BENJAMIN F. VOIGHT
CURRICULUM VITAE

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CV last updated: February 2023

EMPLOYMENT HISTORY

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

EDUCATION

2006	Ph.D., Advised by Drs. Jonathan Pritchard and Nancy Cox Human Genetics, University of Chicago
2001	B.S. in Biology and B.A. Mathematics University of Washington, Seattle [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 provide 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.

2021–2023 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.

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).

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: **B. Voight**, M. den Hoed)
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.

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)
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

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 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
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)

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)

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
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

2013–2019, 2021-Present	Co-Director, *Introduction to Bioinformatics* (CIS/MTR/GCB535) Undergrad/grad/post-doc/MD/MD+PhD, ~55+ students Includes lectures and administrative responsibilities. 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

2021–Present	Da (Mia) Lee (PhD Student, PGG)
2021–Present	Mitch Conery (PhD Student, GCB, joint with Struan Grant) - Selected for Genomics T32 (2022)
2021–Present	Mary Ann Hazuga (PhD Student, GCB, joint with Struan Grant)
2018–Present	Chris Adams (PhD Student, GCB)
2018–Present	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)*

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

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

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 155 PAPERS, H-INDEX=82, CITATIONS=71,579)

LINK TO FULL PUBLICATION LIST:

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

PREPRINTS

[1] Gawronski KAB, Bone W, Park Y, Pashos E, Wang X, Yang W, Rader D, Musunuru K, **Voight BF**, Brown C. Evaluating the contribution of cell-type specific alternative splicing to variation in lipid levels. *bioRxiv,* ***doi:*** https://doi.org/10.1101/659326 [r]

[2] Pividori M, Lu S, Li B, Su C, Johnson ME, Wei W-Q, Feng Q, Namjou B, Kiryluk K, Kullo I, Luo Y, Sullivan BD, **Voight BF**, Skarke C, Ritchie MD, Grant SFA, Greene CS. Projecting genetic associations through gene expression patterns highlights disease etiology and drug mechanisms. *bioRxiv, doi:* https://doi.org/10.1101/2021.07.05.450786 [r]

[3] 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, doi:* https://doi.org/10.1101/2021.12.16.21267869 [r]

[4] 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. *bioRxiv*, *doi:* https://biorxiv.org/cgi/content/short/2022.10.14.512160v1 [r]

In Press

*: DENOTES EQUAL CONTRIBUTION

[1] Huang , Huffman JE, Huang Y, Do Valle Í., Assimes TL, Raghavan S, Voight BF, Barabási A-L, Huang R, Hui Q, Nguyen X-M, Ho Y-L, Djoussé L, Lynch J, Vujkovic M, Tang H, Damrauer SM, Reaven PD, Miller D, Phillips LS, Ng M, Graff M, Haiman CA, Loos RJF, North KE, Yengo L, Smith GD, Saleheen D, Gaziano JM, Rader DJ, Tsao PS, Cho K, Chang K-M, Wilson PWF, VA Million Veteran Program, Sun YV, O'Donnell CJ. Genome-wide and phenome-wide study of genetically determined body mass index reveals a complex adiposity disease network. *Accepted, Nature Communications.*

[2] Levin MG, Tsao NL, Singhal P, Liu C, Vy THM, Paranjpe I, Backman JD, Bellomo TR, Bone WP, Biddinger KJ, Hui Q, Dikilitas O, Satterfield BA,MD, Yang Y, Morley MP, Bradford Y, Burke M, Reza N, Charest B, Regeneron Genetics Center, 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*. Multi-ancestry and Multivariate Genome-Wide Analyses Highlight the Role of Common Genetic Variation in Cardiac Structure, Function, and Heart Failure-related Traits. *Accepted. Nature Communications.*

***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.

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