, Reaven PD, Phillips LS, Muralidhar S, DuVall SL, Lee JS, Assimes TL, Pyarajan S, Cho K, Edwards TL, Damrauer SM, Wilson PW, Gaziano JM, O'Donnell CJ, Khera AV, Grant SFA, Brown CD, Tsao PS, Saleheen D, Lotta LA, Bastarache L, Anstee QM, Daly AK, Meigs JB, Rotter JI, Lynch JA, Rader DJ*, **Voight BF***, Chang KM*. A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nat Genet. 2022 Jun;54(6):761-771.

[81] Babb PL, Gregorič M, Lahens NF, Nicholson DN, Hayashi CY, Higgins L, Kuntner M, Agnarsson I, **Voight BF**. Characterization of the genome and silk-gland transcriptomes of Darwin's bark spider (Caerostris darwini). PLoS One. 2022;17(6):e0268660.

[82] Lorenz K, Thom CS, Adurty S, **Voight BF**. TSABL: Trait Specific Annotation Based Locus predictor. BMC Genomics. 2022 Jun 15;23(1):444.

[83] Liu H, Doke T, Guo D, Sheng X, Ma Z, Park J, Vy HMT, Nadkarni GN, Abedini A, Miao Z, Palmer M, **Voight BF**, Li H, Brown CD, Ritchie MD, Shu Y, Susztak K. Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nat Genet. 2022 Jul;54(7):950-962.

[84] Chen BY, Bone WP, Lorenz K, Levin M, Ritchie MD, **Voight BF**. ColocQuiaL: A QTL-GWAS colocalization pipeline. Bioinformatics. 2022 Jul 27;38(18):4409-11.

[85] Tcheandjieu C, Zhu X, Hilliard AT, Clarke SL, Napolioni V, Ma S, Lee KM, Fang H, Chen F, Lu Y, Tsao NL, Raghavan S, Koyama S, Gorman BR, Vujkovic M, Klarin D, Levin MG, Sinnott-Armstrong N, Wojcik GL, Plomondon ME, Maddox TM, Waldo SW, Bick AG, Pyarajan S, Huang J, Song R, Ho YL, Buyske S, Kooperberg C, Haessler J, Loos RJF, Do R, Verbanck M, Chaudhary K, North KE, Avery CL, Graff M, Haiman CA, Le Marchand L, Wilkens LR, Bis JC, Leonard H, Shen B, Lange LA, Giri A, Dikilitas O, Kullo IJ, Stanaway IB, Jarvik GP, Gordon AS, Hebbring S, Namjou B, Kaufman KM, Ito K, Ishigaki K, Kamatani Y, Verma SS, Ritchie MD, Kember RL, Baras A, Lotta LA; Regeneron Genetics Center; CARDIoGRAMplusC4D Consortium; Biobank Japan; Million Veteran Program, Kathiresan S, Hauser ER, Miller DR, Lee JS, Saleheen D, Reaven PD, Cho K, Gaziano JM, Natarajan P, Huffman JE, **Voight BF**, Rader DJ, Chang KM, Lynch JA, Damrauer SM, Wilson PWF, Tang H, Sun YV, Tsao PS, O'Donnell CJ, Assimes TL. Large-scale genome-wide association study of coronary artery disease in genetically diverse populations. Nat Med. 2022 Aug;28(8):1679-1692.

[86] Ding Z, Ritchie MD, **Voight BF***, Hwang W-T*. Estimating the effect size of a hidden causal factor between SNPs and a continuous trait: a mediation model approach. BMC Bioinformatics. 2022 Oct 13;23(1):420.

[87] A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. Raghavan S, Huang J, Tcheandjieu C, Huffman JE, Litkowski E, Liu C, Ho YA, Hunter-Zinck H, Zhao H, Marouli E, North KE; VA Million Veteran Program, Lange E, Lange LA, **Voight BF**, Gaziano JM, Pyarajan S, Hauser ER, Tsao PS, Wilson PWF, Chang KM, Cho K, O'Donnell CJ, Sun YV, Assimes TL. PLoS Genet. 2022 Jun 2;18(6):e1010193. doi: 10.1371/journal.pgen.1010193. eCollection 2022 Jun.

[88] Johnson KE, Adams CJ, **Voight BF**. Identifying rare variants inconsistent with identity-by-descent in population-scale whole genome sequencing data. Methods Ecol Evol. 2022; 13:2429–2442.

[89] Levin MG, Tsao NL, Singhal P, Liu C, Vy HMT, Paranjpe I, Backman JD, Bellomo TR, Bone WP, Biddinger KJ, Hui Q, Dikilitas O, Satterfield BA, Yang Y, Morley MP, Bradford Y, Burke M, Reza N, Charest B, Judy RL, Puckelwartz MJ, Hakonarson H, Khan A, Kottyan LC, Kullo I, Luo Y, McNally EM, Rasmussen-Torvik LJ, Day SM, Do R, Phillips LS, Ellinor PT, Nadkarni GN, Ritchie MD, Arany Z, Cappola TP, Margulies KB, Aragam KG, Haggerty CM, Joseph J, Sun YV, Voight BF, Damrauer SM. Genome-wide association and multi-trait analyses characterize the common genetic architecture of heart failure. Nat Commun.

2022 Nov 14;13(1):6914. doi: 10.1038/s41467-022-34216-6. PubMed PMID: 36376295; PubMed Central PMCID: PMC9663424.

[90] Huang J, Huffman JE, Huang Y, Do Valle Í, Assimes TL, Raghavan S, **Voight BF**, Liu C, Barabási AL, Huang RDL, Hui Q, Nguyen XT, Ho YL, Djousse L, Lynch JA, Vujkovic M, Tcheandjieu C, Tang H, Damrauer SM, Reaven PD, Miller D, Phillips LS, Ng MCY, Graff M, Haiman CA, Loos RJF, North KE, Yengo L, Smith GD, Saleheen D, Gaziano JM, Rader DJ, Tsao PS, Cho K, Chang KM, Wilson PWF; VA Million Veteran Program; Sun YV, O'Donnell CJ. Genomics and phenomics of body mass index reveals a complex disease network. Nat Commun. 2022 Dec 29;13(1):7973. doi: 10.1038/s41467-022-35553-2.

[91] Ahn K, Penn RB, Rattan S, Panettieri RA Jr, **Voight BF**, An SS. Mendelian Randomization Analysis Reveals a Complex Genetic Interplay among Atopic Dermatitis, Asthma, and Gastroesophageal Reflux Disease. Am J Respir Crit Care Med. 2023 Jan 15;207(2):130-137. doi: 10.1164/rccm.202205-0951OC. PubMed PMID: 36214830; PubMed Central PMCID: PMC9893317.

[92] Gawronski KAB, Bone WP, Park Y, Pashos EE, Wenz BM, Dudek MF, Wang X, Yang W, Rader DJ, Musunuru K, **Voight BF**, Brown CD. Evaluating the Contribution of Cell Type-Specific Alternative Splicing to Variation in Lipid Levels. Circ Genom Precis Med. 2023 Jun;16(3):248-257. doi: 10.1161/CIRCGEN.120.003249. Epub 2023 May 11.

[93] Adams CJ, Conery M, Auerbach BJ, Jensen ST, Mathieson I, **Voight BF**. Regularized sequence-context mutational trees capture variation in mutation rates across the human genome. PLoS Genet. 2023 Jul 7;19(7):e1010807. doi: 10.1371/journal.pgen.1010807.

[94] Pividori M, Lu S, Li B, Su C, Johnson ME, Wei WQ, Feng Q, Namjou B, Kiryluk K, Kullo IJ, Luo Y, Sullivan BD, **Voight BF**, Skarke C, Ritchie MD, Grant SFA; eMERGE Consortium; Greene CS. Projecting genetic associations through gene expression patterns highlights disease etiology and drug mechanisms. Nat Commun. 2023 Sep 9;14(1):5562. doi: 10.1038/s41467-023-41057-4.

## ***ADDITIONAL PUBLICATIONS***

[1] Coverage and characteristics of the Affymetrix GeneChip Human Mapping 100K SNP set. Nicolae DL, Wen X, **Voight BF**, Cox NJ. PLoS Genet. 2006 May;2(5):e67. Doi: 10.1371/journal.pgen.0020067. Epub 2006 May 5.

[2] A common variant of HMGA2 is associated with adult and childhood height in the general population. Weedon MN, Lettre G, Freathy RM, Lindgren CM, **Voight BF**, Perry JR, Elliott KS, Hackett R, Guiducci C, Shields B, Zeggini E, Lango H, Lyssenko V, Timpson NJ, Burtt NP, Rayner NW, Saxena R, Ardlie K, Tobias JH, Ness AR, Ring SM, Palmer CN, Morris AD, Peltonen L, Salomaa V; Diabetes Genetics Initiative; Wellcome Trust Case Control Consortium, Davey Smith G, Groop LC, Hattersley AT, McCarthy MI, Hirschhorn JN, Frayling TM. Nat Genet. 2007 Oct;39(10):1245-50. doi: 10.1038/ng2121. Epub 2007 Sep 2.

[3] Identification of ten loci associated with height highlights new biological pathways in human growth. Lettre G, Jackson AU, Gieger C, Schumacher FR, Berndt SI, Sanna S, Eyheramendy S, **Voight BF**, Butler JL, Guiducci C, Illig T, Hackett R, Heid IM, Jacobs KB, Lyssenko V, Uda M; Diabetes Genetics Initiative; FUSION; KORA; Prostate, Lung Colorectal and Ovarian Cancer Screening Trial; Nurses' Health Study; SardiNIA, Boehnke M, Chanock SJ, Groop LC, Hu FB, Isomaa B, Kraft P, Peltonen L, Salomaa V, Schlessinger D, Hunter DJ, Hayes RB, Abecasis GR, Wichmann HE, Mohlke KL, Hirschhorn JN. Nat Genet. 2008 May;40(5):584-91. doi: 10.1038/ng.125. Epub 2008 Apr 6.

[4] Common variants near MC4R are associated with fat mass, weight and risk of obesity. Loos RJ, Lindgren CM, Li S, Wheeler E, Zhao JH, Prokopenko I, Inouye M, Freathy RM, Attwood AP, Beckmann JS, Berndt SI; Prostate, Lung, Colorectal, and Ovarian (PLCO) Cancer Screening Trial, Jacobs KB, Chanock SJ, Hayes RB, Bergmann S, Bennett AJ, Bingham SA, Bochud M, Brown M, Cauchi S, Connell JM, Cooper C, Smith GD, Day I, Dina C, De S, Dermitzakis ET, Doney AS, Elliott KS, Elliott P, Evans DM, Sadaf Farooqi I, Froguel P, Ghori J, Groves CJ, Gwilliam R, Hadley D, Hall AS, Hattersley AT, Hebebrand J, Heid IM; KORA, Lamina C, Gieger C, Illig T, Meitinger T, Wichmann HE, Herrera B, Hinney A, Hunt SE, Jarvelin MR, Johnson T, Jolley JD, Karpe F, Keniry A, Khaw KT, Luben RN, Mangino M, Marchini J, McArdle WL, McGinnis R, Meyre D, Munroe PB, Morris AD, Ness AR, Neville MJ, Nica AC, Ong KK, O'Rahilly S, Owen KR, Palmer CN, Papadakis K, Potter S, Pouta A, Qi L; Nurses' Health Study, Randall JC, Rayner NW, Ring SM, Sandhu MS, Scherag A, Sims MA, Song K, Soranzo N, Speliotes EK; Diabetes Genetics Initiative, Syddall HE, Teichmann SA, Timpson NJ, Tobias JH, Uda M; SardiNIA Study, Vogel CI, Wallace C, Waterworth DM, Weedon MN; Wellcome Trust Case Control Consortium, Willer CJ; FUSION, Wraight, Yuan X, Zeggini E, Hirschhorn JN, Strachan DP, Ouwehand WH, Caulfield MJ, Samani NJ, Frayling TM, Vollenweider P, Waeber G, Mooser V, Deloukas P, McCarthy MI, Wareham NJ, Barroso I, Jacobs KB, Chanock SJ, Hayes RB, Lamina C, Gieger C, Illig T, Meitinger T, Wichmann HE, Kraft P, Hankinson SE, Hunter DJ, Hu FB, Lyon HN, **Voight BF**, Ridderstrale M, Groop L, Scheet P, Sanna S, Abecasis GR, Albai G, Nagaraja R, Schlessinger D, Jackson AU, Tuomilehto J, Collins FS, Boehnke M, Mohlke KL. Nat Genet. 2008 Jun;40(6):768-75. doi: 10.1038/ng.140. Epub 2008 May 4.

[5] Common missense variant in the glucokinase regulatory protein gene is associated with increased plasma triglyceride and C-reactive protein but lower fasting glucose concentrations. Orho-Melander M, Melander O, Guiducci C, Perez-Martinez P, Corella D,

Roos C, Tewhey R, Rieder MJ, Hall J, Abecasis G, Tai ES, Welch C, Arnett DK, Lyssenko V, Lindholm E, Saxena R, de Bakker PI, Burtt N, **Voight BF**, Hirschhorn JN, Tucker KL, Hedner T, Tuomi T, Isomaa B, Eriksson KF, Taskinen MR, Wahlstrand B, Hughes TE, Parnell LD, Lai CQ, Berglund G, Peltonen L, Vartiainen E, Jousilahti P, Havulinna AS, Salomaa V, Nilsson P, Groop L, Altshuler D, Ordovas JM, Kathiresan S. Diabetes. 2008 Nov;57(11):3112-21. doi: 10.2337/db08-0516. Epub 2008 Aug 4.

[6] Practical aspects of imputation-driven meta-analysis of genome-wide association studies. de Bakker PI, Ferreira MA, Jia X, Neale BM, Raychaudhuri S, **Voight BF**. Hum Mol Genet. 2008 Oct 15;17(R2):R122-8. doi: 10.1093/hmg/ddn288.

[7] Common variants at 30 loci contribute to polygenic dyslipidemia. Kathiresan S, Willer CJ, Peloso GM, Demissie S, Musunuru K, Schadt EE, Kaplan L, Bennett D, Li Y, Tanaka T, **Voight BF**, Bonnycastle LL, Jackson AU, Crawford G, Surti A, Guiducci C, Burtt NP, Parish S, Clarke R, Zelenika D, Kubalanza KA, Morken MA, Scott LJ, Stringham HM, Galan P, Swift AJ, Kuusisto J, Bergman RN, Sundvall J, Laakso M, Ferrucci L, Scheet P, Sanna S, Uda M, Yang Q, Lunetta KL, Dupuis J, de Bakker PI, O'Donnell CJ, Chambers JC, Kooner JS, Hercberg S, Meneton P, Lakatta EG, Scuteri A, Schlessinger D, Tuomilehto J, Collins FS, Groop L, Altshuler D, Collins R, Lathrop GM, Melander O, Salomaa V, Peltonen L, Orho-Melander M, Ordovas JM, Boehnke M, Abecasis GR, Mohlke KL, Cupples LA. Nat Genet. 2009 Jan;41(1):56-65. doi: 10.1038/ng.291. Epub 2008 Dec 7.

[8] Variants in MTNR1B influence fasting glucose levels. Prokopenko I, Langenberg C, Florez JC, Saxena R, Soranzo N, Thorleifsson G, Loos RJ, Manning AK, Jackson AU, Aulchenko Y, Potter SC, Erdos MR, Sanna S, Hottenga JJ, Wheeler E, Kaakinen M, Lyssenko V, Chen WM, Ahmadi K, Beckmann JS, Bergman RN, Bochud M, Bonnycastle LL, Buchanan TA, Cao A, Cervino A, Coin L, Collins FS, Crisponi L, de Geus EJ, Dehghan A, Deloukas P, Doney AS, Elliott P, Freimer N, Gateva V, Herder C, Hofman A, Hughes TE, Hunt S, Illig T, Inouye M, Isomaa B, Johnson T, Kong A, Krestyaninova M, Kuusisto J, Laakso M, Lim N, Lindblad U, Lindgren CM, McCann OT, Mohlke KL, Morris AD, Naitza S, Orrù M, Palmer CN, Pouta A, Randall J, Rathmann W, Saramies J, Scheet P, Scott LJ, Scuteri A, Sharp S, Sijbrands E, Smit JH, Song K, Steinthorsdottir V, Stringham HM, Tuomi T, Tuomilehto J, Uitterlinden AG, **Voight BF**, Waterworth D, Wichmann HE, Willemsen G, Witteman JC, Yuan X, Zhao JH, Zeggini E, Schlessinger D, Sandhu M, Boomsma DI, Uda M, Spector TD, Penninx BW, Altshuler D, Vollenweider P, Jarvelin MR, Lakatta E, Waeber G, Fox CS, Peltonen L, Groop LC, Mooser V, Cupples LA, Thorsteinsdottir U, Boehnke M, Barroso I, Van Duijn C, Dupuis J, Watanabe RM, Stefansson K, McCarthy MI, Wareham NJ, Meigs JB, Abecasis GR. Nat Genet. 2009 Jan;41(1):77-81. doi: 10.1038/ng.290. Epub 2008 Dec 7.

[9] New susceptibility locus for coronary artery disease on chromosome 3q22.3. Erdmann J, Grosshennig A, Braund PS, König IR, Hengstenberg C, Hall AS, Linsel-Nitschke P, Kathiresan S, Wright B, Trégouët DA, Cambien F, Bruse P, Aherrahrou Z, Wagner AK, Stark K, Schwartz SM, Salomaa V, Elosua R, Melander O, **Voight BF**, O'Donnell CJ, Peltonen L, Siscovick DS, Altshuler D, Merlini PA, Peyvandi F, Bernardinelli L, Ardissino D, Schillert A, Blankenberg S, Zeller T, Wild P, Schwarz DF, Tiret L, Perret C, Schreiber S, El Mokhtari NE, Schäfer A, März W, Renner W, Bugert P, Klüter H, Schrezenmeir J, Rubin D, Ball SG, Balmforth AJ, Wichmann HE, Meitinger T, Fischer M, Meisinger C, Baumert J, Peters A, Ouwehand WH; Italian Atherosclerosis, Thrombosis, and Vascular Biology Working Group; Myocardial Infarction Genetics Consortium; Wellcome Trust Case Control

Consortium; Cardiogenics Consortium, Deloukas P, Thompson JR, Ziegler A, Samani NJ, Schunkert H. Nat Genet. 2009 Mar;41(3):280-2. doi: 10.1038/ng.307. Epub 2009 Feb 8.

[10] The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. Choquet H, Cavalcanti-Proença C, Lecoeur C, Dina C, Cauchi S, Vaxillaire M, Hadjadj S, Horber F, Potoczna N, Charpentier G, Ruiz J, Hercberg S, Maimaitiming S, Roussel R, Boenhnke M, Jackson AU, Patsch W, Krempler F, **Voight BF**, Altshuler D, Groop L, Thorleifsson G, Steinthorsdottir V, Stefansson K, Balkau B, Froguel P, Meyre D. Hum Mol Genet. 2009 Jul 1;18(13):2495-501. doi: 10.1093/hmg/ddp169. Epub 2009 Apr 18.

[11] Linkage disequilibrium mapping of the replicated type 2 diabetes linkage signal on chromosome 1q. Prokopenko I, Zeggini E, Hanson RL, Mitchell BD, Rayner NW, Akan P, Baier L, Das SK, Elliott KS, Fu M, Frayling TM, Groves CJ, Gwilliam R, Scott LJ, **Voight BF**, Hattersley AT, Hu C, Morris AD, Ng M, Palmer CN, Tello-Ruiz M, Vaxillaire M, Wang CR, Stein L, Chan J, Jia W, Froguel P, Elbein SC, Deloukas P, Bogardus C, Shuldiner AR, McCarthy MI; International Type 2 Diabetes 1q Consortium. Diabetes. 2009 Jul;58(7):1704-9. doi: 10.2337/db09-0081. Epub 2009 Apr 23.

[12] Genome-wide association study identifies eight loci associated with blood pressure. Newton-Cheh C, Johnson T, Gateva V, Tobin MD, Bochud M, Coin L, Najjar SS, Zhao JH, Heath SC, Eyheramendy S, Papadakis K, **Voight BF**, Scott LJ, Zhang F, Farrall M, Tanaka T, Wallace C, Chambers JC, Khaw KT, Nilsson P, van der Harst P, Polidoro S, Grobbee DE, Onland-Moret NC, Bots ML, Wain LV, Elliott KS, Teumer A, Luan J, Lucas G, Kuusisto J, Burton PR, Hadley D, McArdle WL; Wellcome Trust Case Control Consortium, Brown M, Dominiczak A, Newhouse SJ, Samani NJ, Webster J, Zeggini E, Beckmann JS, Bergmann S, Lim N, Song K, Vollenweider P, Waeber G, Waterworth DM, Yuan X, Groop L, Orho-Melander M, Allione A, Di Gregorio A, Guarrera S, Panico S, Ricceri F, Romanazzi V, Sacerdote C, Vineis P, Barroso I, Sandhu MS, Luben RN, Crawford GJ, Jousilahti P, Perola M, Boehnke M, Bonnycastle LL, Collins FS, Jackson AU, Mohlke KL, Stringham HM, Valle TT, Willer CJ, Bergman RN, Morken MA, Döring A, Gieger C, Illig T, Meitinger T, Org E, Pfeufer A, Wichmann HE, Kathiresan S, Marrugat J, O'Donnell CJ, Schwartz SM, Siscovick DS, Subirana I, Freimer NB, Hartikainen AL, McCarthy MI, O'Reilly PF, Peltonen L, Pouta A, de Jong PE, Snieder H, van Gilst WH, Clarke R, Goel A, Hamsten A, Peden JF, Seedorf U, Syvänen AC, Tognoni G, Lakatta EG, Sanna S, Scheet P, Schlessinger D, Scuteri A, Dörr M, Ernst F, Felix SB, Homuth G, Lorbeer R, Reffelmann T, Rettig R, Völker U, Galan P, Gut IG, Hercberg S, Lathrop GM, Zelenika D, Deloukas P, Soranzo N, Williams FM, Zhai G, Salomaa V, Laakso M, Elosua R, Forouhi NG, Völzke H, Uiterwaal CS, van der Schouw YT, Numans ME, Matullo G, Navis G, Berglund G, Bingham SA, Kooner JS, Connell JM, Bandinelli S, Ferrucci L, Watkins H, Spector TD, Tuomilehto J, Altshuler D, Strachan DP, Laan M, Meneton P, Wareham NJ, Uda M, Jarvelin MR, Mooser V, Melander O, Loos RJ, Elliott P, Abecasis GR, Caulfield M, Munroe PB. Nat Genet. 2009 Jun;41(6):666-76. doi: 10.1038/ng.361. Epub 2009 May 10.

[13] Common body mass index-associated variants confer risk of extreme obesity. Cotsapas C, Speliotes EK, Hatoum IJ, Greenawalt DM, Dobrin R, Lum PY, Suver C, Chudin E, Kemp D, Reitman M, **Voight BF**, Neale BM, Schadt EE, Hirschhorn JN, Kaplan LM, Daly MJ; GIANT Consortium. Hum Mol Genet. 2009 Sep 15;18(18):3502-7. doi: 10.1093/hmg/ddp292. Epub 2009 Jun 24.

[14] Underlying genetic models of inheritance in established type 2 diabetes associations. Salanti G, Southam L, Altshuler D, Ardlie K, Barroso I, Boehnke M, Cornelis MC, Frayling TM, Grallert H, Grarup N, Groop L, Hansen T, Hattersley AT, Hu FB, Hveem K, Illig T, Kuusisto J, Laakso M, Langenberg C, Lyssenko V, McCarthy MI, Morris A, Morris AD, Palmer CN, Payne F, Platou CG, Scott LJ, **Voight BF**, Wareham NJ, Zeggini E, Ioannidis JP. Am J Epidemiol. 2009 Sep 1;170(5):537-45. doi: 10.1093/aje/kwp145. Epub 2009 Jul 14.

[15] A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Soranzo N, Spector TD, Mangino M, Kühnel B, Rendon A, Teumer A, Willenborg C, Wright B, Chen L, Li M, Salo P, **Voight BF**, Burns P, Laskowski RA, Xue Y, Menzel S, Altshuler D, Bradley JR, Bumpstead S, Burnett MS, Devaney J, Döring A, Elosua R, Epstein SE, Erber W, Falchi M, Garner SF, Ghori MJ, Goodall AH, Gwilliam R, Hakonarson HH, Hall AS, Hammond N, Hengstenberg C, Illig T, König IR, Knouff CW, McPherson R, Melander O, Mooser V, Nauck M, Nieminen MS, O'Donnell CJ, Peltonen L, Potter SC, Prokisch H, Rader DJ, Rice CM, Roberts R, Salomaa V, Sambrook J, Schreiber S, Schunkert H, Schwartz SM, Serbanovic-Canic J, Sinisalo J, Siscovick DS, Stark K, Surakka I, Stephens J, Thompson JR, Völker U, Völzke H, Watkins NA, Wells GA, Wichmann HE, Van Heel DA, Tyler-Smith C, Thein SL, Kathiresan S, Perola M, Reilly MP, Stewart AF, Erdmann J, Samani NJ, Meisinger C, Greinacher A, Deloukas P, Ouwehand WH, Gieger C. Nat Genet. 2009 Nov;41(11):1182-90. doi: 10.1038/ng.467. Epub 2009 Oct 11.

[16] Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Saxena R, Hivert MF, Langenberg C, Tanaka T, Pankow JS, Vollenweider P, Lyssenko V, Bouatia-Naji N, Dupuis J, Jackson AU, Kao WH, Li M, Glazer NL, Manning AK, Luan J, Stringham HM, Prokopenko I, Johnson T, Grarup N, Boesgaard TW, Lecoeur C, Shrader P, O'Connell J, Ingelsson E, Couper DJ, Rice K, Song K, Andreasen CH, Dina C, Köttgen A, Le Bacquer O, Pattou F, Taneera J, Steinthorsdottir V, Rybin D, Ardlie K, Sampson M, Qi L, van Hoek M, Weedon MN, Aulchenko YS, **Voight BF**, Grallert H, Balkau B, Bergman RN, Bielinski SJ, Bonnefond A, Bonnycastle LL, Borch-Johnsen K, Böttcher Y, Brunner E, Buchanan TA, Bumpstead SJ, Cavalcanti-Proença C, Charpentier G, Chen YD, Chines PS, Collins FS, Cornelis M, J Crawford G, Delplanque J, Doney A, Egan JM, Erdos MR, Firmann M, Forouhi NG, Fox CS, Goodarzi MO, Graessler J, Hingorani A, Isomaa B, Jørgensen T, Kivimaki M, Kovacs P, Krohn K, Kumari M, Lauritzen T, Lévy-Marchal C, Mayor V, McAteer JB, Meyre D, Mitchell BD, Mohlke KL, Morken MA, Narisu N, Palmer CN, Pakyz R, Pascoe L, Payne F, Pearson D, Rathmann W, Sandbaek A, Sayer AA, Scott LJ, Sharp SJ, Sijbrands E, Singleton A, Siscovick DS, Smith NL, Sparsø T, Swift AJ, Syddall H, Thorleifsson G, Tönjes A, Tuomi T, Tuomilehto J, Valle TT, Waeber G, Walley A, Waterworth DM, Zeggini E, Zhao JH; GIANT consortium; MAGIC investigators, Illig T, Wichmann HE, Wilson JF, van Duijn C, Hu FB, Morris AD, Frayling TM, Hattersley AT, Thorsteinsdottir U, Stefansson K, Nilsson P, Syvänen AC, Shuldiner AR, Walker M, Bornstein SR, Schwarz P, Williams GH, Nathan DM, Kuusisto J, Laakso M, Cooper C, Marmot M, Ferrucci L, Mooser V, Stumvoll M, Loos RJ, Altshuler D, Psaty BM, Rotter JI, Boerwinkle E, Hansen T, Pedersen O, Florez JC, McCarthy MI, Boehnke M, Barroso I, Sladek R, Froguel P, Meigs JB, Groop L, Wareham NJ, Watanabe RM. Nat Genet. 2010 Feb;42(2):142-8. doi: 10.1038/ng.521. Epub 2010 Jan 17.

[17] New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Dupuis J, Langenberg C, Prokopenko I, Saxena R, Soranzo N, Jackson AU,

Wheeler E, Glazer NL, Bouatia-Naji N, Gloyn AL, Lindgren CM, Mägi R, Morris AP, Randall J, Johnson T, Elliott P, Rybin D, Thorleifsson G, Steinthorsdottir V, Henneman P, Grallert H, Dehghan A, Hottenga JJ, Franklin CS, Navarro P, Song K, Goel A, Perry JR, Egan JM, Lajunen T, Grarup N, Sparsø T, Doney A, **Voight BF**, Stringham HM, Li M, Kanoni S, Shrader P, Cavalcanti-Proença C, Kumari M, Qi L, Timpson NJ, Gieger C, Zabena C, Rocheleau G, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Payne F, Roccasecca RM, Pattou F, Sethupathy P, Ardlie K, Ariyurek Y, Balkau B, Barter P, Beilby JP, Ben-Shlomo Y, Benediktsson R, Bennett AJ, Bergmann S, Bochud M, Boerwinkle E, Bonnefond A, Bonnycastle LL, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Charpentier G, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Cornelis M, Crawford G, Crisponi L, Day IN, de Geus EJ, Delplanque J, Dina C, Erdos MR, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Fox CS, Frants R, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Groves CJ, Grundy S, Gwilliam R, Gyllensten U, Hadjadj S, Hallmans G, Hammond N, Han X, Hartikainen AL, Hassanali N, Hayward C, Heath SC, Hercberg S, Herder C, Hicks AA, Hillman DR, Hingorani AD, Hofman A, Hui J, Hung J, Isomaa B, Johnson PR, Jørgensen T, Jula A, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Lyssenko V, Mahley R, Mangino M, Manning AK, Martínez-Larrad MT, McAteer JB, McCulloch LJ, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Morken MA, Mukherjee S, Naitza S, Narisu N, Neville MJ, Oostra BA, Orrù M, Pakyz R, Palmer CN, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Perola M, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Psaty BM, Rathmann W, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Roden M, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Scott LJ, Seedorf U, Sharp SJ, Shields B, Sigurethsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tanaka T, Thorand B, Tichet J, Tönjes A, Tuomi T, Uitterlinden AG, van Dijk KW, van Hoek M, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Walters GB, Ward KL, Watkins H, Weedon MN, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zeggini E, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global BPgen Consortium, Borecki IB, Loos RJ, Meneton P, Magnusson PK, Nathan DM, Williams GH, Hattersley AT, Silander K, Salomaa V, Smith GD, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Dedoussis GV, Serrano-Ríos M, Morris AD, Lind L, Palmer LJ, Hu FB, Franks PW, Ebrahim S, Marmot M, Kao WH, Pankow JS, Sampson MJ, Kuusisto J, Laakso M, Hansen T, Pedersen O, Pramstaller PP, Wichmann HE, Illig T, Rudan I, Wright AF, Stumvoll M, Campbell H, Wilson JF; Anders Hamsten on behalf of Procardis Consortium; MAGIC investigators, Bergman RN, Buchanan TA, Collins FS, Mohlke KL, Tuomilehto J, Valle TT, Altshuler D, Rotter JI, Siscovick DS, Penninx BW, Boomsma DI, Deloukas P, Spector TD, Frayling TM, Ferrucci L, Kong A, Thorsteinsdottir U, Stefansson K, van Duijn CM, Aulchenko YS, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Waterworth DM, Vollenweider P, Peltonen L, Mooser V, Abecasis GR, Wareham NJ, Sladek R, Froguel P, Watanabe RM, Meigs JB, Groop L, Boehnke M, McCarthy MI, Florez JC, Barroso I. Nat Genet. 2010 Feb;42(2):105-16. doi: 10.1038/ng.520. Epub 2010 Jan 17.

[18] PNPLA3 variants specifically confer increased risk for histologic nonalcoholic fatty liver disease but not metabolic disease. Speliotes EK, Butler JL, Palmer CD, **Voight BF**; GIANT Consortium; MIGen Consortium; NASH CRN, Hirschhorn JN. Hepatology. 2010 Sep;52(3):904-12. doi: 10.1002/hep.23768.

[19] Excess of rare variants in genes identified by genome-wide association study of hypertriglyceridemia. Johansen CT, Wang J, Lanktree MB, Cao H, McIntyre AD, Ban MR, Martins RA, Kennedy BA, Hassell RG, Visser ME, Schwartz SM, **Voight BF**, Elosua R, Salomaa V, O'Donnell CJ, Dallinga-Thie GM, Anand SS, Yusuf S, Huff MW, Kathiresan S, Hegele RA. Nat Genet. 2010 Aug;42(8):684-7. doi: 10.1038/ng.628. Epub 2010 Jul 25.

[20] Biological, clinical and population relevance of 95 loci for blood lipids. Teslovich TM, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Ripatti S, Chasman DI, Willer CJ, Johansen CT, Fouchier SW, Isaacs A, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Aulchenko YS, Thorleifsson G, Feitosa MF, Chambers J, Orho-Melander M, Melander O, Johnson T, Li X, Guo X, Li M, Shin Cho Y, Jin Go M, Jin Kim Y, Lee JY, Park T, Kim K, Sim X, Twee-Hee Ong R, Croteau-Chonka DC, Lange LA, Smith JD, Song K, Hua Zhao J, Yuan X, Luan J, Lamina C, Ziegler A, Zhang W, Zee RY, Wright AF, Witteman JC, Wilson JF, Willemsen G, Wichmann HE, Whitfield JB, Waterworth DM, Wareham NJ, Waeber G, Vollenweider P, **Voight BF**, Vitart V, Uitterlinden AG, Uda M, Tuomilehto J, Thompson JR, Tanaka T, Surakka I, Stringham HM, Spector TD, Soranzo N, Smit JH, Sinisalo J, Silander K, Sijbrands EJ, Scuteri A, Scott J, Schlessinger D, Sanna S, Salomaa V, Saharinen J, Sabatti C, Ruokonen A, Rudan I, Rose LM, Roberts R, Rieder M, Psaty BM, Pramstaller PP, Pichler I, Perola M, Penninx BW, Pedersen NL, Pattaro C, Parker AN, Pare G, Oostra BA, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, Meitinger T, McPherson R, McCarthy MI, McArdle W, Masson D, Martin NG, Marroni F, Mangino M, Magnusson PK, Lucas G, Luben R, Loos RJ, Lokki ML, Lettre G, Langenberg C, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, Kronenberg F, König IR, Khaw KT, Kaprio J, Kaplan LM, Johansson A, Jarvelin MR, Janssens AC, Ingelsson E, Igl W, Kees Hovingh G, Hottenga JJ, Hofman A, Hicks AA, Hengstenberg C, Heid IM, Hayward C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Gyllensten U, Guiducci C, Groop LC, Gonzalez E, Gieger C, Freimer NB, Ferrucci L, Erdmann J, Elliott P, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Geus EJ, de Faire U, Crawford G, Collins FS, Chen YD, Caulfield MJ, Campbell H, Burtt NP, Bonnycastle LL, Boomsma DI, Boekholdt SM, Bergman RN, Barroso I, Bandinelli S, Ballantyne CM, Assimes TL, Quertermous T, Altshuler D, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Adair LS, Taylor HA Jr, Borecki IB, Gabriel SB, Wilson JG, Holm H, Thorsteinsdottir U, Gudnason V, Krauss RM, Mohlke KL, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Rotter JI, Boerwinkle E, Strachan DP, Mooser V, Stefansson K, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, van Duijn CM, Peltonen L, Abecasis GR, Boehnke M, Kathiresan S. Nature. 2010 Aug 5;466(7307):707-13. doi: 10.1038/nature09270.

[20] Common variants at 10 genomic loci influence hemoglobin $A_1$(C) levels via glycemic and nonglycemic pathways. Soranzo N, Sanna S, Wheeler E, Gieger C, Radke D, Dupuis J, Bouatia-Naji N, Langenberg C, Prokopenko I, Stolerman E, Sandhu MS, Heeney MM, Devaney JM, Reilly MP, Ricketts SL, Stewart AF, **Voight BF**, Willenborg C, Wright B, Altshuler D, Arking D, Balkau B, Barnes D, Boerwinkle E, Böhm B, Bonnefond A, Bonnycastle LL, Boomsma DI, Bornstein SR, Böttcher Y, Bumpstead S, Burnett-Miller MS, Campbell H, Cao A, Chambers J, Clark R, Collins FS, Coresh J, de Geus EJ, Dei M, Deloukas P, Döring A, Egan JM, Elosua R, Ferrucci L, Forouhi N, Fox CS, Franklin C, Franzosi MG, Gallina S, Goel A, Graessler J, Grallert H, Greinacher A, Hadley D, Hall A, Hamsten A, Hayward C, Heath S, Herder C, Homuth G, Hottenga JJ, Hunter-Merrill R, Illig T, Jackson AU, Jula A, Kleber M, Knouff CW, Kong A, Kooner J, Köttgen A, Kovacs P,

Krohn K, Kühnel B, Kuusisto J, Laakso M, Lathrop M, Lecoeur C, Li M, Li M, Loos RJ, Luan J, Lyssenko V, Mägi R, Magnusson PK, Mälarstig A, Mangino M, Martínez-Larrad MT, März W, McArdle WL, McPherson R, Meisinger C, Meitinger T, Melander O, Mohlke KL, Mooser VE, Morken MA, Narisu N, Nathan DM, Nauck M, O'Donnell C, Oexle K, Olla N, Pankow JS, Payne F, Peden JF, Pedersen NL, Peltonen L, Perola M, Polasek O, Porcu E, Rader DJ, Rathmann W, Ripatti S, Rocheleau G, Roden M, Rudan I, Salomaa V, Saxena R, Schlessinger D, Schunkert H, Schwarz P, Seedorf U, Selvin E, Serrano-Ríos M, Shrader P, Silveira A, Siscovick D, Song K, Spector TD, Stefansson K, Steinthorsdottir V, Strachan DP, Strawbridge R, Stumvoll M, Surakka I, Swift AJ, Tanaka T, Teumer A, Thorleifsson G, Thorsteinsdottir U, Tönjes A, Usala G, Vitart V, Völzke H, Wallaschofski H, Waterworth DM, Watkins H, Wichmann HE, Wild SH, Willemsen G, Williams GH, Wilson JF, Winkelmann J, Wright AF; WTCCC, Zabena C, Zhao JH, Epstein SE, Erdmann J, Hakonarson HH, Kathiresan S, Khaw KT, Roberts R, Samani NJ, Fleming MD, Sladek R, Abecasis G, Boehnke M, Froguel P, Groop L, McCarthy MI, Kao WH, Florez JC, Uda M, Wareham NJ, Barroso I, Meigs JB. Diabetes. 2010 Dec;59(12):3229-39. doi: 10.2337/db10-0502. Epub 2010 Sep 21.

[21] Hundreds of variants clustered in genomic loci and biological pathways affect human height. Lango Allen H, Estrada K, Lettre G, Berndt SI, Weedon MN, Rivadeneira F, Willer CJ, Jackson AU, Vedantam S, Raychaudhuri S, Ferreira T, Wood AR, Weyant RJ, Segrè AV, Speliotes EK, Wheeler E, Soranzo N, Park JH, Yang J, Gudbjartsson D, Heard-Costa NL, Randall JC, Qi L, Vernon Smith A, Mägi R, Pastinen T, Liang L, Heid IM, Luan J, Thorleifsson G, Winkler TW, Goddard ME, Sin Lo K, Palmer C, Workalemahu T, Aulchenko YS, Johansson A, Zillikens MC, Feitosa MF, Esko T, Johnson T, Ketkar S, Kraft P, Mangino M, Prokopenko I, Absher D, Albrecht E, Ernst F, Glazer NL, Hayward C, Hottenga JJ, Jacobs KB, Knowles JW, Kutalik Z, Monda KL, Polasek O, Preuss M, Rayner NW, Robertson NR, Steinthorsdottir V, Tyrer JP, **Voight BF**, Wiklund F, Xu J, Zhao JH, Nyholt DR, Pellikka N, Perola M, Perry JR, Surakka I, Tammesoo ML, Altmaier EL, Amin N, Aspelund T, Bhangale T, Boucher G, Chasman DI, Chen C, Coin L, Cooper MN, Dixon AL, Gibson Q, Grundberg E, Hao K, Juhani Junttila M, Kaplan LM, Kettunen J, König IR, Kwan T, Lawrence RW, Levinson DF, Lorentzon M, McKnight B, Morris AP, Müller M, Suh Ngwa J, Purcell S, Rafelt S, Salem RM, Salvi E, Sanna S, Shi J, Sovio U, Thompson JR, Turchin MC, Vandenput L, Verlaan DJ, Vitart V, White CC, Ziegler A, Almgren P, Balmforth AJ, Campbell H, Citterio L, De Grandi A, Dominiczak A, Duan J, Elliott P, Elosua R, Eriksson JG, Freimer NB, Geus EJ, Glorioso N, Haiqing S, Hartikainen AL, Havulinna AS, Hicks AA, Hui J, Igl W, Illig T, Jula A, Kajantie E, Kilpeläinen TO, Koiranen M, Kolcic I, Koskinen S, Kovacs P, Laitinen J, Liu J, Lokki ML, Marusic A, Maschio A, Meitinger T, Mulas A, Paré G, Parker AN, Peden JF, Petersmann A, Pichler I, Pietiläinen KH, Pouta A, Ridderstråle M, Rotter JI, Sambrook JG, Sanders AR, Schmidt CO, Sinisalo J, Smit JH, Stringham HM, Bragi Walters G, Widen E, Wild SH, Willemsen G, Zagato L, Zgaga L, Zitting P, Alavere H, Farrall M, McArdle WL, Nelis M, Peters MJ, Ripatti S, van Meurs JB, Aben KK, Ardlie KG, Beckmann JS, Beilby JP, Bergman RN, Bergmann S, Collins FS, Cusi D, den Heijer M, Eiriksdottir G, Gejman PV, Hall AS, Hamsten A, Huikuri HV, Iribarren C, Kähönen M, Kaprio J, Kathiresan S, Kiemeney L, Kocher T, Launer LJ, Lehtimäki T, Melander O, Mosley TH Jr, Musk AW, Nieminen MS, O'Donnell CJ, Ohlsson C, Oostra B, Palmer LJ, Raitakari O, Ridker PM, Rioux JD, Rissanen A, Rivolta C, Schunkert H, Shuldiner AR, Siscovick DS, Stumvoll M, Tönjes A, Tuomilehto J, van Ommen GJ, Viikari J, Heath AC, Martin NG, Montgomery GW, Province MA, Kayser M, Arnold AM, Atwood LD, Boerwinkle E, Chanock SJ, Deloukas P, Gieger C, Grönberg H, Hall P, Hattersley AT,

Hengstenberg C, Hoffman W, Lathrop GM, Salomaa V, Schreiber S, Uda M, Waterworth D, Wright AF, Assimes TL, Barroso I, Hofman A, Mohlke KL, Boomsma DI, Caulfield MJ, Cupples LA, Erdmann J, Fox CS, Gudnason V, Gyllensten U, Harris TB, Hayes RB, Jarvelin MR, Mooser V, Munroe PB, Ouwehand WH, Penninx BW, Pramstaller PP, Quertermous T, Rudan I, Samani NJ, Spector TD, Völzke H, Watkins H, Wilson JF, Groop LC, Haritunians T, Hu FB, Kaplan RC, Metspalu A, North KE, Schlessinger D, Wareham NJ, Hunter DJ, O'Connell JR, Strachan DP, Wichmann HE, Borecki IB, van Duijn CM, Schadt EE, Thorsteinsdottir U, Peltonen L, Uitterlinden AG, Visscher PM, Chatterjee N, Loos RJ, Boehnke M, McCarthy MI, Ingelsson E, Lindgren CM, Abecasis GR, Stefansson K, Frayling TM, Hirschhorn JN. Nature. 2010 Oct 14;467(7317):832-8. doi: 10.1038/nature09410. Epub 2010 Sep 29.

[22] Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study: A Genome-wide association meta-analysis involving more than 22 000 cases and 60 000 controls. Preuss M, König IR, Thompson JR, Erdmann J, Absher D, Assimes TL, Blankenberg S, Boerwinkle E, Chen L, Cupples LA, Hall AS, Halperin E, Hengstenberg C, Holm H, Laaksonen R, Li M, März W, McPherson R, Musunuru K, Nelson CP, Burnett MS, Epstein SE, O'Donnell CJ, Quertermous T, Rader DJ, Roberts R, Schillert A, Stefansson K, Stewart AF, Thorleifsson G, **Voight BF**, Wells GA, Ziegler A, Kathiresan S, Reilly MP, Samani NJ, Schunkert H; CARDIoGRAM Consortium. Circ Cardiovasc Genet. 2010 Oct;3(5):475-83. doi: 10.1161/CIRCGENETICS.109.899443. Epub 2010 Oct 5.

[23] Lack of association between the Trp719Arg polymorphism in kinesin-like protein-6 and coronary artery disease in 19 case-control studies. Assimes TL, Hólm H, Kathiresan S, Reilly MP, Thorleifsson G, **Voight BF**, Erdmann J, Willenborg C, Vaidya D, Xie C, Patterson CC, Morgan TM, Burnett MS, Li M, Hlatky MA, Knowles JW, Thompson JR, Absher D, Iribarren C, Go A, Fortmann SP, Sidney S, Risch N, Tang H, Myers RM, Berger K, Stoll M, Shah SH, Thorgeirsson G, Andersen K, Havulinna AS, Herrera JE, Faraday N, Kim Y, Kral BG, Mathias RA, Ruczinski I, Suktitipat B, Wilson AF, Yanek LR, Becker LC, Linsel-Nitschke P, Lieb W, König IR, Hengstenberg C, Fischer M, Stark K, Reinhard W, Winogradow J, Grassl M, Grosshennig A, Preuss M, Schreiber S, Wichmann HE, Meisinger C, Yee J, Friedlander Y, Do R, Meigs JB, Williams G, Nathan DM, MacRae CA, Qu L, Wilensky RL, Matthai WH Jr, Qasim AN, Hakonarson H, Pichard AD, Kent KM, Satler L, Lindsay JM, Waksman R, Knouff CW, Waterworth DM, Walker MC, Mooser VE, Marrugat J, Lucas G, Subirana I, Sala J, Ramos R, Martinelli N, Olivieri O, Trabetti E, Malerba G, Pignatti PF, Guiducci C, Mirel D, Parkin M, Hirschhorn JN, Asselta R, Duga S, Musunuru K, Daly MJ, Purcell S, Eifert S, Braund PS, Wright BJ, Balmforth AJ, Ball SG; Myocardial Infarction Genetics Consortium; Wellcome Trust Case Control Consortium; Cardiogenics, Ouwehand WH, Deloukas P, Scholz M, Cambien F, Huge A, Scheffold T, Salomaa V, Girelli D, Granger CB, Peltonen L, McKeown PP, Altshuler D, Melander O, Devaney JM, Epstein SE, Rader DJ, Elosua R, Engert JC, Anand SS, Hall AS, Ziegler A, O'Donnell CJ, Spertus JA, Siscovick D, Schwartz SM, Becker D, Thorsteinsdottir U, Stefansson K, Schunkert H, Samani NJ, Quertermous T. J Am Coll Cardiol. 2010 Nov 2;56(19):1552-63. doi: 10.1016/j.jacc.2010.06.022.

[24] Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Heid IM, Jackson AU, Randall JC, Winkler TW, Qi L, Steinthorsdottir V, Thorleifsson G, Zillikens MC, Speliotes EK, Mägi R, Workalemahu T, White CC, Bouatia-Naji N, Harris TB, Berndt SI, Ingelsson E, Willer CJ,

Weedon MN, Luan J, Vedantam S, Esko T, Kilpeläinen TO, Kutalik Z, Li S, Monda KL, Dixon AL, Holmes CC, Kaplan LM, Liang L, Min JL, Moffatt MF, Molony C, Nicholson G, Schadt EE, Zondervan KT, Feitosa MF, Ferreira T, Lango Allen H, Weyant RJ, Wheeler E, Wood AR; MAGIC, Estrada K, Goddard ME, Lettre G, Mangino M, Nyholt DR, Purcell S, Smith AV, Visscher PM, Yang J, McCarroll SA, Nemesh J, **Voight BF**, Absher D, Amin N, Aspelund T, Coin L, Glazer NL, Hayward C, Heard-Costa NL, Hottenga JJ, Johansson A, Johnson T, Kaakinen M, Kapur K, Ketkar S, Knowles JW, Kraft P, Kraja AT, Lamina C, Leitzmann MF, McKnight B, Morris AP, Ong KK, Perry JR, Peters MJ, Polasek O, Prokopenko I, Rayner NW, Ripatti S, Rivadeneira F, Robertson NR, Sanna S, Sovio U, Surakka I, Teumer A, van Wingerden S, Vitart V, Zhao JH, Cavalcanti-Proença C, Chines PS, Fisher E, Kulzer JR, Lecoeur C, Narisu N, Sandholt C, Scott LJ, Silander K, Stark K, Tammesoo ML, Teslovich TM, Timpson NJ, Watanabe RM, Welch R, Chasman DI, Cooper MN, Jansson JO, Kettunen J, Lawrence RW, Pellikka N, Perola M, Vandenput L, Alavere H, Almgren P, Atwood LD, Bennett AJ, Biffar R, Bonnycastle LL, Bornstein SR, Buchanan TA, Campbell H, Day IN, Dei M, Dörr M, Elliott P, Erdos MR, Eriksson JG, Freimer NB, Fu M, Gaget S, Geus EJ, Gjesing AP, Grallert H, Grässler J, Groves CJ, Guiducci C, Hartikainen AL, Hassanali N, Havulinna AS, Herzig KH, Hicks AA, Hui J, Igl W, Jousilahti P, Jula A, Kajantie E, Kinnunen L, Kolcic I, Koskinen S, Kovacs P, Kroemer HK, Krzelj V, Kuusisto J, Kvaloy K, Laitinen J, Lantieri O, Lathrop GM, Lokki ML, Luben RN, Ludwig B, McArdle WL, McCarthy A, Morken MA, Nelis M, Neville MJ, Paré G, Parker AN, Peden JF, Pichler I, Pietiläinen KH, Platou CG, Pouta A, Ridderstråle M, Samani NJ, Saramies J, Sinisalo J, Smit JH, Strawbridge RJ, Stringham HM, Swift AJ, Teder-Laving M, Thomson B, Usala G, van Meurs JB, van Ommen GJ, Vatin V, Volpato CB, Wallaschofski H, Walters GB, Widen E, Wild SH, Willemsen G, Witte DR, Zgaga L, Zitting P, Beilby JP, James AL, Kähönen M, Lehtimäki T, Nieminen MS, Ohlsson C, Palmer LJ, Raitakari O, Ridker PM, Stumvoll M, Tönjes A, Viikari J, Balkau B, Ben-Shlomo Y, Bergman RN, Boeing H, Smith GD, Ebrahim S, Froguel P, Hansen T, Hengstenberg C, Hveem K, Isomaa B, Jørgensen T, Karpe F, Khaw KT, Laakso M, Lawlor DA, Marre M, Meitinger T, Metspalu A, Midthjell K, Pedersen O, Salomaa V, Schwarz PE, Tuomi T, Tuomilehto J, Valle TT, Wareham NJ, Arnold AM, Beckmann JS, Bergmann S, Boerwinkle E, Boomsma DI, Caulfield MJ, Collins FS, Eiriksdottir G, Gudnason V, Gyllensten U, Hamsten A, Hattersley AT, Hofman A, Hu FB, Illig T, Iribarren C, Jarvelin MR, Kao WH, Kaprio J, Launer LJ, Munroe PB, Oostra B, Penninx BW, Pramstaller PP, Psaty BM, Quertermous T, Rissanen A, Rudan I, Shuldiner AR, Soranzo N, Spector TD, Syvanen AC, Uda M, Uitterlinden A, Völzke H, Vollenweider P, Wilson JF, Witteman JC, Wright AF, Abecasis GR, Boehnke M, Borecki IB, Deloukas P, Frayling TM, Groop LC, Haritunians T, Hunter DJ, Kaplan RC, North KE, O'Connell JR, Peltonen L, Schlessinger D, Strachan DP, Hirschhorn JN, Assimes TL, Wichmann HE, Thorsteinsdottir U, van Duijn CM, Stefansson K, Cupples LA, Loos RJ, Barroso I, McCarthy MI, Fox CS, Mohlke KL, Lindgren CM. Nat Genet. 2010 Nov;42(11):949-60. doi: 10.1038/ng.685. Epub 2010 Oct 10.

[25] Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Speliotes EK, Willer CJ, Berndt SI, Monda KL, Thorleifsson G, Jackson AU, Lango Allen H, Lindgren CM, Luan J, Mägi R, Randall JC, Vedantam S, Winkler TW, Qi L, Workalemahu T, Heid IM, Steinthorsdottir V, Stringham HM, Weedon MN, Wheeler E, Wood AR, Ferreira T, Weyant RJ, Segrè AV, Estrada K, Liang L, Nemesh J, Park JH, Gustafsson S, Kilpeläinen TO, Yang J, Bouatia-Naji N, Esko T, Feitosa MF, Kutalik Z, Mangino M, Raychaudhuri S, Scherag A, Smith AV, Welch R, Zhao JH, Aben KK, Absher DM, Amin N, Dixon AL, Fisher E, Glazer NL, Goddard ME, Heard-Costa NL, Hoesel V,

Hottenga JJ, Johansson A, Johnson T, Ketkar S, Lamina C, Li S, Moffatt MF, Myers RH, Narisu N, Perry JR, Peters MJ, Preuss M, Ripatti S, Rivadeneira F, Sandholt C, Scott LJ, Timpson NJ, Tyrer JP, van Wingerden S, Watanabe RM, White CC, Wiklund F, Barlassina C, Chasman DI, Cooper MN, Jansson JO, Lawrence RW, Pellikka N, Prokopenko I, Shi J, Thiering E, Alavere H, Alibrandi MT, Almgren P, Arnold AM, Aspelund T, Atwood LD, Balkau B, Balmforth AJ, Bennett AJ, Ben-Shlomo Y, Bergman RN, Bergmann S, Biebermann H, Blakemore AI, Boes T, Bonnycastle LL, Bornstein SR, Brown MJ, Buchanan TA, Busonero F, Campbell H, Cappuccio FP, Cavalcanti-Proença C, Chen YD, Chen CM, Chines PS, Clarke R, Coin L, Connell J, Day IN, den Heijer M, Duan J, Ebrahim S, Elliott P, Elosua R, Eiriksdottir G, Erdos MR, Eriksson JG, Facheris MF, Felix SB, Fischer-Posovszky P, Folsom AR, Friedrich N, Freimer NB, Fu M, Gaget S, Gejman PV, Geus EJ, Gieger C, Gjesing AP, Goel A, Goyette P, Grallert H, Grässler J, Greenawalt DM, Groves CJ, Gudnason V, Guiducci C, Hartikainen AL, Hassanali N, Hall AS, Havulinna AS, Hayward C, Heath AC, Hengstenberg C, Hicks AA, Hinney A, Hofman A, Homuth G, Hui J, Igl W, Iribarren C, Isomaa B, Jacobs KB, Jarick I, Jewell E, John U, Jørgensen T, Jousilahti P, Jula A, Kaakinen M, Kajantie E, Kaplan LM, Kathiresan S, Kettunen J, Kinnunen L, Knowles JW, Kolcic I, König IR, Koskinen S, Kovacs P, Kuusisto J, Kraft P, Kvaløy K, Laitinen J, Lantieri O, Lanzani C, Launer LJ, Lecoeur C, Lehtimäki T, Lettre G, Liu J, Lokki ML, Lorentzon M, Luben RN, Ludwig B; MAGIC, Manunta P, Marek D, Marre M, Martin NG, McArdle WL, McCarthy A, McKnight B, Meitinger T, Melander O, Meyre D, Midthjell K, Montgomery GW, Morken MA, Morris AP, Mulic R, Ngwa JS, Nelis M, Neville MJ, Nyholt DR, O'Donnell CJ, O'Rahilly S, Ong KK, Oostra B, Paré G, Parker AN, Perola M, Pichler I, Pietiläinen KH, Platou CG, Polasek O, Pouta A, Rafelt S, Raitakari O, Rayner NW, Ridderstråle M, Rief W, Ruokonen A, Robertson NR, Rzehak P, Salomaa V, Sanders AR, Sandhu MS, Sanna S, Saramies J, Savolainen MJ, Scherag S, Schipf S, Schreiber S, Schunkert H, Silander K, Sinisalo J, Siscovick DS, Smit JH, Soranzo N, Sovio U, Stephens J, Surakka I, Swift AJ, Tammesoo ML, Tardif JC, Teder-Laving M, Teslovich TM, Thompson JR, Thomson B, Tönjes A, Tuomi T, van Meurs JB, van Ommen GJ, Vatin V, Viikari J, Visvikis-Siest S, Vitart V, Vogel CI, **Voight BF**, Waite LL, Wallaschofski H, Walters GB, Widen E, Wiegand S, Wild SH, Willemsen G, Witte DR, Witteman JC, Xu J, Zhang Q, Zgaga L, Ziegler A, Zitting P, Beilby JP, Farooqi IS, Hebebrand J, Huikuri HV, James AL, Kähönen M, Levinson DF, Macciardi F, Nieminen MS, Ohlsson C, Palmer LJ, Ridker PM, Stumvoll M, Beckmann JS, Boeing H, Boerwinkle E, Boomsma DI, Caulfield MJ, Chanock SJ, Collins FS, Cupples LA, Smith GD, Erdmann J, Froguel P, Grönberg H, Gyllensten U, Hall P, Hansen T, Harris TB, Hattersley AT, Hayes RB, Heinrich J, Hu FB, Hveem K, Illig T, Jarvelin MR, Kaprio J, Karpe F, Khaw KT, Kiemeney LA, Krude H, Laakso M, Lawlor DA, Metspalu A, Munroe PB, Ouwehand WH, Pedersen O, Penninx BW, Peters A, Pramstaller PP, Quertermous T, Reinehr T, Rissanen A, Rudan I, Samani NJ, Schwarz PE, Shuldiner AR, Spector TD, Tuomilehto J, Uda M, Uitterlinden A, Valle TT, Wabitsch M, Waeber G, Wareham NJ, Watkins H; Procardis Consortium, Wilson JF, Wright AF, Zillikens MC, Chatterjee N, McCarroll SA, Purcell S, Schadt EE, Visscher PM, Assimes TL, Borecki IB, Deloukas P, Fox CS, Groop LC, Haritunians T, Hunter DJ, Kaplan RC, Mohlke KL, O'Connell JR, Peltonen L, Schlessinger D, Strachan DP, van Duijn CM, Wichmann HE, Frayling TM, Thorsteinsdottir U, Abecasis GR, Barroso I, Boehnke M, Stefansson K, North KE, McCarthy MI, Hirschhorn JN, Ingelsson E, Loos RJ. Nat Genet. 2010 Nov;42(11):937-48. doi: 10.1038/ng.686. Epub 2010 Oct 10.

[26] Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Schunkert H, König IR, Kathiresan S, Reilly MP, Assimes TL, Holm H,

Preuss M, Stewart AF, Barbalic M, Gieger C, Absher D, Aherrahrou Z, Allayee H, Altshuler D, Anand SS, Andersen K, Anderson JL, Ardissino D, Ball SG, Balmforth AJ, Barnes TA, Becker DM, Becker LC, Berger K, Bis JC, Boekholdt SM, Boerwinkle E, Braund PS, Brown MJ, Burnett MS, Buysschaert I; Cardiogenics, Carlquist JF, Chen L, Cichon S, Codd V, Davies RW, Dedoussis G, Dehghan A, Demissie S, Devaney JM, Diemert P, Do R, Doering A, Eifert S, Mokhtari NE, Ellis SG, Elosua R, Engert JC, Epstein SE, de Faire U, Fischer M, Folsom AR, Freyer J, Gigante B, Girelli D, Gretarsdottir S, Gudnason V, Gulcher JR, Halperin E, Hammond N, Hazen SL, Hofman A, Horne BD, Illig T, Iribarren C, Jones GT, Jukema JW, Kaiser MA, Kaplan LM, Kastelein JJ, Khaw KT, Knowles JW, Kolovou G, Kong A, Laaksonen R, Lambrechts D, Leander K, Lettre G, Li M, Lieb W, Loley C, Lotery AJ, Mannucci PM, Maouche S, Martinelli N, McKeown PP, Meisinger C, Meitinger T, Melander O, Merlini PA, Mooser V, Morgan T, Mühleisen TW, Muhlestein JB, Münzel T, Musunuru K, Nahrstaedt J, Nelson CP, Nöthen MM, Olivieri O, Patel RS, Patterson CC, Peters A, Peyvandi F, Qu L, Quyyumi AA, Rader DJ, Rallidis LS, Rice C, Rosendaal FR, Rubin D, Salomaa V, Sampietro ML, Sandhu MS, Schadt E, Schäfer A, Schillert A, Schreiber S, Schrezenmeir J, Schwartz SM, Siscovick DS, Sivananthan M, Sivapalaratnam S, Smith A, Smith TB, Snoep JD, Soranzo N, Spertus JA, Stark K, Stirrups K, Stoll M, Tang WH, Tennstedt S, Thorgeirsson G, Thorleifsson G, Tomaszewski M, Uitterlinden AG, van Rij AM, **Voight BF**, Wareham NJ, Wells GA, Wichmann HE, Wild PS, Willenborg C, Witteman JC, Wright BJ, Ye S, Zeller T, Ziegler A, Cambien F, Goodall AH, Cupples LA, Quertermous T, März W, Hengstenberg C, Blankenberg S, Ouwehand WH, Hall AS, Deloukas P, Thompson JR, Stefansson K, Roberts R, Thorsteinsdottir U, O'Donnell CJ, McPherson R, Erdmann J; CARDIoGRAM Consortium, Samani NJ. Nat Genet. 2011 Mar 6;43(4):333-8. doi: 10.1038/ng.784.

[27] Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. Speliotes EK, Yerges-Armstrong LM, Wu J, Hernaez R, Kim LJ, Palmer CD, Gudnason V, Eiriksdottir G, Garcia ME, Launer LJ, Nalls MA, Clark JM, Mitchell BD, Shuldiner AR, Butler JL, Tomas M, Hoffmann U, Hwang SJ, Massaro JM, O'Donnell CJ, Sahani DV, Salomaa V, Schadt EE, Schwartz SM, Siscovick DS; NASH CRN; GIANT Consortium; MAGIC Investigators, **Voight BF**, Carr JJ, Feitosa MF, Harris TB, Fox CS, Smith AV, Kao WH, Hirschhorn JN, Borecki IB; GOLD Consortium. PLoS Genet. 2011 Mar;7(3):e1001324. doi: 10.1371/journal.pgen.1001324. Epub 2011 Mar 10.

[28] An increased burden of common and rare lipid-associated risk alleles contributes to the phenotypic spectrum of hypertriglyceridemia. Johansen CT, Wang J, Lanktree MB, McIntyre AD, Ban MR, Martins RA, Kennedy BA, Hassell RG, Visser ME, Schwartz SM, **Voight BF**, Elosua R, Salomaa V, O'Donnell CJ, Dallinga-Thie GM, Anand SS, Yusuf S, Huff MW, Kathiresan S, Cao H, Hegele RA. Arterioscler Thromb Vasc Biol. 2011 Aug;31(8):1916-26. doi: 10.1161/ATVBAHA.111.226365. Epub 2011 May 19.

[29] A genome-wide association study identifies LIPA as a susceptibility gene for coronary artery disease. Wild PS, Zeller T, Schillert A, Szymczak S, Sinning CR, Deiseroth A, Schnabel RB, Lubos E, Keller T, Eleftheriadis MS, Bickel C, Rupprecht HJ, Wilde S, Rossmann H, Diemert P, Cupples LA, Perret C, Erdmann J, Stark K, Kleber ME, Epstein SE, **Voight BF**, Kuulasmaa K, Li M, Schäfer AS, Klopp N, Braund PS, Sager HB, Demissie S, Proust C, König IR, Wichmann HE, Reinhard W, Hoffmann MM, Virtamo J, Burnett MS, Siscovick D, Wiklund PG, Qu L, El Mokthari NE, Thompson JR, Peters A, Smith AV, Yon E, Baumert J, Hengstenberg C, März W, Amouyel P, Devaney J, Schwartz

SM, Saarela O, Mehta NN, Rubin D, Silander K, Hall AS, Ferrieres J, Harris TB, Melander O, Kee F, Hakonarson H, Schrezenmeir J, Gudnason V, Elosua R, Arveiler D, Evans A, Rader DJ, Illig T, Schreiber S, Bis JC, Altshuler D, Kavousi M, Witteman JC, Uitterlinden AG, Hofman A, Folsom AR, Barbalic M, Boerwinkle E, Kathiresan S, Reilly MP, O'Donnell CJ, Samani NJ, Schunkert H, Cambien F, Lackner KJ, Tiret L, Salomaa V, Munzel T, Ziegler A, Blankenberg S. Circ Cardiovasc Genet. 2011 Aug 1;4(4):403-12. doi: 10.1161/CIRCGENETICS.110.958728. Epub 2011 May 23.

[30] Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. Strawbridge RJ, Dupuis J, Prokopenko I, Barker A, Ahlqvist E, Rybin D, Petrie JR, Travers ME, Bouatia-Naji N, Dimas AS, Nica A, Wheeler E, Chen H, **Voight BF**, Taneera J, Kanoni S, Peden JF, Turrini F, Gustafsson S, Zabena C, Almgren P, Barker DJ, Barnes D, Dennison EM, Eriksson JG, Eriksson P, Eury E, Folkersen L, Fox CS, Frayling TM, Goel A, Gu HF, Horikoshi M, Isomaa B, Jackson AU, Jameson KA, Kajantie E, Kerr-Conte J, Kuulasmaa T, Kuusisto J, Loos RJ, Luan J, Makrilakis K, Manning AK, Martínez-Larrad MT, Narisu N, Nastase Mannila M, Ohrvik J, Osmond C, Pascoe L, Payne F, Sayer AA, Sennblad B, Silveira A, Stancáková A, Stirrups K, Swift AJ, Syvänen AC, Tuomi T, van 't Hooft FM, Walker M, Weedon MN, Xie W, Zethelius B; DIAGRAM Consortium; GIANT Consortium; MuTHER Consortium; CARDIoGRAM Consortium; C4D Consortium, Ongen H, Mälarstig A, Hopewell JC, Saleheen D, Chambers J, Parish S, Danesh J, Kooner J, Ostenson CG, Lind L, Cooper CC, Serrano-Ríos M, Ferrannini E, Forsen TJ, Clarke R, Franzosi MG, Seedorf U, Watkins H, Froguel P, Johnson P, Deloukas P, Collins FS, Laakso M, Dermitzakis ET, Boehnke M, McCarthy MI, Wareham NJ, Groop L, Pattou F, Gloyn AL, Dedoussis GV, Lyssenko V, Meigs JB, Barroso I, Watanabe RM, Ingelsson E, Langenberg C, Hamsten A, Florez JC. Diabetes. 2011 Oct;60(10):2624-34. doi: 10.2337/db11-0415. Epub 2011 Aug 26.

[31] Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Wain LV, Verwoert GC, O'Reilly PF, Shi G, Johnson T, Johnson AD, Bochud M, Rice KM, Henneman P, Smith AV, Ehret GB, Amin N, Larson MG, Mooser V, Hadley D, Dörr M, Bis JC, Aspelund T, Esko T, Janssens AC, Zhao JH, Heath S, Laan M, Fu J, Pistis G, Luan J, Arora P, Lucas G, Pirastu N, Pichler I, Jackson AU, Webster RJ, Zhang F, Peden JF, Schmidt H, Tanaka T, Campbell H, Igl W, Milaneschi Y, Hottenga JJ, Vitart V, Chasman DI, Trompet S, Bragg-Gresham JL, Alizadeh BZ, Chambers JC, Guo X, Lehtimäki T, Kühnel B, Lopez LM, Polašek O, Boban M, Nelson CP, Morrison AC, Pihur V, Ganesh SK, Hofman A, Kundu S, Mattace-Raso FU, Rivadeneira F, Sijbrands EJ, Uitterlinden AG, Hwang SJ, Vasan RS, Wang TJ, Bergmann S, Vollenweider P, Waeber G, Laitinen J, Pouta A, Zitting P, McArdle WL, Kroemer HK, Völker U, Völzke H, Glazer NL, Taylor KD, Harris TB, Alavere H, Haller T, Keis A, Tammesoo ML, Aulchenko Y, Barroso I, Khaw KT, Galan P, Hercberg S, Lathrop M, Eyheramendy S, Org E, Sõber S, Lu X, Nolte IM, Penninx BW, Corre T, Masciullo C, Sala C, Groop L, **Voight BF**, Melander O, O'Donnell CJ, Salomaa V, d'Adamo AP, Fabretto A, Faletra F, Ulivi S, Del Greco F, Facheris M, Collins FS, Bergman RN, Beilby JP, Hung J, Musk AW, Mangino M, Shin SY, Soranzo N, Watkins H, Goel A, Hamsten A, Gider P, Loitfelder M, Zeginigg M, Hernandez D, Najjar SS, Navarro P, Wild SH, Corsi AM, Singleton A, de Geus EJ, Willemsen G, Parker AN, Rose LM, Buckley B, Stott D, Orru M, Uda M; LifeLines Cohort Study, van der Klauw MM, Zhang W, Li X, Scott J, Chen YD, Burke GL, Kähönen M, Viikari J, Döring A, Meitinger T, Davies G, Starr JM, Emilsson V, Plump A, Lindeman JH, Hoen PA, König IR;

EchoGen consortium, Felix JF, Clarke R, Hopewell JC, Ongen H, Breteler M, Debette S, Destefano AL, Fornage M; AortaGen Consortium, Mitchell GF; CHARGE Consortium Heart Failure Working Group, Smith NL; KidneyGen consortium, Holm H, Stefansson K, Thorleifsson G, Thorsteinsdottir U; CKDGen consortium; Cardiogenics consortium; CardioGram, Samani NJ, Preuss M, Rudan I, Hayward C, Deary IJ, Wichmann HE, Raitakari OT, Palmas W, Kooner JS, Stolk RP, Jukema JW, Wright AF, Boomsma DI, Bandinelli S, Gyllensten UB, Wilson JF, Ferrucci L, Schmidt R, Farrall M, Spector TD, Palmer LJ, Tuomilehto J, Pfeufer A, Gasparini P, Siscovick D, Altshuler D, Loos RJ, Toniolo D, Snieder H, Gieger C, Meneton P, Wareham NJ, Oostra BA, Metspalu A, Launer L, Rettig R, Strachan DP, Beckmann JS, Witteman JC, Erdmann J, van Dijk KW, Boerwinkle E, Boehnke M, Ridker PM, Jarvelin MR, Chakravarti A, Abecasis GR, Gudnason V, Newton-Cheh C, Levy D, Munroe PB, Psaty BM, Caulfield MJ, Rao DC, Tobin MD, Elliott P, van Duijn CM. Nat Genet. 2011 Sep 11;43(10):1005-11. doi: 10.1038/ng.922.

[32] Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. International Consortium for Blood Pressure Genome-Wide Association Studies, Ehret GB, Munroe PB, Rice KM, Bochud M, Johnson AD, Chasman DI, Smith AV, Tobin MD, Verwoert GC, Hwang SJ, Pihur V, Vollenweider P, O'Reilly PF, Amin N, Bragg-Gresham JL, Teumer A, Glazer NL, Launer L, Zhao JH, Aulchenko Y, Heath S, Sõber S, Parsa A, Luan J, Arora P, Dehghan A, Zhang F, Lucas G, Hicks AA, Jackson AU, Peden JF, Tanaka T, Wild SH, Rudan I, Igl W, Milaneschi Y, Parker AN, Fava C, Chambers JC, Fox ER, Kumari M, Go MJ, van der Harst P, Kao WH, Sjögren M, Vinay DG, Alexander M, Tabara Y, Shaw-Hawkins S, Whincup PH, Liu Y, Shi G, Kuusisto J, Tayo B, Seielstad M, Sim X, Nguyen KD, Lehtimäki T, Matullo G, Wu Y, Gaunt TR, Onland-Moret NC, Cooper MN, Platou CG, Org E, Hardy R, Dahgam S, Palmen J, Vitart V, Braund PS, Kuznetsova T, Uiterwaal CS, Adeyemo A, Palmas W, Campbell H, Ludwig B, Tomaszewski M, Tzoulaki I, Palmer ND; CARDIoGRAM consortium; CKDGen Consortium; KidneyGen Consortium; EchoGen consortium; CHARGE-HF consortium, Aspelund T, Garcia M, Chang YP, O'Connell JR, Steinle NI, Grobbee DE, Arking DE, Kardia SL, Morrison AC, Hernandez D, Najjar S, McArdle WL, Hadley D, Brown MJ, Connell JM, Hingorani AD, Day IN, Lawlor DA, Beilby JP, Lawrence RW, Clarke R, Hopewell JC, Ongen H, Dreisbach AW, Li Y, Young JH, Bis JC, Kähönen M, Viikari J, Adair LS, Lee NR, Chen MH, Olden M, Pattaro C, Bolton JA, Köttgen A, Bergmann S, Mooser V, Chaturvedi N, Frayling TM, Islam M, Jafar TH, Erdmann J, Kulkarni SR, Bornstein SR, Grässler J, Groop L, **Voight BF**, Kettunen J, Howard P, Taylor A, Guarrera S, Ricceri F, Emilsson V, Plump A, Barroso I, Khaw KT, Weder AB, Hunt SC, Sun YV, Bergman RN, Collins FS, Bonnycastle LL, Scott LJ, Stringham HM, Peltonen L, Perola M, Vartiainen E, Brand SM, Staessen JA, Wang TJ, Burton PR, Soler Artigas M, Dong Y, Snieder H, Wang X, Zhu H, Lohman KK, Rudock ME, Heckbert SR, Smith NL, Wiggins KL, Doumatey A, Shriner D, Veldre G, Viigimaa M, Kinra S, Prabhakaran D, Tripathy V, Langefeld CD, Rosengren A, Thelle DS, Corsi AM, Singleton A, Forrester T, Hilton G, McKenzie CA, Salako T, Iwai N, Kita Y, Ogihara T, Ohkubo T, Okamura T, Ueshima H, Umemura S, Eyheramendy S, Meitinger T, Wichmann HE, Cho YS, Kim HL, Lee JY, Scott J, Sehmi JS, Zhang W, Hedblad B, Nilsson P, Smith GD, Wong A, Narisu N, Stančáková A, Raffel LJ, Yao J, Kathiresan S, O'Donnell CJ, Schwartz SM, Ikram MA, Longstreth WT Jr, Mosley TH, Seshadri S, Shrine NR, Wain LV, Morken MA, Swift AJ, Laitinen J, Prokopenko I, Zitting P, Cooper JA, Humphries SE, Danesh J, Rasheed A, Goel A, Hamsten A, Watkins H, Bakker SJ, van Gilst WH, Janipalli CS, Mani KR, Yajnik CS, Hofman A, Mattace-Raso FU, Oostra BA, Demirkan A, Isaacs A,

Rivadeneira F, Lakatta EG, Orru M, Scuteri A, Ala-Korpela M, Kangas AJ, Lyytikäinen LP, Soininen P, Tukiainen T, Würtz P, Ong RT, Dörr M, Kroemer HK, Völker U, Völzke H, Galan P, Hercberg S, Lathrop M, Zelenika D, Deloukas P, Mangino M, Spector TD, Zhai G, Meschia JF, Nalls MA, Sharma P, Terzic J, Kumar MV, Denniff M, Zukowska-Szczechowska E, Wagenknecht LE, Fowkes FG, Charchar FJ, Schwarz PE, Hayward C, Guo X, Rotimi C, Bots ML, Brand E, Samani NJ, Polasek O, Talmud PJ, Nyberg F, Kuh D, Laan M, Hveem K, Palmer LJ, van der Schouw YT, Casas JP, Mohlke KL, Vineis P, Raitakari O, Ganesh SK, Wong TY, Tai ES, Cooper RS, Laakso M, Rao DC, Harris TB, Morris RW, Dominiczak AF, Kivimaki M, Marmot MG, Miki T, Saleheen D, Chandak GR, Coresh J, Navis G, Salomaa V, Han BG, Zhu X, Kooner JS, Melander O, Ridker PM, Bandinelli S, Gyllensten UB, Wright AF, Wilson JF, Ferrucci L, Farrall M, Tuomilehto J, Pramstaller PP, Elosua R, Soranzo N, Sijbrands EJ, Altshuler D, Loos RJ, Shuldiner AR, Gieger C, Meneton P, Uitterlinden AG, Wareham NJ, Gudnason V, Rotter JI, Rettig R, Uda M, Strachan DP, Witteman JC, Hartikainen AL, Beckmann JS, Boerwinkle E, Vasan RS, Boehnke M, Larson MG, Järvelin MR, Psaty BM, Abecasis GR, Chakravarti A, Elliott P, van Duijn CM, Newton-Cheh C, Levy D, Caulfield MJ, Johnson T. Nature. 2011 Sep 11;478(7367):103-9. doi: 10.1038/nature10405.

[33] Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. O'Donnell CJ, Kavousi M, Smith AV, Kardia SL, Feitosa MF, Hwang SJ, Sun YV, Province MA, Aspelund T, Dehghan A, Hoffmann U, Bielak LF, Zhang Q, Eiriksdottir G, van Duijn CM, Fox CS, de Andrade M, Kraja AT, Sigurdsson S, Elias-Smale SE, Murabito JM, Launer LJ, van der Lugt A, Kathiresan S; CARDIoGRAM Consortium, Krestin GP, Herrington DM, Howard TD, Liu Y, Post W, Mitchell BD, O'Connell JR, Shen H, Shuldiner AR, Altshuler D, Elosua R, Salomaa V, Schwartz SM, Siscovick DS, **Voight BF**, Bis JC, Glazer NL, Psaty BM, Boerwinkle E, Heiss G, Blankenberg S, Zeller T, Wild PS, Schnabel RB, Schillert A, Ziegler A, Münzel TF, White CC, Rotter JI, Nalls M, Oudkerk M, Johnson AD, Newman AB, Uitterlinden AG, Massaro JM, Cunningham J, Harris TB, Hofman A, Peyser PA, Borecki IB, Cupples LA, Gudnason V, Witteman JC. Circulation. 2011 Dec 20;124(25):2855-64. doi: 10.1161/CIRCULATIONAHA.110.974899. Epub 2011 Dec 5.

[34] A genome-wide association search for type 2 diabetes genes in African Americans. Palmer ND, McDonough CW, Hicks PJ, Roh BH, Wing MR, An SS, Hester JM, Cooke JN, Bostrom MA, Rudock ME, Talbert ME, Lewis JP; DIAGRAM Consortium; MAGIC Investigators, Ferrara A, Lu L, Ziegler JT, Sale MM, Divers J, Shriner D, Adeyemo A, Rotimi CN, Ng MC, Langefeld CD, Freedman BI, Bowden DW, **Voight BF**, Scott LJ, Steinthorsdottir V, Morris AP, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Langenberg C, Hofmann OM, Dupuis J, Qi L, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Couper DJ, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Klopp N, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Perry JR, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M,

Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Mohlke KL, Morris AD, Palmer CN, Pramstaller PP, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Wareham NJ, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Hu FB, Meigs JB, Pankow JS, Pedersen O, Wichmann HE, Barroso I, Florez JC, Frayling TM, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, Boehnke M, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Johnson T, Elliott P, Rybin D, Henneman P, Dehghan A, Hottenga JJ, Song K, Goel A, Egan JM, Lajunen T, Doney A, Kanoni S, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Frants R, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hicks AA, Hillman DR, Hingorani AD, Hui J, Hung J, Jula A, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Manning AK, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Oostra BA, Orrù M, Pakyz R, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Perola M, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Psaty BM, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tanaka T, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC, Borecki IB, Loos RJ, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Salomaa V, Smith GD, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Dedoussis GV, Serrano-Ríos M, Lind L, Palmer LJ, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A, Buchanan TA, Valle TT, Rotter JI, Siscovick DS, Penninx BW, Boomsma DI, Deloukas P, Spector TD, Ferrucci L, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Waterworth DM, Vollenweider P, Peltonen L, Mooser V, Sladek R. PLoS One. 2012;7(1):e29202. doi: 10.1371/journal.pone.0029202. Epub 2012 Jan 4.

[35] Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. Saxena R, Elbers CC, Guo Y, Peter I, Gaunt TR, Mega JL, Lanktree MB, Tare A, Castillo BA, Li YR, Johnson T, Bruinenberg M, Gilbert-Diamond D, Rajagopalan R, Voight BF, Balasubramanyam A, Barnard J, Bauer F, Baumert J, Bhangale T, Böhm BO, Braund PS, Burton PR, Chandrupatla HR, Clarke R, Cooper-DeHoff RM, Crook ED, Davey-Smith G, Day IN, de Boer A, de Groot MC, Drenos F, Ferguson J, Fox CS, Furlong CE, Gibson Q, Gieger C, Gilhuijs-Pederson LA, Glessner JT, Goel A, Gong Y, Grant SF, Grobbee DE, Hastie C, Humphries SE, Kim CE, Kivimaki M, Kleber M, Meisinger C, Kumari M, Langaee

TY, Lawlor DA, Li M, Lobmeyer MT, Maitland-van der Zee AH, Meijs MF, Molony CM, Morrow DA, Murugesan G, Musani SK, Nelson CP, Newhouse SJ, O'Connell JR, Padmanabhan S, Palmen J, Patel SR, Pepine CJ, Pettinger M, Price TS, Rafelt S, Ranchalis J, Rasheed A, Rosenthal E, Ruczinski I, Shah S, Shen H, Silbernagel G, Smith EN, Spijkerman AW, Stanton A, Steffes MW, Thorand B, Trip M, van der Harst P, van der A DL, van Iperen EP, van Setten J, van Vliet-Ostaptchouk JV, Verweij N, Wolffenbuttel BH, Young T, Zafarmand MH, Zmuda JM; Look AHEAD Research Group; DIAGRAM consortium, Boehnke M, Altshuler D, McCarthy M, Kao WH, Pankow JS, Cappola TP, Sever P, Poulter N, Caulfield M, Dominiczak A, Shields DC, Bhatt DL, Zhang L, Curtis SP, Danesh J, Casas JP, van der Schouw YT, Onland-Moret NC, Doevendans PA, Dorn GW 2nd, Farrall M, FitzGerald GA, Hamsten A, Hegele R, Hingorani AD, Hofker MH, Huggins GS, Illig T, Jarvik GP, Johnson JA, Klungel OH, Knowler WC, Koenig W, März W, Meigs JB, Melander O, Munroe PB, Mitchell BD, Bielinski SJ, Rader DJ, Reilly MP, Rich SS, Rotter JI, Saleheen D, Samani NJ, Schadt EE, Shuldiner AR, Silverstein R, Kottke-Marchant K, Talmud PJ, Watkins H, Asselbergs FW, de Bakker PI, McCaffery J, Wijmenga C, Sabatine MS, Wilson JG, Reiner A, Bowden DW, Hakonarson H, Siscovick DS, Keating BJ. Am J Hum Genet. 2012 Mar 9;90(3):410-25. doi: 10.1016/j.ajhg.2011.12.022. Epub 2012 Feb 9.

[36] Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. Dastani Z, Hivert MF, Timpson N, Perry JR, Yuan X, Scott RA, Henneman P, Heid IM, Kizer JR, Lyytikäinen LP, Fuchsberger C, Tanaka T, Morris AP, Small K, Isaacs A, Beekman M, Coassin S, Lohman K, Qi L, Kanoni S, Pankow JS, Uh HW, Wu Y, Bidulescu A, Rasmussen-Torvik LJ, Greenwood CM, Ladouceur M, Grimsby J, Manning AK, Liu CT, Kooner J, Mooser VE, Vollenweider P, Kapur KA, Chambers J, Wareham NJ, Langenberg C, Frants R, Willems-Vandijk K, Oostra BA, Willems SM, Lamina C, Winkler TW, Psaty BM, Tracy RP, Brody J, Chen I, Viikari J, Kähönen M, Pramstaller PP, Evans DM, St Pourcain B, Sattar N, Wood AR, Bandinelli S, Carlson OD, Egan JM, Böhringer S, van Heemst D, Kedenko L, Kristiansson K, Nuotio ML, Loo BM, Harris T, Garcia M, Kanaya A, Haun M, Klopp N, Wichmann HE, Deloukas P, Katsareli E, Couper DJ, Duncan BB, Kloppenburg M, Adair LS, Borja JB; DIAGRAM+ Consortium; MAGIC Consortium; GLGC Investigators; MuTHER Consortium, Wilson JG, Musani S, Guo X, Johnson T, Semple R, Teslovich TM, Allison MA, Redline S, Buxbaum SG, Mohlke KL, Meulenbelt I, Ballantyne CM, Dedoussis GV, Hu FB, Liu Y, Paulweber B, Spector TD, Slagboom PE, Ferrucci L, Jula A, Perola M, Raitakari O, Florez JC, Salomaa V, Eriksson JG, Frayling TM, Hicks AA, Lehtimäki T, Smith GD, Siscovick DS, Kronenberg F, van Duijn C, Loos RJ, Waterworth DM, Meigs JB, Dupuis J, Richards JB, **Voight BF**, Scott LJ, Steinthorsdottir V, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Hofmann OM, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T,

Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Morris AD, Palmer CN, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Pedersen O, Barroso I, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, Boehnke M, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Elliott P, Rybin D, Dehghan A, Hottenga JJ, Song K, Goel A, Lajunen T, Doney A, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hillman DR, Hingorani AD, Hui J, Hung J, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Orrù M, Pakyz R, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sigurðsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global B Pgen Consortium, Borecki IB, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Serrano-Ríos M, Lind L, Palmer LJ, Hu FB 1st, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A; Procardis Consortium, Buchanan TA, Valle TT, Rotter JI, Penninx BW, Boomsma DI, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Peltonen L, Mooser V, Sladek R; MAGIC investigators; GLGC Consortium, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Chasman DI, Johansen CT, Fouchier SW, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Feitosa MF, Orho-Melander M, Melander O, Li X, Li M, Cho YS, Go MJ, Kim YJ, Lee JY, Park T, Kim K, Sim X, Ong RT, Croteau-Chonka DC, Lange LA, Smith JD, Ziegler A, Zhang W, Zee RY, Whitfield JB, Thompson JR, Surakka I, Spector TD, Smit JH, Sinisalo J, Scott J, Saharinen J, Sabatti C, Rose LM, Roberts R, Rieder M, Parker AN, Pare G, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, McArdle W, Masson D, Martin NG, Marroni F, Lucas G, Luben R, Lokki ML, Lettre G, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, König IR, Khaw KT, Kaplan LM, Johansson Å, Janssens AC, Igl W, Hovingh GK, Hengstenberg C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Groop LC, Gonzalez E, Freimer NB, Erdmann J, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Faire U, Crawford G, Chen YD, Caulfield MJ, Boekholdt SM, Assimes TL, Quertermous T, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Taylor HA Jr,

Gabriel SB, Holm H, Gudnason V, Krauss RM, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Strachan DP, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, Kathiresan S. PLoS Genet. 2012;8(3):e1002607. doi: 10.1371/journal.pgen.1002607. Epub 2012 Mar 29.

[37] Evaluation of the metabochip genotyping array in African Americans and implications for fine mapping of GWAS-identified loci: the PAGE study. Buyske S, Wu Y, Carty CL, Cheng I, Assimes TL, Dumitrescu L, Hindorff LA, Mitchell S, Ambite JL, Boerwinkle E, Buzkova P, Carlson CS, Cochran B, Duggan D, Eaton CB, Fesinmeyer MD, Franceschini N, Haessler J, Jenny N, Kang HM, Kooperberg C, Lin Y, Le Marchand L, Matise TC, Robinson JG, Rodriguez C, Schumacher FR, **Voight BF**, Young A, Manolio TA, Mohlke KL, Haiman CA, Peters U, Crawford DC, North KE. PLoS One. 2012;7(4):e35651. doi: 10.1371/journal.pone.0035651. Epub 2012 Apr 23.

[38] Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Ellinor PT, Lunetta KL, Albert CM, Glazer NL, Ritchie MD, Smith AV, Arking DE, Müller-Nurasyid M, Krijthe BP, Lubitz SA, Bis JC, Chung MK, Dörr M, Ozaki K, Roberts JD, Smith JG, Pfeufer A, Sinner MF, Lohman K, Ding J, Smith NL, Smith JD, Rienstra M, Rice KM, Van Wagoner DR, Magnani JW, Wakili R, Clauss S, Rotter JI, Steinbeck G, Launer LJ, Davies RW, Borkovich M, Harris TB, Lin H, Völker U, Völzke H, Milan DJ, Hofman A, Boerwinkle E, Chen LY, Soliman EZ, **Voight BF**, Li G, Chakravarti A, Kubo M, Tedrow UB, Rose LM, Ridker PM, Conen D, Tsunoda T, Furukawa T, Sotoodehnia N, Xu S, Kamatani N, Levy D, Nakamura Y, Parvez B, Mahida S, Furie KL, Rosand J, Muhammad R, Psaty BM, Meitinger T, Perz S, Wichmann HE, Witteman JC, Kao WH, Kathiresan S, Roden DM, Uitterlinden AG, Rivadeneira F, McKnight B, Sjögren M, Newman AB, Liu Y, Gollob MH, Melander O, Tanaka T, Stricker BH, Felix SB, Alonso A, Darbar D, Barnard J, Chasman DI, Heckbert SR, Benjamin EJ, Gudnason V, Kääb S. Nat Genet. 2012 Apr 29;44(6):670-5. doi: 10.1038/ng.2261.

[39] A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Manning AK, Hivert MF, Scott RA, Grimsby JL, Bouatia-Naji N, Chen H, Rybin D, Liu CT, Bielak LF, Prokopenko I, Amin N, Barnes D, Cadby G, Hottenga JJ, Ingelsson E, Jackson AU, Johnson T, Kanoni S, Ladenvall C, Lagou V, Lahti J, Lecoeur C, Liu Y, Martinez-Larrad MT, Montasser ME, Navarro P, Perry JR, Rasmussen-Torvik LJ, Salo P, Sattar N, Shungin D, Strawbridge RJ, Tanaka T, van Duijn CM, An P, de Andrade M, Andrews JS, Aspelund T, Atalay M, Aulchenko Y, Balkau B, Bandinelli S, Beckmann JS, Beilby JP, Bellis C, Bergman RN, Blangero J, Boban M, Boehnke M, Boerwinkle E, Bonnycastle LL, Boomsma DI, Borecki IB, Böttcher Y, Bouchard C, Brunner E, Budimir D, Campbell H, Carlson O, Chines PS, Clarke R, Collins FS, Corbatón-Anchuelo A, Couper D, de Faire U, Dedoussis GV, Deloukas P, Dimitriou M, Egan JM, Eiriksdottir G, Erdos MR, Eriksson JG, Eury E, Ferrucci L, Ford I, Forouhi NG, Fox CS, Franzosi MG, Franks PW, Frayling TM, Froguel P, Galan P, de Geus E, Gigante B, Glazer NL, Goel A, Groop L, Gudnason V, Hallmans G, Hamsten A, Hansson O, Harris TB, Hayward C, Heath S, Hercberg S, Hicks AA, Hingorani A, Hofman A, Hui J, Hung J, Jarvelin MR, Jhun MA, Johnson PC, Jukema JW, Jula A, Kao WH, Kaprio J, Kardia SL, Keinanen-Kiukaanniemi S, Kivimaki M, Kolcic I, Kovacs P, Kumari M, Kuusisto J, Kyvik KO, Laakso M, Lakka T, Lannfelt L, Lathrop GM, Launer LJ, Leander K, Li G, Lind L, Lindstrom J, Lobbens S, Loos RJ, Luan J, Lyssenko V, Mägi R, Magnusson PK, Marmot M, Meneton P, Mohlke KL, Mooser V, Morken MA, Miljkovic I, Narisu N, O'Connell J, Ong KK, Oostra BA, Palmer LJ, Palotie A, Pankow JS, Peden JF,

Pedersen NL, Pehlic M, Peltonen L, Penninx B, Pericic M, Perola M, Perusse L, Peyser PA, Polasek O, Pramstaller PP, Province MA, Räikkönen K, Rauramaa R, Rehnberg E, Rice K, Rotter JI, Rudan I, Ruokonen A, Saaristo T, Sabater-Lleal M, Salomaa V, Savage DB, Saxena R, Schwarz P, Seedorf U, Sennblad B, Serrano-Rios M, Shuldiner AR, Sijbrands EJ, Siscovick DS, Smit JH, Small KS, Smith NL, Smith AV, Stančáková A, Stirrups K, Stumvoll M, Sun YV, Swift AJ, Tönjes A, Tuomilehto J, Trompet S, Uitterlinden AG, Uusitupa M, Vikström M, Vitart V, Vohl MC, **Voight BF**, Vollenweider P, Waeber G, Waterworth DM, Watkins H, Wheeler E, Widen E, Wild SH, Willems SM, Willemsen G, Wilson JF, Witteman JC, Wright AF, Yaghootkar H, Zelenika D, Zemunik T, Zgaga L; DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium; Multiple Tissue Human Expression Resource (MUTHER) Consortium, Wareham NJ, McCarthy MI, Barroso I, Watanabe RM, Florez JC, Dupuis J, Meigs JB, Langenberg C. Nat Genet. 2012 May 13;44(6):659-69. doi: 10.1038/ng.2274.

[40] Impact of common variation in bone-related genes on type 2 diabetes and related traits. Billings LK, Hsu YH, Ackerman RJ, Dupuis J, **Voight BF**, Rasmussen-Torvik LJ, Hercberg S, Lathrop M, Barnes D, Langenberg C, Hui J, Fu M, Bouatia-Naji N, Lecoeur C, An P, Magnusson PK, Surakka I, Ripatti S, Christiansen L, Dalgård C, Folkersen L, Grundberg E; MAGIC Investigators; DIAGRAM + Consortium; MuTHER Consortium; ASCOT Investigators; GEFOS Consortium, Eriksson P, Kaprio J, Ohm Kyvik K, Pedersen NL, Borecki IB, Province MA, Balkau B, Froguel P, Shuldiner AR, Palmer LJ, Wareham N, Meneton P, Johnson T, Pankow JS, Karasik D, Meigs JB, Kiel DP, Florez JC. Diabetes. 2012 Aug;61(8):2176-86. doi: 10.2337/db11-1515. Epub 2012 Jun 14.

[41] Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Scott RA, Lagou V, Welch RP, Wheeler E, Montasser ME, Luan J, Mägi R, Strawbridge RJ, Rehnberg E, Gustafsson S, Kanoni S, Rasmussen-Torvik LJ, Yengo L, Lecoeur C, Shungin D, Sanna S, Sidore C, Johnson PC, Jukema JW, Johnson T, Mahajan A, Verweij N, Thorleifsson G, Hottenga JJ, Shah S, Smith AV, Sennblad B, Gieger C, Salo P, Perola M, Timpson NJ, Evans DM, Pourcain BS, Wu Y, Andrews JS, Hui J, Bielak LF, Zhao W, Horikoshi M, Navarro P, Isaacs A, O'Connell JR, Stirrups K, Vitart V, Hayward C, Esko T, Mihailov E, Fraser RM, Fall T, **Voight BF**, Raychaudhuri S, Chen H, Lindgren CM, Morris AP, Rayner NW, Robertson N, Rybin D, Liu CT, Beckmann JS, Willems SM, Chines PS, Jackson AU, Kang HM, Stringham HM, Song K, Tanaka T, Peden JF, Goel A, Hicks AA, An P, Müller-Nurasyid M, Franco-Cereceda A, Folkersen L, Marullo L, Jansen H, Oldehinkel AJ, Bruinenberg M, Pankow JS, North KE, Forouhi NG, Loos RJ, Edkins S, Varga TV, Hallmans G, Oksa H, Antonella M, Nagaraja R, Trompet S, Ford I, Bakker SJ, Kong A, Kumari M, Gigante B, Herder C, Munroe PB, Caulfield M, Antti J, Mangino M, Small K, Miljkovic I, Liu Y, Atalay M, Kiess W, James AL, Rivadeneira F, Uitterlinden AG, Palmer CN, Doney AS, Willemsen G, Smit JH, Campbell S, Polasek O, Bonnycastle LL, Hercberg S, Dimitriou M, Bolton JL, Fowkes GR, Kovacs P, Lindström J, Zemunik T, Bandinelli S, Wild SH, Basart HV, Rathmann W, Grallert H; DIAbetes Genetics Replication and Meta-analysis (DIAGRAM) Consortium, Maerz W, Kleber ME, Boehm BO, Peters A, Pramstaller PP, Province MA, Borecki IB, Hastie ND, Rudan I, Campbell H, Watkins H, Farrall M, Stumvoll M, Ferrucci L, Waterworth DM, Bergman RN, Collins FS, Tuomilehto J, Watanabe RM, de Geus EJ, Penninx BW, Hofman A, Oostra BA, Psaty BM, Vollenweider P, Wilson JF, Wright AF, Hovingh GK, Metspalu A, Uusitupa M, Magnusson PK, Kyvik KO, Kaprio J, Price JF, Dedoussis GV, Deloukas P, Meneton P, Lind L, Boehnke M, Shuldiner

AR, van Duijn CM, Morris AD, Toenjes A, Peyser PA, Beilby JP, Körner A, Kuusisto J, Laakso M, Bornstein SR, Schwarz PE, Lakka TA, Rauramaa R, Adair LS, Smith GD, Spector TD, Illig T, de Faire U, Hamsten A, Gudnason V, Kivimaki M, Hingorani A, Keinanen-Kiukaanniemi SM, Saaristo TE, Boomsma DI, Stefansson K, van der Harst P, Dupuis J, Pedersen NL, Sattar N, Harris TB, Cucca F, Ripatti S, Salomaa V, Mohlke KL, Balkau B, Froguel P, Pouta A, Jarvelin MR, Wareham NJ, Bouatia-Naji N, McCarthy MI, Franks PW, Meigs JB, Teslovich TM, Florez JC, Langenberg C, Ingelsson E, Prokopenko I, Barroso I. Nat Genet. 2012 Sep;44(9):991-1005. doi: 10.1038/ng.2385. Epub 2012 Aug 12.

[42] Identification of the BCAR1-CFDP1-TMEM170A locus as a determinant of carotid intima-media thickness and coronary artery disease risk. Gertow K, Sennblad B, Strawbridge RJ, Ohrvik J, Zabaneh D, Shah S, Veglia F, Fava C, Kavousi M, McLachlan S, Kivimäki M, Bolton JL, Folkersen L, Gigante B, Leander K, Vikström M, Larsson M, Silveira A, Deanfield J, **Voight BF**, Fontanillas P, Sabater-Lleal M, Colombo GI, Kumari M, Langenberg C, Wareham NJ, Uitterlinden AG, Gabrielsen A, Hedin U, Franco-Cereceda A, Nyyssönen K, Rauramaa R, Tuomainen TP, Savonen K, Smit AJ, Giral P, Mannarino E, Robertson CM, Talmud PJ, Hedblad B, Hofman A, Erdmann J, Reilly MP, O'Donnell CJ, Farrall M, Clarke R, Franzosi MG, Seedorf U, Syvänen AC, Hansson GK, Eriksson P, Samani NJ, Watkins H, Price JF, Hingorani AD, Melander O, Witteman JC, Baldassarre D, Tremoli E, de Faire U, Humphries SE, Hamsten A. Circ Cardiovasc Genet. 2012 Dec;5(6):656-65. doi: 10.1161/CIRCGENETICS.112.963660. Epub 2012 Nov 14.

[43] Large-scale association analysis identifies new risk loci for coronary artery disease. CARDIoGRAMplusC4D Consortium, Deloukas P, Kanoni S, Willenborg C, Farrall M, Assimes TL, Thompson JR, Ingelsson E, Saleheen D, Erdmann J, Goldstein BA, Stirrups K, König IR, Cazier JB, Johansson A, Hall AS, Lee JY, Willer CJ, Chambers JC, Esko T, Folkersen L, Goel A, Grundberg E, Havulinna AS, Ho WK, Hopewell JC, Eriksson N, Kleber ME, Kristiansson K, Lundmark P, Lyytikäinen LP, Rafelt S, Shungin D, Strawbridge RJ, Thorleifsson G, Tikkanen E, Van Zuydam N, **Voight BF**, Waite LL, Zhang W, Ziegler A, Absher D, Altshuler D, Balmforth AJ, Barroso I, Braund PS, Burgdorf C, Claudi-Boehm S, Cox D, Dimitriou M, Do R; DIAGRAM Consortium; CARDIOGENICS Consortium, Doney AS, El Mokhtari N, Eriksson P, Fischer K, Fontanillas P, Franco-Cereceda A, Gigante B, Groop L, Gustafsson S, Hager J, Hallmans G, Han BG, Hunt SE, Kang HM, Illig T, Kessler T, Knowles JW, Kolovou G, Kuusisto J, Langenberg C, Langford C, Leander K, Lokki ML, Lundmark A, McCarthy MI, Meisinger C, Melander O, Mihailov E, Maouche S, Morris AD, Müller-Nurasyid M; MuTHER Consortium, Nikus K, Peden JF, Rayner NW, Rasheed A, Rosinger S, Rubin D, Rumpf MP, Schäfer A, Sivananthan M, Song C, Stewart AF, Tan ST, Thorgeirsson G, van der Schoot CE, Wagner PJ; Wellcome Trust Case Control Consortium, Wells GA, Wild PS, Yang TP, Amouyel P, Arveiler D, Basart H, Boehnke M, Boerwinkle E, Brambilla P, Cambien F, Cupples AL, de Faire U, Dehghan A, Diemert P, Epstein SE, Evans A, Ferrario MM, Ferrières J, Gauguier D, Go AS, Goodall AH, Gudnason V, Hazen SL, Holm H, Iribarren C, Jang Y, Kähönen M, Kee F, Kim HS, Klopp N, Koenig W, Kratzer W, Kuulasmaa K, Laakso M, Laaksonen R, Lee JY, Lind L, Ouwehand WH, Parish S, Park JE, Pedersen NL, Peters A, Quertermous T, Rader DJ, Salomaa V, Schadt E, Shah SH, Sinisalo J, Stark K, Stefansson K, Trégouët DA, Virtamo J, Wallentin L, Wareham N, Zimmermann ME, Nieminen MS, Hengstenberg C, Sandhu MS, Pastinen T, Syvänen AC, Hovingh GK, Dedoussis G, Franks PW, Lehtimäki T, Metspalu A, Zalloua PA, Siegbahn A, Schreiber S, Ripatti S, Blankenberg SS, Perola M,

Clarke R, Boehm BO, O'Donnell C, Reilly MP, März W, Collins R, Kathiresan S, Hamsten A, Kooner JS, Thorsteinsdottir U, Danesh J, Palmer CN, Roberts R, Watkins H, Schunkert H, Samani NJ. Nat Genet. 2013 Jan;45(1):25-33. doi: 10.1038/ng.2480. Epub 2012 Dec 2.

[44] Common variants associated with plasma triglycerides and risk for coronary artery disease. Do R, Willer CJ, Schmidt EM, Sengupta S, Gao C, Peloso GM, Gustafsson S, Kanoni S, Ganna A, Chen J, Buchkovich ML, Mora S, Beckmann JS, Bragg-Gresham JL, Chang HY, Demirkan A, Den Hertog HM, Donnelly LA, Ehret GB, Esko T, Feitosa MF, Ferreira T, Fischer K, Fontanillas P, Fraser RM, Freitag DF, Gurdasani D, Heikkilä K, Hyppönen E, Isaacs A, Jackson AU, Johansson A, Johnson T, Kaakinen M, Kettunen J, Kleber ME, Li X, Luan J, Lyytikäinen LP, Magnusson PK, Mangino M, Mihailov E, Montasser ME, Müller-Nurasyid M, Nolte IM, O'Connell JR, Palmer CD, Perola M, Petersen AK, Sanna S, Saxena R, Service SK, Shah S, Shungin D, Sidore C, Song C, Strawbridge RJ, Surakka I, Tanaka T, Teslovich TM, Thorleifsson G, Van den Herik EG, **Voight BF**, Volcik KA, Waite LL, Wong A, Wu Y, Zhang W, Absher D, Asiki G, Barroso I, Been LF, Bolton JL, Bonnycastle LL, Brambilla P, Burnett MS, Cesana G, Dimitriou M, Doney AS, Döring A, Elliott P, Epstein SE, Eyjolfsson GI, Gigante B, Goodarzi MO, Grallert H, Gravito ML, Groves CJ, Hallmans G, Hartikainen AL, Hayward C, Hernandez D, Hicks AA, Holm H, Hung YJ, Illig T, Jones MR, Kaleebu P, Kastelein JJ, Khaw KT, Kim E, Klopp N, Komulainen P, Kumari M, Langenberg C, Lehtimäki T, Lin SY, Lindström J, Loos RJ, Mach F, McArdle WL, Meisinger C, Mitchell BD, Müller G, Nagaraja R, Narisu N, Nieminen TV, Nsubuga RN, Olafsson I, Ong KK, Palotie A, Papamarkou T, Pomilla C, Pouta A, Rader DJ, Reilly MP, Ridker PM, Rivadeneira F, Rudan I, Ruokonen A, Samani N, Scharnagl H, Seeley J, Silander K, Stančáková A, Stirrups K, Swift AJ, Tiret L, Uitterlinden AG, van Pelt LJ, Vedantam S, Wainwright N, Wijmenga C, Wild SH, Willemsen G, Wilsgaard T, Wilson JF, Young EH, Zhao JH, Adair LS, Arveiler D, Assimes TL, Bandinelli S, Bennett F, Bochud M, Boehm BO, Boomsma DI, Borecki IB, Bornstein SR, Bovet P, Burnier M, Campbell H, Chakravarti A, Chambers JC, Chen YD, Collins FS, Cooper RS, Danesh J, Dedoussis G, de Faire U, Feranil AB, Ferrières J, Ferrucci L, Freimer NB, Gieger C, Groop LC, Gudnason V, Gyllensten U, Hamsten A, Harris TB, Hingorani A, Hirschhorn JN, Hofman A, Hovingh GK, Hsiung CA, Humphries SE, Hunt SC, Hveem K, Iribarren C, Järvelin MR, Jula A, Kähönen M, Kaprio J, Kesäniemi A, Kivimaki M, Kooner JS, Koudstaal PJ, Krauss RM, Kuh D, Kuusisto J, Kyvik KO, Laakso M, Lakka TA, Lind L, Lindgren CM, Martin NG, März W, McCarthy MI, McKenzie CA, Meneton P, Metspalu A, Moilanen L, Morris AD, Munroe PB, Njølstad I, Pedersen NL, Power C, Pramstaller PP, Price JF, Psaty BM, Quertermous T, Rauramaa R, Saleheen D, Salomaa V, Sanghera DK, Saramies J, Schwarz PE, Sheu WH, Shuldiner AR, Siegbahn A, Spector TD, Stefansson K, Strachan DP, Tayo BO, Tremoli E, Tuomilehto J, Uusitupa M, van Duijn CM, Vollenweider P, Wallentin L, Wareham NJ, Whitfield JB, Wolffenbuttel BH, Altshuler D, Ordovas JM, Boerwinkle E, Palmer CN, Thorsteinsdottir U, Chasman DI, Rotter JI, Franks PW, Ripatti S, Cupples LA, Sandhu MS, Rich SS, Boehnke M, Deloukas P, Mohlke KL, Ingelsson E, Abecasis GR, Daly MJ, Neale BM, Kathiresan S. Nat Genet. 2013 Nov;45(11):1345-52. doi: 10.1038/ng.2795. Epub 2013 Oct 6.

[45] Discovery and refinement of loci associated with lipid levels. Willer CJ, Schmidt EM, Sengupta S, Peloso GM, Gustafsson S, Kanoni S, Ganna A, Chen J, Buchkovich ML, Mora S, Beckmann JS, Bragg-Gresham JL, Chang HY, Demirkan A, Den Hertog HM, Do R, Donnelly LA, Ehret GB, Esko T, Feitosa MF, Ferreira T, Fischer K, Fontanillas P, Fraser RM, Freitag DF, Gurdasani D, Heikkilä K, Hyppönen E, Isaacs A, Jackson AU, Johansson

Å, Johnson T, Kaakinen M, Kettunen J, Kleber ME, Li X, Luan J, Lyytikäinen LP, Magnusson PKE, Mangino M, Mihailov E, Montasser ME, Müller-Nurasyid M, Nolte IM, O'Connell JR, Palmer CD, Perola M, Petersen AK, Sanna S, Saxena R, Service SK, Shah S, Shungin D, Sidore C, Song C, Strawbridge RJ, Surakka I, Tanaka T, Teslovich TM, Thorleifsson G, Van den Herik EG, **Voight BF**, Volcik KA, Waite LL, Wong A, Wu Y, Zhang W, Absher D, Asiki G, Barroso I, Been LF, Bolton JL, Bonnycastle LL, Brambilla P, Burnett MS, Cesana G, Dimitriou M, Doney ASF, Döring A, Elliott P, Epstein SE, Ingi Eyjolfsson G, Gigante B, Goodarzi MO, Grallert H, Gravito ML, Groves CJ, Hallmans G, Hartikainen AL, Hayward C, Hernandez D, Hicks AA, Holm H, Hung YJ, Illig T, Jones MR, Kaleebu P, Kastelein JJP, Khaw KT, Kim E, Klopp N, Komulainen P, Kumari M, Langenberg C, Lehtimäki T, Lin SY, Lindström J, Loos RJF, Mach F, McArdle WL, Meisinger C, Mitchell BD, Müller G, Nagaraja R, Narisu N, Nieminen TVM, Nsubuga RN, Olafsson I, Ong KK, Palotie A, Papamarkou T, Pomilla C, Pouta A, Rader DJ, Reilly MP, Ridker PM, Rivadeneira F, Rudan I, Ruokonen A, Samani N, Scharnagl H, Seeley J, Silander K, Stančáková A, Stirrups K, Swift AJ, Tiret L, Uitterlinden AG, van Pelt LJ, Vedantam S, Wainwright N, Wijmenga C, Wild SH, Willemsen G, Wilsgaard T, Wilson JF, Young EH, Zhao JH, Adair LS, Arveiler D, Assimes TL, Bandinelli S, Bennett F, Bochud M, Boehm BO, Boomsma DI, Borecki IB, Bornstein SR, Bovet P, Burnier M, Campbell H, Chakravarti A, Chambers JC, Chen YI, Collins FS, Cooper RS, Danesh J, Dedoussis G, de Faire U, Feranil AB, Ferrières J, Ferrucci L, Freimer NB, Gieger C, Groop LC, Gudnason V, Gyllensten U, Hamsten A, Harris TB, Hingorani A, Hirschhorn JN, Hofman A, Hovingh GK, Hsiung CA, Humphries SE, Hunt SC, Hveem K, Iribarren C, Järvelin MR, Jula A, Kähönen M, Kaprio J, Kesäniemi A, Kivimaki M, Kooner JS, Koudstaal PJ, Krauss RM, Kuh D, Kuusisto J, Kyvik KO, Laakso M, Lakka TA, Lind L, Lindgren CM, Martin NG, März W, McCarthy MI, McKenzie CA, Meneton P, Metspalu A, Moilanen L, Morris AD, Munroe PB, Njølstad I, Pedersen NL, Power C, Pramstaller PP, Price JF, Psaty BM, Quertermous T, Rauramaa R, Saleheen D, Salomaa V, Sanghera DK, Saramies J, Schwarz PEH, Sheu WH, Shuldiner AR, Siegbahn A, Spector TD, Stefansson K, Strachan DP, Tayo BO, Tremoli E, Tuomilehto J, Uusitupa M, van Duijn CM, Vollenweider P, Wallentin L, Wareham NJ, Whitfield JB, Wolffenbuttel BHR, Ordovas JM, Boerwinkle E, Palmer CNA, Thorsteinsdottir U, Chasman DI, Rotter JI, Franks PW, Ripatti S, Cupples LA, Sandhu MS, Rich SS, Boehnke M, Deloukas P, Kathiresan S, Mohlke KL, Ingelsson E, Abecasis GR; Global Lipids Genetics Consortium. Nat Genet. 2013 Nov;45(11):1274-1283. doi: 10.1038/ng.2797. Epub 2013 Oct 6.

[46] Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium; Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium; South Asian Type 2 Diabetes (SAT2D) Consortium; Mexican American Type 2 Diabetes (MAT2D) Consortium; Type 2 Diabetes Genetic Exploration by Nex-generation sequencing in muylti-Ethnic Samples (T2D-GENES) Consortium, Mahajan A, Go MJ, Zhang W, Below JE, Gaulton KJ, Ferreira T, Horikoshi M, Johnson AD, Ng MC, Prokopenko I, Saleheen D, Wang X, Zeggini E, Abecasis GR, Adair LS, Almgren P, Atalay M, Aung T, Baldassarre D, Balkau B, Bao Y, Barnett AH, Barroso I, Basit A, Been LF, Beilby J, Bell GI, Benediktsson R, Bergman RN, Boehm BO, Boerwinkle E, Bonnycastle LL, Burtt N, Cai Q, Campbell H, Carey J, Cauchi S, Caulfield M, Chan JC, Chang LC, Chang TJ, Chang YC, Charpentier G, Chen CH, Chen H, Chen YT, Chia KS, Chidambaram M, Chines PS, Cho NH, Cho YM, Chuang LM, Collins FS, Cornelis MC, Couper DJ, Crenshaw AT, van Dam RM, Danesh J, Das D, de Faire U, Dedoussis G,

Deloukas P, Dimas AS, Dina C, Doney AS, Donnelly PJ, Dorkhan M, van Duijn C, Dupuis J, Edkins S, Elliott P, Emilsson V, Erbel R, Eriksson JG, Escobedo J, Esko T, Eury E, Florez JC, Fontanillas P, Forouhi NG, Forsen T, Fox C, Fraser RM, Frayling TM, Froguel P, Frossard P, Gao Y, Gertow K, Gieger C, Gigante B, Grallert H, Grant GB, Grrop LC, Groves CJ, Grundberg E, Guiducci C, Hamsten A, Han BG, Hara K, Hassanali N, Hattersley AT, Hayward C, Hedman AK, Herder C, Hofman A, Holmen OL, Hovingh K, Hreidarsson AB, Hu C, Hu FB, Hui J, Humphries SE, Hunt SE, Hunter DJ, Hveem K, Hydrie ZI, Ikegami H, Illig T, Ingelsson E, Islam M, Isomaa B, Jackson AU, Jafar T, James A, Jia W, Jöckel KH, Jonsson A, Jowett JB, Kadowaki T, Kang HM, Kanoni S, Kao WH, Kathiresan S, Kato N, Katulanda P, Keinanen-Kiukaanniemi KM, Kelly AM, Khan H, Khaw KT, Khor CC, Kim HL, Kim S, Kim YJ, Kinnunen L, Klopp N, Kong A, Korpi-Hyövälti E, Kowlessur S, Kraft P, Kravic J, Kristensen MM, Krithika S, Kumar A, Kumate J, Kuusisto J, Kwak SH, Laakso M, Lagou V, Lakka TA, Langenberg C, Langford C, Lawrence R, Leander K, Lee JM, Lee NR, Li M, Li X, Li Y, Liang J, Liju S, Lim WY, Lind L, Lindgren CM, Lindholm E, Liu CT, Liu JJ, Lobbens S, Long J, Loos RJ, Lu W, Luan J, Lyssenko V, Ma RC, Maeda S, Mägi R, Männisto S, Matthews DR, Meigs JB, Melander O, Metspalu A, Meyer J, Mirza G, Mihailov E, Moebus S, Mohan V, Mohlke KL, Morris AD, Mühleisen TW, Müller-Nurasyid M, Musk B, Nakamura J, Nakashima E, Navarro P, Ng PK, Nica AC, Nilsson PM, Njølstad I, Nöthen MM, Ohnaka K, Ong TH, Owen KR, Palmer CN, Pankow JS, Park KS, Parkin M, Pechlivanis S, Pedersen NL, Peltonen L, Perry JR, Peters A, Pinidiyapathirage JM, Platou CG, Potter S, Price JF, Qi L, Radha V, Rallidis L, Rasheed A, Rathman W, Rauramaa R, Raychaudhuri S, Rayner NW, Rees SD, Rehnberg E, Ripatti S, Robertson N, Roden M, Rossin EJ, Rudan I, Rybin D, Saaristo TE, Salomaa V, Saltevo J, Samuel M, Sanghera DK, Saramies J, Scott J, Scott LJ, Scott RA, Segrè AV, Sehmi J, Sennblad B, Shah N, Shah S, Shera AS, Shu XO, Shuldiner AR, Sigurđsson G, Sijbrands E, Silveira A, Sim X, Sivapalaratnam S, Small KS, So WY, Stančáková A, Stefansson K, Steinbach G, Steinthorsdottir V, Stirrups K, Strawbridge RJ, Stringham HM, Sun Q, Suo C, Syvänen AC, Takayanagi R, Takeuchi F, Tay WT, Teslovich TM, Thorand B, Thorleifsson G, Thorsteinsdottir U, Tikkanen E, Trakalo J, Tremoli E, Trip MD, Tsai FJ, Tuomi T, Tuomilehto J, Uitterlinden AG, Valladares-Salgado A, Vedantam S, Veglia F, **Voight BF**, Wang C, Wareham NJ, Wennauer R, Wickremasinghe AR, Wilsgaard T, Wilson JF, Wiltshire S, Winckler W, Wong TY, Wood AR, Wu JY, Wu Y, Yamamoto K, Yamauchi T, Yang M, Yengo L, Yokota M, Young R, Zabaneh D, Zhang F, Zhang R, Zheng W, Zimmet PZ, Altshuler D, Bowden DW, Cho YS, Cox NJ, Cruz M, Hanis CL, Kooner J, Lee JY, Seielstad M, Teo YY, Boehnke M, Parra EJ, Chambers JC, Tai ES, McCarthy MI, Morris AP. Nat Genet. 2014 Mar;46(3):234-44. doi: 10.1038/ng.2897. Epub 2014 Feb 9.

[47] Pleiotropic genes for metabolic syndrome and inflammation. Kraja AT, Chasman DI, North KE, Reiner AP, Yanek LR, Kilpeläinen TO, Smith JA, Dehghan A, Dupuis J, Johnson AD, Feitosa MF, Tekola-Ayele F, Chu AY, Nolte IM, Dastani Z, Morris A, Pendergrass SA, Sun YV, Ritchie MD, Vaez A, Lin H, Ligthart S, Marullo L, Rohde R, Shao Y, Ziegler MA, Im HK; Cross Consortia Pleiotropy Group; Cohorts for Heart and; Aging Research in Genetic Epidemiology; Genetic Investigation of Anthropometric Traits Consortium; Global Lipids Genetics Consortium; Meta-Analyses of Glucose; Insulin-related traits Consortium; Global BPgen Consortium; ADIPOGen Consortium; Women's Genome Health Study; Howard University Family Study, Schnabel RB, Jørgensen T, Jørgensen ME, Hansen T, Pedersen O, Stolk RP, Snieder H, Hofman A, Uitterlinden AG, Franco OH, Ikram MA, Richards JB, Rotimi C, Wilson JG, Lange L, Ganesh SK, Nalls M, Rasmussen-Torvik LJ, Pankow JS, Coresh J, Tang W, Linda Kao WH, Boerwinkle E, Morrison AC, Ridker PM,

Becker DM, Rotter JI, Kardia SL, Loos RJ, Larson MG, Hsu YH, Province MA, Tracy R, **Voight BF**, Vaidya D, O'Donnell CJ, Benjamin EJ, Alizadeh BZ, Prokopenko I, Meigs JB, Borecki IB. Mol Genet Metab. 2014 Aug;112(4):317-38. doi: 10.1016/j.ymgme.2014.04.007. Epub 2014 May 9.

[48] Human genetics shines a light on ischaemic stroke. **Voight BF**, Rader DJ. Lancet Neurol. 2016 Feb;15(2):130-131. doi: 10.1016/S1474-4422(15)00400-7. Epub 2015 Dec 19.

[49] Pathway and network-based strategies to translate genetic discoveries into effective therapies. Greene CS, **Voight BF**. Hum Mol Genet. 2016 Oct 1;25(R2):R94-R98. doi: 10.1093/hmg/ddw160. Epub 2016 Jun 23.

[50] The genetic architecture of type 2 diabetes. Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SCJ, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, **Voight BF**, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MCY, Palmer ND, Balkau B, Stančáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JMM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VKL, Park KS, Saleheen D, So WY, Tam CHT, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, van der Schouw YT, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA Jr, Thameem F, Wilson G Sr, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney ASF, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, de Angelis MH, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CNA, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JCN, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RCW, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJF, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean

G, Hanis CL, Wilson JG, Seielstad M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Burtt NP, Mohlke KL, Meitinger T, Groop L, Abecasis G, Florez JC, Scott LJ, Morris AP, Kang HM, Boehnke M, Altshuler D, McCarthy MI. Nature. 2016 Aug 4;536(7614):41-47. doi: 10.1038/nature18642. Epub 2016 Jul 11.

[51] Disentangling the Causal Association of Plasma Lipid Traits and Type 2 Diabetes Using Human Genetics. Saleheen D, Rader DJ, **Voight BF**. JAMA Cardiol. 2016 Sep 1;1(6):631-3. doi: 10.1001/jamacardio.2016.2298.

[52] The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Ehret GB, Ferreira T, Chasman DI, Jackson AU, Schmidt EM, Johnson T, Thorleifsson G, Luan J, Donnelly LA, Kanoni S, Petersen AK, Pihur V, Strawbridge RJ, Shungin D, Hughes MF, Meirelles O, Kaakinen M, Bouatia-Naji N, Kristiansson K, Shah S, Kleber ME, Guo X, Lyytikäinen LP, Fava C, Eriksson N, Nolte IM, Magnusson PK, Salfati EL, Rallidis LS, Theusch E, Smith AJP, Folkersen L, Witkowska K, Pers TH, Joehanes R, Kim SK, Lataniotis L, Jansen R, Johnson AD, Warren H, Kim YJ, Zhao W, Wu Y, Tayo BO, Bochud M; CHARGE-EchoGen consortium; CHARGE-HF consortium; Wellcome Trust Case Control Consortium, Absher D, Adair LS, Amin N, Arking DE, Axelsson T, Baldassarre D, Balkau B, Bandinelli S, Barnes MR, Barroso I, Bevan S, Bis JC, Bjornsdottir G, Boehnke M, Boerwinkle E, Bonnycastle LL, Boomsma DI, Bornstein SR, Brown MJ, Burnier M, Cabrera CP, Chambers JC, Chang IS, Cheng CY, Chines PS, Chung RH, Collins FS, Connell JM, Döring A, Dallongeville J, Danesh J, de Faire U, Delgado G, Dominiczak AF, Doney ASF, Drenos F, Edkins S, Eicher JD, Elosua R, Enroth S, Erdmann J, Eriksson P, Esko T, Evangelou E, Evans A, Fall T, Farrall M, Felix JF, Ferrières J, Ferrucci L, Fornage M, Forrester T, Franceschini N, Duran OHF, Franco-Cereceda A, Fraser RM, Ganesh SK, Gao H, Gertow K, Gianfagna F, Gigante B, Giulianini F, Goel A, Goodall AH, Goodarzi MO, Gorski M, Gräßler J, Groves C, Gudnason V, Gyllensten U, Hallmans G, Hartikainen AL, Hassinen M, Havulinna AS, Hayward C, Hercberg S, Herzig KH, Hicks AA, Hingorani AD, Hirschhorn JN, Hofman A, Holmen J, Holmen OL, Hottenga JJ, Howard P, Hsiung CA, Hunt SC, Ikram MA, Illig T, Iribarren C, Jensen RA, Kähönen M, Kang H, Kathiresan S, Keating BJ, Khaw KT, Kim YK, Kim E, Kivimaki M, Klopp N, Kolovou G, Komulainen P, Kooner JS, Kosova G, Krauss RM, Kuh D, Kutalik Z, Kuusisto J, Kvaløy K, Lakka TA, Lee NR, Lee IT, Lee WJ, Levy D, Li X, Liang KW, Lin H, Lin L, Lindström J, Lobbens S, Männistö S, Müller G, Müller-Nurasyid M, Mach F, Markus HS, Marouli E, McCarthy MI, McKenzie CA, Meneton P, Menni C, Metspalu A, Mijatovic V, Moilanen L, Montasser ME, Morris AD, Morrison AC, Mulas A, Nagaraja R, Narisu N, Nikus K, O'Donnell CJ, O'Reilly PF, Ong KK, Paccaud F, Palmer CD, Parsa A, Pedersen NL, Penninx BW, Perola M, Peters A, Poulter N, Pramstaller PP, Psaty BM, Quertermous T, Rao DC, Rasheed A, Rayner NWNWR, Renström F, Rettig R, Rice KM, Roberts R, Rose LM, Rossouw J, Samani NJ, Sanna S, Saramies J, Schunkert H, Sebert S, Sheu WH, Shin YA, Sim X, Smit JH, Smith AV, Sosa MX, Spector TD, Stančáková A, Stanton A, Stirrups KE, Stringham HM, Sundstrom J, Swift AJ, Syvänen AC, Tai ES, Tanaka T, Tarasov KV, Teumer A, Thorsteinsdottir U, Tobin MD, Tremoli E, Uitterlinden AG, Uusitupa M, Vaez A, Vaidya D, van Duijn CM, van Iperen EPA, Vasan RS, Verwoert GC, Virtamo J, Vitart V, **Voight BF**, Vollenweider P, Wagner A, Wain LV, Wareham NJ, Watkins H, Weder AB, Westra HJ, Wilks R, Wilsgaard T, Wilson JF, Wong TY, Yang TP, Yao J, Yengo L, Zhang W, Zhao JH, Zhu X, Bovet P, Cooper RS, Mohlke KL, Saleheen D, Lee JY, Elliott P, Gierman HJ, Willer CJ, Franke L, Hovingh GK, Taylor KD, Dedoussis G, Sever P, Wong A, Lind L, Assimes TL, Njølstad I, Schwarz PE, Langenberg C, Snieder H,

Caulfield MJ, Melander O, Laakso M, Saltevo J, Rauramaa R, Tuomilehto J, Ingelsson E, Lehtimäki T, Hveem K, Palmas W, März W, Kumari M, Salomaa V, Chen YI, Rotter JI, Froguel P, Jarvelin MR, Lakatta EG, Kuulasmaa K, Franks PW, Hamsten A, Wichmann HE, Palmer CNA, Stefansson K, Ridker PM, Loos RJF, Chakravarti A, Deloukas P, Morris AP, Newton-Cheh C, Munroe PB. Nat Genet. 2016 Oct;48(10):1171-1184. doi: 10.1038/ng.3667. Epub 2016 Sep 12.

[53] Type 2 Diabetes Genes Gleaned by Making a β-Cell Screen Routine. **Voight BF**, Grant SF. Diabetes. 2016 Dec;65(12):3541-3543. doi: 10.2337/dbi16-0054.

[54] An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Scott RA, Scott LJ, Mägi R, Marullo L, Gaulton KJ, Kaakinen M, Pervjakova N, Pers TH, Johnson AD, Eicher JD, Jackson AU, Ferreira T, Lee Y, Ma C, Steinthorsdottir V, Thorleifsson G, Qi L, Van Zuydam NR, Mahajan A, Chen H, Almgren P, **Voight BF**, Grallert H, Müller-Nurasyid M, Ried JS, Rayner NW, Robertson N, Karssen LC, van Leeuwen EM, Willems SM, Fuchsberger C, Kwan P, Teslovich TM, Chanda P, Li M, Lu Y, Dina C, Thuillier D, Yengo L, Jiang L, Sparso T, Kestler HA, Chheda H, Eisele L, Gustafsson S, Frånberg M, Strawbridge RJ, Benediktsson R, Hreidarsson AB, Kong A, Sigurðsson G, Kerrison ND, Luan J, Liang L, Meitinger T, Roden M, Thorand B, Esko T, Mihailov E, Fox C, Liu CT, Rybin D, Isomaa B, Lyssenko V, Tuomi T, Couper DJ, Pankow JS, Grarup N, Have CT, Jørgensen ME, Jørgensen T, Linneberg A, Cornelis MC, van Dam RM, Hunter DJ, Kraft P, Sun Q, Edkins S, Owen KR, Perry JRB, Wood AR, Zeggini E, Tajes-Fernandes J, Abecasis GR, Bonnycastle LL, Chines PS, Stringham HM, Koistinen HA, Kinnunen L, Sennblad B, Mühleisen TW, Nöthen MM, Pechlivanis S, Baldassarre D, Gertow K, Humphries SE, Tremoli E, Klopp N, Meyer J, Steinbach G, Wennauer R, Eriksson JG, Männistö S, Peltonen L, Tikkanen E, Charpentier G, Eury E, Lobbens S, Gigante B, Leander K, McLeod O, Bottinger EP, Gottesman O, Ruderfer D, Blüher M, Kovacs P, Tonjes A, Maruthur NM, Scapoli C, Erbel R, Jöckel KH, Moebus S, de Faire U, Hamsten A, Stumvoll M, Deloukas P, Donnelly PJ, Frayling TM, Hattersley AT, Ripatti S, Salomaa V, Pedersen NL, Boehm BO, Bergman RN, Collins FS, Mohlke KL, Tuomilehto J, Hansen T, Pedersen O, Barroso I, Lannfelt L, Ingelsson E, Lind L, Lindgren CM, Cauchi S, Froguel P, Loos RJF, Balkau B, Boeing H, Franks PW, Barricarte Gurrea A, Palli D, van der Schouw YT, Altshuler D, Groop LC, Langenberg C, Wareham NJ, Sijbrands E, van Duijn CM, Florez JC, Meigs JB, Boerwinkle E, Gieger C, Strauch K, Metspalu A, Morris AD, Palmer CNA, Hu FB, Thorsteinsdottir U, Stefansson K, Dupuis J, Morris AP, Boehnke M, McCarthy MI, Prokopenko I; DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium. Diabetes. 2017 Nov;66(11):2888-2902. doi: 10.2337/db16-1253. Epub 2017 May 31.

[55] Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Flannick J, Fuchsberger C, Mahajan A, Teslovich TM, Agarwala V, Gaulton KJ, Caulkins L, Koesterer R, Ma C, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SCJ, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, **Voight BF**, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MCY, Palmer ND,

Balkau B, Stančáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JMM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VKL, Park KS, Saleheen D, So WY, Tam CHT, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney ASF, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, de Angelis MH, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CNA, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JC, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RCW, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJF, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, Seielstad M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Mohlke KL, Meitinger T, Groop L, Abecasis G, Scott LJ, Morris AP, Kang HM, Altshuler D, Burtt NP, Florez JC, Boehnke M, McCarthy MI. Sci Data. 2017 Dec 19;4:170179. doi: 10.1038/sdata.2017.179.

[56] Dissecting an adiposity locus with an arsenal of genomics. Lorenz K, **Voight BF**. Genome Biol. 2018 Jun 7;19(1):74. doi: 10.1186/s13059-018-1460-y.

[57] Keen on the tenure track job, are you? Know these things, you should. **Voight BF**. Genome Biol. 2019 Jan 7;20(1):6. doi: 10.1186/s13059-018-1617-8.

[58] Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. van Zuydam NR, Ladenvall C, **Voight BF**, Strawbridge RJ, Fernandez-Tajes J, Rayner NW, Robertson NR, Mahajan A, Vlachopoulou E, Goel A, Kleber ME, Nelson CP, Kwee LC, Esko T, Mihailov E, Mägi R, Milani L, Fischer K, Kanoni S, Kumar J, Song C, Hartiala JA, Pedersen NL, Perola M, Gieger C, Peters A, Qu L, Willems SM, Doney ASF, Morris AD, Zheng Y, Sesti G, Hu FB, Qi L, Laakso M, Thorsteinsdottir U, Grallert H, van Duijn C, Reilly MP, Ingelsson E, Deloukas P, Kathiresan S, Metspalu A, Shah SH, Sinisalo J, Salomaa V, Hamsten A, Samani NJ, März W, Hazen SL, Watkins H, Saleheen D, Morris AP, Colhoun HM, Groop L, McCarthy MI, Palmer CNA; SUMMIT Steering Committee; CARDIOGRAMplusC4D Steering Committee*. Circ Genom Precis Med. 2020 Dec;13(6):e002769. doi: 10.1161/CIRCGEN.119.002769. Epub 2020 Aug 13.

[59] Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. Cousminer DL, Wagley Y, Pippin JA,

Elhakeem A, Way GP, Pahl MC, McCormack SE, Chesi A, Mitchell JA, Kindler JM, Baird D, Hartley A, Howe L, Kalkwarf HJ, Lappe JM, Lu S, Leonard ME, Johnson ME, Hakonarson H, Gilsanz V, Shepherd JA, Oberfield SE, Greene CS, Kelly A, Lawlor DA, **Voight BF**, Wells AD, Zemel BS, Hankenson KD, Grant SFA. Genome Biol. 2021 Jan 4;22(1):1. doi: 10.1186/s13059-020-02207-9.

[60] Golden orb-weaving spider (Trichonephila clavipes) silk genes with sex-biased expression and atypical architectures. Correa-Garhwal SM, Babb PL, **Voight BF**, Hayashi CY. G3 (Bethesda). 2021 Jan 18;11(1):jkaa039. doi: 10.1093/g3journal/jkaa039.

[61] Prioritizing the Role of Major Lipoproteins and Subfractions as Risk Factors for Peripheral Artery Disease. Levin MG, Zuber V, Walker VM, Klarin D, Lynch J, Malik R, Aday AW, Bottolo L, Pradhan AD, Dichgans M, Chang KM, Rader DJ, Tsao PS, **Voight BF**, Gill D, Burgess S, Damrauer SM. Circulation. 2021 Aug 3;144(5):353-364. doi: 10.1161/CIRCULATIONAHA.121.053797. Epub 2021 Jun 18.

[62] Genetic Evidence for Repurposing of GLP1R (Glucagon-Like Peptide-1 Receptor) Agonists to Prevent Heart Failure. Daghlas I, Karhunen V, Ray D, Zuber V, Burgess S, Tsao PS, Lynch JA, Lee KM, **Voight BF**, Chang KM, Baker EH, Damrauer SM, Howson JMM, Vujkovic M, Gill D. J Am Heart Assoc. 2021 Jul 6;10(13):e020331. doi: 10.1161/JAHA.120.020331. Epub 2021 Jun 29.

[63] Cis-regulatory architecture of human ESC-derived hypothalamic neuron differentiation aids in variant-to-gene mapping of relevant complex traits. Pahl MC, Doege CA, Hodge KM, Littleton SH, Leonard ME, Lu S, Rausch R, Pippin JA, De Rosa MC, Basak A, Bradfield JP, Hammond RK, Boehm K, Berkowitz RI, Lasconi C, Su C, Chesi A, Johnson ME, Wells AD, **Voight BF**, Leibel RL, Cousminer DL, Grant SFA. Nat Commun. 2021 Nov 19;12(1):6749. doi: 10.1038/s41467-021-27001-4.

[64] Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Temprano-Sagrera G, Sitlani CM, Bone WP, Martin-Bornez M, **Voight BF**, Morrison AC, Damrauer SM, de Vries PS, Smith NL, Sabater-Lleal M. J Thromb Haemost. 2022 Jun;20(6):1331-1349. doi: 10.1111/jth.15698. Epub 2022 Mar 29.

[65] Yarmolinsky J, Bouras E, Constantinescu A, Burrows K, Bull CJ, Vincent EE, Martin RM, Dimopoulou O, Lewis SJ, Moreno V, Vujkovic M, Chang KM, **Voight BF**, Tsao PS, Gunter MJ, Hampe J, Pellatt AJ, Pharoah PDP, Schoen RE, Gallinger S, Jenkins MA, Pai RK; PRACTICAL consortium; VA Million Veteran Program; Gill D, Tsilidis KK. Genetically proxied glucose-lowering drug target perturbation and risk of cancer: a Mendelian randomisation analysis. Diabetologia. 2023 Aug;66(8):1481-1500. doi: 10.1007/s00125-023-05925-4. Epub 2023 May 12.