

# CURRICULUM VITAE FOR CWRU SCHOOL OF MEDICINE

## PERSONAL INFORMATION

---

Name: Crawford, Dana Colleen

### EDUCATION

School: Vanderbilt University, Nashville, TN  
Degree: Bachelor of Science (Molecular Biology)  
Dates: 1991-1995

School: Emory University, Atlanta, GA  
Degree: Doctor of Philosophy (Genetics and Molecular Biology)  
Dates: 1995-2000

### POST-GRADUATE TRAINING

Institution: Centers for Disease Control and Prevention, Atlanta, GA  
Position, Epidemic Intelligence Service Officer, National Center on Birth Defects and  
Developmental Disabilities  
Dates: July 2000-July 2002

Institution: University of Washington, Seattle, WA  
Position: Post-doctoral fellow with Dr. Deborah Nickerson, Department of Genome Sciences,  
Dates: July 2002- January 2006

### PH.D. THESIS

Title: Factors involved in fragile X CGG repeat instability and their ultimate impact on world  
populations  
Ph.D. Thesis Committee: Drs. Stephanie L. Sherman (advisor), Judy Fridovich Keil, Douglas  
Wallace, and Stephen T. Warren.

### CONTACT INFORMATION

Office Address: Wolstein Research Building, 2103 Cornell Road, Suite 2527, Cleveland, Ohio  
44106-7295  
Office Phone: (216) 368-5546  
E-mail: [dana.crawford@case.edu](mailto:dana.crawford@case.edu)

### PROFESSIONAL/ACADEMIC APPOINTMENTS

---

Position/Rank: Professor (with tenure)  
Institution/Department: Department of Population and Quantitative Health Sciences  
Case Western Reserve University  
Dates: July 1, 2020 – present

Curriculum Vitae: DANA C. CRAWFORD

Position/Rank: Associate Director for Population and Diversity Research  
Institution/Department: Cleveland Institute for Computational Biology  
(formerly Institute for Computational Biology)  
Case Western Reserve University  
Dates: January 13, 2015 – present

Position/Rank: Associate Professor (secondary appointment)  
Institution/Department: Department of Genetics and Genome Sciences  
Case Western Reserve University  
Dates: June 2016 – present

Position/Rank: Associate Professor (with tenure)  
Institution/Department: Department of Population and Quantitative Health Sciences  
(formerly Epidemiology and Biostatistics)  
Case Western Reserve University  
Dates: January 13, 2015 – June 30, 2020

Position/Rank: Visiting Associate Professor  
Institution/Department: Department of Epidemiology and Biostatistics and Institute for  
Computational Biology  
Case Western Reserve University  
Dates: July 8, 2014 – January 12, 2015

Position/Rank: Associate Professor (with tenure)  
Institution/Department: Department of Molecular Physiology and Biophysics  
Vanderbilt University  
Dates: July 2012 – July 2014

Position/Rank: Assistant Director  
Institution/Department: Center for Human Genetics Research  
Vanderbilt University  
Dates: July 2013 – March 2014

Position/Rank: Assistant Professor (tenure-track)  
Institution/Department: Division of Human Genomics  
Department of Molecular Physiology and Biophysics  
Vanderbilt University  
Dates: September 18, 2006 – 2012

Position/Rank: Investigator  
Institution/Department: Center for Human Genetics Research  
Vanderbilt University  
Dates: September 18, 2006 – 2012

Position/Rank: Acting Assistant Professor  
Institution/Department: Department of Genome Sciences

University of Washington  
Dates: February 1 – September 1, 2006

### **HONORS AND AWARDS**

---

Collierville High School Valedictorian	1991
Vanderbilt University's Chancellor's Scholar	1991-1995
Vanderbilt Undergraduate Howard Hughes Research Fellowship	1993
Vanderbilt University, graduated Cum Laude	1995
C.W. Cotterman Award (post-doctoral paper deemed to have made outstanding scientific contributions to the field of human genetics published in the previous year of the <i>American Journal of Human Genetics</i> ) <i>American Journal of Human Genetics</i> 76(2):197 (2005) <a href="https://pubmed.ncbi.nlm.nih.gov/1196360/">PMCID1196360</a>	2004
NCMHD/NIH Health Disparities Research Scholar	2005-2011
Rippel Scholars Award for New Investigators (finalist)	2007
Tomorrow's PI, Genome Technology	2007
Vanderbilt Clinical and Translational Research Scholar	2008-2009
FASEB MARC Travel Award for Genetics and Genomics of Infectious Disease (GGID) meeting in Singapore	2009
Fellow, Keystone Symposia on Molecular and Cellular Biology	2009-2010
Pacific Symposium on Biocomputing Travel Award	2013
Kavli Frontiers of Science fellow	2012-2014
Society for Advancement of Chicanos and Native Americans in Science (SACNAS) Distinguished Research Mentor Award <a href="https://www.youtube.com/watch?v=alstHidCyhY">https://www.youtube.com/watch?v=alstHidCyhY</a>	2014
Case Western Reserve University School of Medicine Faculty Diversity Award	2017
Annual Biomedical Research Conference for Minority Students (ABRCMS) Judges Travel Award	2017
Case Western Reserve University Shared Training to Advance Integrity in Research (STAIR) Mentor Fellows Program, senior mentor fellow with junior mentee fellow Dr. Farren Briggs	2019-2020

American Association for the Advancement of Science (AAAS) Elected Fellow, for distinguished contributions in pioneering phenome-wide association studies and in developing and leading genetic studies in under-represented minority populations, Biological Sciences  
*Science* 370 (6520):1048 (2020) 2020

**CONTINUING EDUCATION AND TRAINING**

---

Epidemiology in Action: Intermediate Methods Course. Philip S. Brachman, Coordinator. The Rollins School of Public Health, Emory University and the Centers for Disease Control and Prevention. Atlanta, Georgia, Feb. 26-March 2, 2001.

Genetic Analysis of Complex Human Disease. Marcy C. Speer, Margaret A. Pericak-Vance, Jonathan L. Haines, Co-organizers. Duke University. Durham, North Carolina, May 6-9, 2001.

What's Next? A Leadership and Professional Development Program for Tenured Women Faculty, Flora Stone Mather Center for Women, Case Western Reserve University. Cleveland, OH, September 2015 – January 2016.

**MEMBERSHIP IN PROFESSIONAL SOCIETIES**

---

American Society of Human Genetics (ASHG)	1997-present
American Public Health Association	2010
Human Genome Organisation (HUGO)	2012
American Association for the Advancement of Science (AAAS)	2013-present
American Heart Association (AHA)	2013-present
Society for the Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS)	2014-present
American Medical Informatics Association (AMIA)	2016-present

**PROFESSIONAL SERVICES**

---

**ADVISORY GROUPS**

Population Architecture using Genomics and Epidemiology (PAGE) Inflammation and Autoimmunity Working Group chair and Lipids Project Group chair	2008-2013
Northwest Institute of Genetic Medicine External Advisory Board	2009-2010
Electronic Medical Records & Genomics (eMERGE)	

Genomics Working Group co-chair	2009-2014
Illumina Genetics Advisory Panel	2011
Pharmacogenomics Research Network (PGRN) Statistical Analysis Resource (P-STAR) expert consultant	2010-2015
Indonesian-American Kavli Frontiers of Science Symposium Organizer	2013-2014
Southern Community Cohort Study (SCCS) Publications Committee	2013-2014
National Institutes of Health (NIH) Workshops	
○ NHGRI Future Directions for the eMERGE Network (Invited participant)	Jan 2014
○ NIH All of Us Workshop. Informatics, Methodologies, Ethical/Legal, and Statistical Research and Cardio-Respiratory and Blood (Invited participant)	Mar 2018
○ NHGRI Strategic Planning Meeting. From Genome to Phenotype: Genomic Variation Identification, Association, and Function in Human Health and Disease Invited panelist, Topic 3: Predicting and Characterizing Functional Consequences of Genome Variation, Including Beyond Single Variant/ Gene	Jan 2019
Association for Computing Machinery (ACM) 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB) Program Committee	2014
Pacific Symposium on Biocomputing (PSB) Session/Workshop Co-Organizer	
○ Detecting and Characterizing Pleiotropy: New Methods for Uncovering the Connection Between the Complexity of Genomic Architecture and Multiple Phenotypes. Co-chairs: Anna L. Tyler, Dana C. Crawford, Sarah A. Pendergrass	2014
○ Precision Medicine: From Genotypes and Molecular Phenotypes Towards Improved Health and Therapies. Co-chairs: Bruce Aronow, Steven E. Brenner, Dana C. Crawford, Joshua C. Denny, Sean D. Mooney, Alexander A. Morgan	2017
○ Precision Medicine: From Diplotypes to Disparities Towards Improved Health and Therapies. Co-chairs: Bruce Aronow, Steven E. Brenner, Dana C. Crawford, Joshua C. Denny, Alexander A. Morgan	2018
○ Integrating Community-level Data Resources for Precision Medicine Research. Co-chairs: Dana C. Crawford and William S. Bush	2018
○ Precision Medicine: Improving Health Through High-Resolution Analysis of Personal Data. Co-chairs: Steven E. Brenner, Martha Bulyk, Dana C. Crawford, Jill Mesirov, Alexander A. Morgan, Predrag Radivojac	2019

Curriculum Vitae: DANA C. CRAWFORD

○ Precision Medicine: Addressing the Challenges of Sharing, Analysis, and Privacy at Scale. Co-chairs: Steven E. Brenner, Martha Bulyk, Dana C. Crawford, Alexander A. Morgan, Predrag Radivojac, Nicholas Tatonetti	2020
○ Computational Challenges and Artificial Intelligence in Precision Medicine. Co-chairs: Olga Afanasiev, Joanne Berghout, Steven Brenner, Martha L. Bulyk, Dana Crawford, Jonathan H. Chen, Roxana Daneshjou, Łukasz Kidziński	2021
○ Precision Medicine: Using Artificial Intelligence to Improve Diagnostics and Healthcare. Co-chairs: Steven E. Brenner, Martha L. Bulyk, Jonathan Chen, Dana C. Crawford, Roxana Daneshjou, Sam Finlayson, Łukasz Kidziński	2022
○ Precision Medicine: Using Computation and Artificial Intelligence to Improve Healthcare and Public Health. Co-chairs: Steven E. Brenner, Jonathan Chen, Dana C. Crawford, Roxana Daneshjou, Łukasz Kidziński, David Ouyang, Michelle Whirl-Carrillo	2023
 American Society of Human Genetics (ASHG)	
Moderator or co-moderator	
Session 31: Neurogenetics, San Diego, CA	2007
Session 29: Genomics II, Philadelphia, PA	2008
Session 61: Missing Heritability, Interactions, & Sequencing, San Francisco, CA	2012
Session 104. Advancing Drug Discovery by Genetic Analysis in Large Cohorts, Orlando, FL	2017
Abstract reviewer	
Topic 5: Complex Traits and Polygenic Disorders	June 2012
Topic 2: Complex Traits and Polygenic Disorders	June 2019
Annual DNA Day Essay Contest	
Judge, Round One	2015
Judge, Round Two	2016
Judge, Round One	2017-2018
Judge, Round Three	2019-2021
Diversity Breakfast	
Panelist	2018
Invited session speaker	
What about the phenotype? Integrating Electronic Health Records to Drive Discovery in Precision Health	2019
Board of Directors	
Elected member	2019-2021
Professional Conduct Working Group, member	2019-2021
Diversity and Inclusion Task Force, chair	2020-2021
Nominating Committee	
Member	2022
Incoming Chair	2023
Chair	2024-2025

Annual Biomedical Research Conference for Minority Students (ABRCMS)	
Poster judge	2015-2019
Travel award judge	2018-2019, 2022
Ambassador, Computational and Systems Biology	2018-2019, 2022
Live Chat Facilitator, Computational and Systems Biology	2020
Live Mentor, Computational and Systems Biology	2021
Invited session speaker	
○ Precision Medicine: Where genomics meets big data biomedical informatics. Phoenix Convention Center, Phoenix, AZ	2017
○ Genomic research enabled by electronic health records. Anaheim Convention Center, Anaheim, CA.	2019
Society for the Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS)	
National conference scientific session organizer and speaker	
○ Genomic Discovery, Collaboration, and Translation Using Electronic Health Records. Speakers: Drs. Dana Crawford (CWRU), Sarah Pendergrass (Geisinger), and Janina Jeff (Mount Sinai). Gaylord National Resort and Convention Center, Washington, DC (Speaker and organizer).	2015
○ The ABCs of Diversity in Genomic Research: Ascertainment, Bioinformatics, and Computation. Speakers: Drs. Farren Briggs (CWRU), Janina Jeff (Illumina), William Bush (CWRU), and Sarah Pendergrass (Geisinger). Long Beach Convention Center, Long Beach, CA (Organizer).	2016
○ The Importance of Diversity in Precision Medicine Research. Speakers: Drs. William Bush (CWRU), Janina Jeff (Illumina), and Dana Crawford (CWRU). Henry B. González Convention Center, San Antonio, TX (Speaker and organizer).	2018
○ Precisely Precision Medicine: A Primer on Translational Research. Speakers: Drs. Jessica Cooke Bailey (CWRU), Farren Briggs (CWRU), William Bush (CWRU), and Dana Crawford (CWRU). Virtual due to SARS-CoV-2/COVID-19 (Speaker and organizer).	2020
○ Quantitative Approaches to Understand Diseases with Electronic Health Record Data. Speakers: Drs. Dana Crawford (CWRU), Blanca Himes (University of Pennsylvania), Farren Briggs (CWRU), and Rebecca Hubbard (University of Pennsylvania). Virtual due to SARS-CoV-2/COVID-19 (Speaker).	2021
Undergraduate research presentations reviewer	2019-2021

Keystone Symposia Health Disparities Workshops Working Group	2016-2019
Million Veteran Program (MVP)	
Statistical Genetics Working Group	2016-present
Publication and Presentation Committee	2021-present
AMIA Informatics Summit (formerly Joint Summits on Translational Science)	
Summit on Translational Bioinformatics (TBI), Scientific Program Committee	2016-2017
Student Paper Competition Judge	2017
Reviewer	2017, 2019, 2022
Orofacial Pain: Prospective Evaluation and Risk Assessment (OPPERA), External Advisory Committee member	2016-2017
Translational Bioinformatics Conference, Long Beach, CA	
Manuscript reviewer	2017
Informatics Enterprise Committee (formerly the Informatics Domain Task Force (iDTF) member, Clinical & Translational Science Awards (CTSA)	2017-present
GpGx Computational Methods for Target Identification and Validation Scientific Input Engagement, Merck Research Labs	Dec 2017
Association for Clinical and Translational Science	
Translational Science Abstract Reviewer	2019
Artificial Intelligence in Oncology: Advancements and Policy, Session IV – Policy & Ethical Considerations for AI, panelist	Oct 24, 2019
American Association for the Advancement of Science	
STEMM Equity Achievement (SEA) Change Departmental Awards Framework Drafting Group	2020
Dog Aging Project, Scientific Advisory Board member	2022-present
National Academy of Sciences planning committee member for "Workshop on Considerations for Returning Individual Genomic Results from Population-Based Surveys: Focus on the National Health and Nutrition Examination Survey"	2022-2023
The National Institutes of Health's Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium, External Scientific Panel (ESP) member	2022-present



**NIH STUDY SECTIONS/GRANT REVIEW COMMITTEES**

Center for Scientific Review Special Emphasis Panel 2008/01 ZRG1 HOP-D (03) M	Nov 28, 2007
Center for Scientific Review Special Emphasis Panel ZRG1 HOP-D (02)	July 24, 2008
Center for Scientific Review, Behavioral Genetics and Epidemiology Study (BGES) Section	Feb 5-6, 2009
Challenge Grants Panels (RFA-OD-09-003): 2009/10 ZRG1 PSE-J (58) R (Panel 1), 2009/10 ZRG1 CVRS-B (58) R (Panel 19), 2009/10 ZRG1 PSE-C (58) R	Jun 12, 2009
Grand Opportunity Grants Panels (RFA-OD-09-004): NIA ZRG1 CVRS B (58) and NCI ZCA1 RTRB-2 (O9)	July 29, 2009 Aug 5-6, 2009
National Institute of Neurological Disorders and Stroke, Udall Centers Review: 2011/08 ZNS1 SRB-E (51)	Jul 14-15, 2011
National Heart, Lung, and Blood Institute Special Emphasis Panel, RFA-HL-13-007: Targeted Analyses of Jackson Heart Study Data (R01)	Aug 15, 2012
National Heart Lung and Blood Institute Re-sequencing and Genotyping (RSnG) Program	Oct 2, 2008 Dec 29, 2008 Dec 16, 2009 Aug 27, 2010 Apr 25, 2012 Sept 12, 2012 Sept 13, 2013 Dec 4, 2014 Mar 17, 2015 June 19, 2015 Sept 14, 2015 Dec 2, 2015
National Heart, Lung, and Blood Institute Special Emphasis Panel, 2015/05 HLBP 1	Feb 2, 2015 Sept 10, 2015
National Human Genomic Research Institute (NHGRI) Genome Research Review Committee (GNOM-G): study section member	2010-2016
National Human Genome Research Institute (NHGRI) Special Emphasis Panel ZHG1 HGR-M (J1) U41 SEP	Nov 8, 2016

Center for Scientific Review Special Emphasis Panel 2017/01 ZRG1 BDCN-N (90) Epilepsy and Alcohol Dependence	Dec 20, 2016
Center for Scientific Review Special Emphasis Panel 2017/05 ZDK1 GRB-N (M2) 1 Inflammatory Bowel Disease Genetics Consortium	March 7, 2017
Infectious Diseases, Reproductive Health, Asthma and Pulmonary Conditions Member Conflicts 2017/05 ZRG1 PSE-U (02)M	April 7, 2017
National Heart, Lung, and Blood Institute (NHLBI) TOPMED: Omics, Phenotypes of Heart, Lung and Blood Disorders (X01) 2017/10 ZHL1 CSR-G(01)1	May 12, 2017
National Institute of Neurological Disorders and Stroke (NINDS) ZNS1 SRB-A(16) Special Emphasis Panel (SEP) Project Grant Proposals (P01)	Mar 12, 2018
National Human Genome Research Institute (NHGRI), 2018/05 ZHG1 HGR-M (M3) 1 – DAP (Diversity Action Plan)	Mar 20, 2018
National Human Genome Research Institute (NHGRI), 2018/08 ZHG1 HGR-P (O1) 1 – DAP (Diversity Action Plan)	July 10, 2018
National Human Genome Research Institute (NHGRI), 2019/05 GNOM-G 1	Mar 7, 2019
Center for Scientific Review, Conflict Special Emphasis Panel, ZRG1 BST-R (02)	June 20, 2019
Center for Scientific Review, Special Emphasis Panel, 2020/05 KNOD	Feb 5-7, 2020
National Human Genome Research Institute (NHGRI), 2020/10 GNOM-G 2	June 4, 2020
Center for Inherited Disease Research (CIDR) Access Committee	July 2020- present
National Human Genome Research Institute (NHGRI), Special Emphasis Panel, Predictive Modeling, 2021/05 ZHG1 HGR-M (M3) 2	Mar 23, 2021
National Human Genome Research Institute (NHGRI), Special Emphasis Panel, Advancing Genomic Medicine Research, 2021/10 ZHG1 HGR-P (O1) 1	July 28, 2021

**OTHER REVIEWS**

NHANES: Genetic Component Technical Review for the National Center for Health Statistics, Centers for Disease Control and Prevention	Feb, Aug, and October 2009;
---	--------------------------------

	June 2017
Ontario Research Fund	Dec 14, 2009
Wellcome Trust	Jan 14, 2011
Vanderbilt Physician Scientist Development (VPSD) Program and Vanderbilt Clinical & Translational Research Scholars (VCTRS) Program Review Committee	Apr 30, 2012 Feb 28, 2013
Centers for Disease Control and Prevention Field Review DD12-006 Coordinating Center for Research and Training to Promote the Health of People with Developmental and Other Disabilities	Jun 19, 2014
Austrian Science Fund	Mar 24, 2017
Joint Biomedical Laboratory Research and Development and Clinical Science Research and Development Services, Scientific Merit Review Board, Subcommittee for Special Emphasis on Million Veteran Program SPLM	Jul 11-12, 2017 Jan 11-12, 2018
Swiss National Science Foundation/Innosuisse, Bridge Discovery review	July 2020
Case Comprehensive Cancer Center, Cancer Data Sciences Pilot Program review	January 2021
Chronic Renal Insufficiency Cohort (CRIC) Study Opportunity Pool Program, Reviewer	October 2021
<b><u>EDITORIAL DUTIES</u></b>	
Academic Editor, <i>PLoS One</i>	2012-present
Editor (Genetics section), <i>Pediatric Research</i>	2012-2016
Guest Associate Editor, <i>PLoS Genetics</i>	2016-2017, 2019, 2022
Specialty Chief Editor (Applied Genetic Epidemiology), <i>Frontiers in Genetics</i>	2017-present
Guest Editor, Special Issue "Data Resources and Approaches for Precision Medicine Research: New Developments and Applications" <i>Journal of Personalized Medicine</i>	2021

**AD HOC JOURNAL REVIEWER**

*Acta Cardiologica*  
*American Heart Journal*  
*American Journal of Epidemiology*  
*American Journal of Human Genetics*  
*American Journal of Hypertension*  
*American Journal of Medical Genetics*  
*American Journal of Obstetrics and Gynecology*  
*American Medical Informatics Association Joint Summits on Translational Science*  
*Annals of Human Genetics*  
*BioData Mining*  
*Bioinformatics and Biology Insights*  
*BMC Evolutionary Biology*  
*BMC Infectious Diseases*  
*BMC Medical Genetics*  
*BMC Sports Science, Medicine and Rehabilitation*  
*Cancer Epidemiology*  
*Cell Genomics*  
*Circulation: Cardiovascular Research*  
*Circulation Research*  
*Clinical and Experimental Medicine*  
*Computers in Biology and Medicine*  
*Coronary Artery Disease*  
*Diabetes*  
*EBioMedicine*  
*Epidemiology and Infection*  
*Ethnicity & Disease*  
*European Journal of Human Genetics*  
*European Journal of Medical Genetics*  
*Expert Review of Precision Medicine and Drug Development*  
*Frontiers in Neurology (Neurogenetics)*  
*Gene*  
*Genetic Epidemiology*  
*Genetics*  
*Genetics in Medicine*  
*Genome Medicine*  
*Genomic Medicine*  
*Genome Research*  
*Heart*  
*Hepatology*  
*Human Biology*  
*Human Molecular Genetics*  
*Human Mutation*  
*Influenza and Other Respiratory Viruses*  
*International Journal of Medical Informatics*

*Investigative Ophthalmology & Visual Science*  
*Journal of the American College of Cardiology*  
*Journal of American Medical Association*  
*Journal of the American Medical Informatics Association*  
*Journal of the American Society of Nephrology*  
*Journal of Biomedical Informatics*  
*Journal of Cellular and Molecular Medicine*  
*Journal of Human Genetics*  
*Journal of Pediatric Endocrinology and Metabolism*  
*Mayo Clinic Proceedings*  
*Molecular Biology and Evolution*  
*Molecular Genetics and Metabolism*  
*Nature Genetics*  
*Neurogenetics*  
*Neurosurgery*  
*New England Journal of Medicine*  
*Pacific Symposium on Biocomputing*  
*Pediatric and Blood Cancer*  
*PLoS Computational Biology*  
*PLoS Genetics*  
*PLoS One*  
*Physiological Genomics*  
*Science*  
*Scientific Reports*  
*The Pharmacogenomics Journal*  
*Trends in Genetics*  
*Tropical Medicine*

## **COMMITTEE SERVICE**

---

### **VANDERBILT UNIVERSITY**

Center for Human Genetics Research Annual Genetics Symposium  
Vanderbilt University, Nashville TN  
“Making Sense of the Senses”  
Speakers: Drs. Toni Pollin (University of Maryland), Stephen Wooding  
(UT Southwestern Medical Center), Jane Gitschier (University of California  
San Francisco), Jennifer Blackford (Vanderbilt University), David Calkins  
(Vanderbilt University), and Samuel Crish (Vanderbilt University)  
Organizing Committee Chair 2008

Vanderbilt University Program in Human Genetics Oversight Committee 2007-2014

Vanderbilt Institute for Clinical and Translational Research (VICTR) Studio  
expert and panel member, ad-hoc 2008-2013

Vanderbilt University Medical Scientist Training Program Faculty Advisory Committee	2011-2014
Vanderbilt University BioVU Operations and Oversight Board	Jul 2011-2014
Vanderbilt University BioVU Review Committee	
Member	Jun 2011-2014
Vice-chair	Aug 2013-2014
Vanderbilt University Center for Human Genetics Faculty Search Committee	2012
Vanderbilt University Molecular Physiology and Biophysics Curriculum Review Committee	2012
Vanderbilt University Endowed Genomics Chair Faculty Search Committee	2013
Vanderbilt University Prize Scholar Award Committee	2013

**CASE WESTERN RESERVE UNIVERSITY**

Case Western Reserve University Committee on Appointments, Promotion, and Tenure (CAPT), Department of Population and Quantitative Health Sciences committee member	2015-2019, 2021-present
Case Western Reserve University, Department of Epidemiology and Biostatistics, Population Genomics Search Committee, Chair	2015
Case Western Reserve University, Department of Epidemiology and Biostatistics, Grievance Committee	2015
Case Western Reserve University, Department of Epidemiology and Biostatistics, EPBI Ad hoc Seminar Committee, Chair	2015
Case Western Reserve University, Department of Epidemiology and Biostatistics, Health Disparities Search Committee, member	2015-2016
Case Western Reserve University, Cleveland Institute for Computational Biology Annual Symposium (North Coast Conference on Precision Medicine), Cleveland, OH, Organizing Committee Chair	2015-present
Case Western Reserve University, School of Medicine, Committee on Appointments, Promotion, & Tenure	
Member	2016-2019
Co-chair	2018-2019

Curriculum Vitae: DANA C. CRAWFORD

Departmental Search Committee Officer for Inclusion, Diversity and Equal Opportunity	
Biomedical Data Science Search Committee, member	
Cancer Epidemiology Search Committee, member	
Director of the MPH Program Search Committee, member	
Spatial Epidemiology Search Committee, ex officio	
Biostatistics Search Committee, ex officio	
MPH Non-Tenure Track Faculty Position Search Committee, member	
Computational Genetic Epidemiology Instructor Search Committee, member	2016-2019
Case Western Reserve University, Cleveland Institute for Computational Biology and Cleveland Clinic Lerner Research Institute, Quantitative Health Sciences, Bioinformatics Search Committee, member	2017-2018
MetroHealth System Medicine Chair Search Committee, member	2018
Case Western Reserve University, Nutrition Department Search Committee, member	2019-2020
Postbaccalaureate Research Education Program (PREP)	
Steering Committee, member	2019-2020
Associate Director	2019-2021
Co-Director	2021-present
MetroHealth System Biorepository Committee	2019
Case Western Reserve University, Department of Population and Quantitative Health Sciences, Epidemiology and Biostatistics PhD Program, Exam Committee, member	2019-present
Case Western Reserve University, Department of Population and Quantitative Health Sciences Biostatistics Search Committee, member	2020-2021
Case Western Reserve University, School of Medicine, Dean's Ad Hoc Committee on Diversity and Inclusion Excellence	2020
Case Western Reserve University Institutional Review Board (IRB)	2020-present
Case Western Reserve University, Senior Vice President for Research and Technology Management Search Committee, member	2022
Case Western Reserve University Medical Scientist Training Program (MSTP) Steering Committee, member	2022-present
Case Western Reserve University, Department of Genetics and Genomics	

Chair Search Committee, member

2022-present

## **TEACHING ACTIVITIES**

---

### **INVITED PRESENTATIONS (LOCAL; NASHVILLE, TN)**

1. *VLDLR*, carotid artery disease, and lipids. Center for Human Genetics Research, Genetic Interest Group, Vanderbilt University, Nashville, TN, October 19, 2006.
2. DNA resources for rare outcomes. An example in *Neisseria meningitidis*. Center for Human Genetics Research retreat, Vanderbilt University, Nashville, TN, June 13, 2007.
3. *VKORC1* and its association with bone mineral density in the general population. Department of Molecular Physiology and Biophysics, Vanderbilt University, May 8, 2008.
4. *VKORC1* and its association with bone mineral density in the general population. Vanderbilt Epidemiology Center, Nashville, TN, May 27, 2008.
5. The genetics of quantitative traits related to cardiovascular disease. Vascular Biology retreat, Vanderbilt University, Nashville, TN, October 31, 2008.
6. Of Biobanks and Cohorts: Using Large DNA Collections for Discovery and Characterization in the Era of Genome-Wide Association Studies. Vanderbilt Epidemiology Center, Nashville, TN, May 12, 2009.
7. Characterization of lipid-associated SNPs in the National Health and Nutrition Examination Surveys (NHANES). Vanderbilt Epidemiology Center, Nashville, TN, January 12, 2010.
8. Race Research and You: Genomic Tools for Health Disparities Research. Meharry Medical College, Nashville, TN, March 25, 2010.
9. Epidemiologic Architecture for Genes Linked to Environment. Department of Molecular Physiology and Biophysics, External Review, Nashville, TN, September 7, 2010.
10. The Genetics of Common Quantitative Traits in Diverse Populations. 11<sup>th</sup> Annual Vanderbilt Genetics Symposium (Beyond Disease Dichotomy. Quantitative traits and intermediate phenotypes), Nashville, TN, October 13, 2010.
11. Moving DNA from Bench to Bedside at Vanderbilt. Canby Robinson Society Board of Directors Meeting, Vanderbilt University, Nashville, TN, April 19, 2011.
12. On the Generalization of GWAS-identified variants in Diverse Populations. Illumina User Group Meeting, Nashville, TN, September 15, 2011.
13. Genomics and race/ethnicity. Vanderbilt Meharry CFAR Scientific Retreat, Nashville, TN, February 8, 2013.



14. The Center for Human Genetics Research (CHGR) and the Population Architecture using Genomics and Epidemiology (PAGE) Study: An Overview. Vanderbilt Epidemiology Center, Nashville, TN, February 21, 2013.
15. Genomic Predictors of Ages at Reproductive Milestones in African American Women. Meharry Medical College, 11<sup>th</sup> Annual Research Symposium, Nashville, TN, April 10, 2014.

**INVITED PRESENTATIONS (LOCAL; CLEVELAND, OH)**

1. EHRs and Large-scale Comparative Effectiveness Research. 2014 Biomedical & Health Informatics Workshop, Case Western Reserve University, Cleveland, OH, September 16, 2014.
2. All In! Cleveland and Precision Medicine. Genetics and Genome Sciences, Case Western Reserve University, September 30, 2015.
3. Precision Medicine Initiative: Challenges for Vision Research, Ophthalmology Grand Rounds, University Hospitals, March 23, 2016.
4. Crawford's in Cleveland. Graduate School and Beyond. Postbaccalaureate Research Education Program (PREP), Case Western Reserve University, February 15, 2017.
5. MetroHealth-Institute for Computational Biology Pilot study (MIPs): A Burgeoning Biobank in Cleveland, Genomic Medicine, Lerner Research Institute, Cleveland Clinic, June 12, 2017.
6. Academic Job Search Series (Panelist). Facilitated by Dr. Kristine-Ann Buela (post-doctoral fellow in Pathology) and organized by Rachel Begley, Director of the Professional Development Center, School of Graduate Studies, Case Western Reserve University, December 8, 2017.
7. Faculty ToolKit Series: Session on Promotion for Faculty in the Tenure Track (Panelist). Facilitated and organized by Nicole Deming, Assistant Dean for Faculty Affairs and Human Resources, Case Western Reserve University, February 20, 2018.
8. Crawford's in Cleveland. Graduate School and Beyond. Postbaccalaureate Research Education Program (PREP), Case Western Reserve University, February 21, 2018.
9. Different Ways Data Are Endangered (Panelist). Endangered Data Week, Kelvin Smith Library, Case Western Reserve University, February 28, 2018.
10. The Importance of an Online Presence in Science. Developing a Professional Online Presence, Women in Sciences and Humanities Earning Doctorates (WISHED), Case Western Reserve University, November 5, 2018.

11. Cleveland's Gone Computational. Postbaccalaureate Research Education Program (PREP), Case Western Reserve University, February 26, 2019.
12. Faculty ToolKit Series: Session on Senior Level Promotions for Faculty in the Tenure Track (Panelist). Facilitated and organized by Nicole Deming, Assistant Dean for Faculty Affairs and Human Resources, Case Western Reserve University, March 19, 2019.
13. Precision Medicine Research and Issues Related to Return of Results and Other Stuff. Heart, Lung, and Blood (HLB) Summer Research Program, Case Western Reserve University (virtual), July 9, 2020.
14. Big Data Bias: The Output is Only as Good as the Input. Women in Sciences and Humanities Earning Doctorates (WISHED), Case Western Reserve University (virtual), February 25, 2021.

### **CONSORTIA PRESENTATIONS**

1. EAGLE Overview. PAGE Steering Committee Meeting, Bethesda, MD, October 6, 2008.
2. EAGLE: Allele Frequencies and Associations. PAGE Steering Committee Meeting, Bethesda, MD, October 6, 2008.
3. EAGLE: Associations and Context Dependencies. PAGE Steering Committee Meeting, Bethesda, MD, October 6, 2008.
4. Genome-wide association study identified novel genomic regions associated with drug-induced Long QT Syndrome. Fifth Statistical Analysis Workshop of the Pharmacogenomics Research Network (PGRN), Rochester, MN, April 15, 2009.
5. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, April 27, 2009.
6. EAGLE Update. PAGE Steering Committee Meeting, Seattle, WA, September 24, 2009.
7. Inflammation Workgroup Update. PAGE Steering Committee Meeting, Seattle, WA, September 24, 2009.
8. Preliminary Lipids Analysis in EAGLE. PAGE Steering Committee Meeting and External Scientific Panel, Seattle, WA, September 24-25, 2009.
9. Preliminary Data from Vanderbilt Genome-Electronic Records (VGER) QRS Study. eMERGE Steering Committee Meeting, Bethesda, MD, November 19, 2009.
10. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, January 14, 2010.
11. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, January 14, 2010.

12. Vanderbilt Genome-Electronic Records (VGER) QRS Study. eMERGE Steering Committee Meeting, Bethesda, MD, April 12, 2010.
13. Genomics Workgroup: Next Steps in Genomics. eMERGE Steering Committee Meeting, Bethesda, MD, April 12, 2010.
14. EAGLE Update. PAGE Steering Committee Meeting, Nashville, TN, June 8, 2010.
15. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Nashville, TN, June 8, 2010.
16. Fine mapping in African American samples for QRS and T2D. eMERGE Steering Committee Meeting, Bethesda, MD, August 30, 2010.
17. Hypothyroidism. eMERGE Steering Committee Meeting and External Scientific Panel, Bethesda, MD, August 31, 2010.
18. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, October 19, 2010.
19. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting and External Scientific Panel, Bethesda, MD, October 19-20, 2010.
20. EAGLE Update. PAGE Steering Committee Meeting, Marina del Rey, CA, February 14, 2011.
21. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Marina del Rey, CA, February 14, 2011.
22. Network-wide Phenotype Update: Hypothyroidism. eMERGE Steering Committee Meeting, Bethesda, MD, April 25, 2011.
23. Fine mapping and admixture mapping associated with ECG traits and type II diabetes in African Americans. eMERGE Steering Committee Meeting, Bethesda, MD, April 26, 2011.
24. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, June 8, 2011.
25. Phase 1 Genomics Workgroup Highlights. eMERGE Steering Committee Meeting, Bethesda, MD, July 25, 2011.
26. Hypothyroidism/TSH: eMERGE Network-wide Projects eMERGE Steering Committee Meeting, Bethesda, MD, July 26, 2011.
27. Resistant Hypertension Update: eMERGE Network-wide Project. eMERGE Steering Committee Meeting, Bethesda, MD, July 26, 2011.

28. Genomics Workgroup eMERGE II Goals. eMERGE Steering Committee Meeting and External Scientific Panel, Rockville, MD, October 18, 2011.
29. Genetic risk scores and eMERGE. eMERGE Steering Committee Meeting, Bethesda, MD, February 9, 2012.
30. EAGLE Update. PAGE Steering Committee Meeting, Chapel Hill, NC, March 5, 2012.
31. PAGE-wide lipids analysis. PAGE Steering Committee Meeting, Chapel Hill, NC, March 6, 2012.
32. Genomics Workgroup Update. eMERGE Steering Committee Meeting, Minneapolis, MN, June 5, 2012.
33. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, June 19, 2012.
34. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, June 20, 2012.
35. PAGE Reproduction Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, June 20, 2012.
36. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, October 18, 2012.
37. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, October 19, 2012.
38. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Seattle, WA, March 14, 2013.
39. EAGLE Summary. PAGE Steering Committee Meeting, Seattle, WA, March 15, 2013.
40. Resistant Hypertension Update. eMERGE Steering Committee Meeting, Philadelphia, PA, June 3, 2013.
41. Null Variants. eMERGE Steering Committee Meeting, Bethesda, MD, October 7, 2013.
42. Genome-based Biomarker Quantification Process for Susceptibility/Risk. Informatics Domain Task Force (iDTF) Spring Face-to-Face Meeting, Clinical and Translational Science Awards (CTSA) Program, San Francisco, CA, March 16, 2018.
43. Engaging the Digitally Underserved in Clinical Research. Informatics Domain Task Force (iDTF) Spring Face-to-Face Meeting, Clinical and Translational Science Awards (CTSA) Program, San Francisco, CA, March 16, 2018.
44. eQTL Mapping in KPMP. Lightning Talks, Steering Committee Meeting, Kidney Precision

Medicine Project (KPMP), virtual, April 7, 2021.

**INVITED PRESENTATIONS (NATIONAL AND INTERNATIONAL)**

1. Cluster investigation of orofacial clefts in Dickson County, Tennessee, 1997-2000. Epidemic Intelligence Service Conference, Atlanta, GA, April 23-27, 2001.  
\*\*\*Featured in “The Rewards, and the Roadblocks, of Medical Sleuthing” by Lawrence K. Altaman, MD, NYTimes.com on May 1, 2001\*\*\*
2. Human diversity: Impact on genetic testing and screening. Information Conference on the Human Genome Project: Challenges and Impact of Human Genome Research for the Minority Communities, Atlanta, GA, July 20-21, 2001.
3. Examining the factors involved in fragile X CGG repeat instability—multifaceted approach. Department of Genome Sciences (Dr. Deborah Nickerson), University of Washington, Seattle, WA, September 7, 2001.
4. Examining the factors involved in fragile X CGG repeat instability—multifaceted approach. Department of Pediatrics, Arkansas Center for Birth Defects Research and Prevention (Director: Dr. Charlotte Hobbs), University of Arkansas for Medical Sciences, Little Rock, AR, January 24, 2002.
5. Examining the factors involved in fragile X CGG repeat instability—multifaceted approach. Program in Human Genetics (Director: Dr. Jonathan Haines), Vanderbilt University, Nashville, TN, January 31, 2002.
6. Examining the factors involved in fragile X CGG repeat instability—multifaceted approach. Center for Statistical Genetics (Director: Dr. Michael Boehnke), Department of Biostatistics, University of Michigan, Ann Arbor, MI, February 20, 2002.
7. Applying from the PGA Resource - Haplotypes. BayGenomics Program for Genomic Applications, San Francisco, CA, April 27, 2004.
8. SeattleSNPs and Applications in Pharmacogenetics. Rosetta, Seattle, WA, July 22, 2005.
9. Assessing the impact of candidate gene variation on quantitative phenotypes. Division of Statistical Genomics (Head: Michael Province), Washington University, St. Louis, MO, December 15, 2005.
10. Assessing the impact of candidate gene variation on quantitative phenotypes. Center for Human Genetics Research (Director: Jonathan Haines), Vanderbilt University, Nashville, TN, February 9, 2006.
11. Assessing the impact of candidate gene variation on quantitative phenotypes. Center for the Study of Weight Regulation and Associated Disorders (Director: Roger Cone), Oregon Health and Science University, Portland, OR, February 22, 2006.

12. Assessing the impact of candidate gene variation on quantitative phenotypes. The McDermott Center for Human Growth and Development (Director: Helen Hobbs), Center for Human Genetics, UT Southwestern, Dallas, TX, March 13, 2006
13. Assessing the impact of candidate gene variation on quantitative phenotypes. Division of Endocrinology, Diabetes and Nutrition (Head: Alan Shuldiner), University of Maryland, Baltimore, MD, April 4, 2006.
14. Genetic association study designs for influenza vaccine clinical trials. Keynote speaker for the Clinical Immunization Safety Assessment (CISA) annual meeting. Centers for Disease Control and Prevention, Atlanta, GA, April 23-24, 2007.
15. Genomics and Vaccine Safety. Understanding the Genomic Basis of Vaccine Safety. Centers for Disease Control and Prevention, Atlanta, GA, January 30-31, 2008.
16. *APOA1/C3/A4/A5* gene cluster SNPs and their interaction with dietary intake are associated with triglyceride levels in the Third National Health and Nutrition Examination Survey. Keystone Symposia on Complex Traits: Biologic and Therapeutic Insights, Santa Fe, NM, February 29-March 5, 2008.
17. Designing Association Analyses. From SNPs to Haplotypes, the Importance of Leveraging Linkage Disequilibrium. American Society for Clinical Pharmacology and Therapeutics, Orlando, FL, April 5, 2008.
18. Genetic determinants of lipids among nonfasting children. Department of Medical Genetics (Chair: Dr. Philip Giampietro), Marshfield, WI, August 13, 2008.
19. Of Biobanks and Cohorts: Using Large DNA Collections for Discovery and Characterization in the Era of Genome-Wide Association Studies. HudsonAlpha, Huntsville, AL, March 11, 2009.
20. Genome-wide association study identified novel genomic regions associated with drug-induced long QT-syndrome. Pharmacogenetic Research Network (PGRN) Statistical Analysis Workshop V, Rochester, MN, April 15, 2009.
21. Using NHANES to Determine the Epidemiologic Architecture for Genes Linked to Environment. National Center for Health Statistics, Centers for Disease Control and Prevention, Hyattsville, MD, October 7, 2009.
22. Using NHANES to determine the Epidemiologic Architecture for Genes Linked to Environment (EAGLE). HudsonAlpha Spring Symposium, Huntsville, AL, March 30, 2010.
23. Population Architecture using Genomics and Epidemiology (PAGE) – from SNPs to GWAS and beyond. American Public Health Association, Denver, CO, November 6-10, 2010.

24. Using Biobanks Linked to Electronic Health Records to Move from Base Pairs to Bedside. Illumina Discovery Symposium, Montreal, Canada, October 11, 2011.
25. On the Generalization of GWAS-identified Variants in Diverse Populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. Human Genetics and Genomics Seminar Series, University of Miami, Miami, FL, November 15, 2011.
26. Using biobanks linked to electronic health records to move from base pairs to bedside. Inaugural Symposium, Penn State Hershey Institute for Personalized Medicine, Penn State Hershey University Conference Center, Hershey, PA, June 8, 2012.
27. Trans-ethnic comparisons for the role of genetics in diabetes: the PAGE Study. American Diabetes Association, Philadelphia, PA, June 9, 2012.
28. Genetic Association Studies in Diverse Populations. Departments of Epidemiology and Biostatistics (Chair: Jonathan Haines) and Genetics and Genomics Sciences (Chair: Anthony Wynshaw-Boris), Case Western Reserve University, Cleveland, OH, September 20, 2013.
29. Big Genetic Epidemiology. American College of Epidemiology. Louisville, KY, September 24, 2013.
30. Genetic Association Studies in Diverse Populations. Division of Human Genetics (Director: Ray Hershberger), The Ohio State University, Columbus, OH, October 28, 2013.
31. Genetic Association Studies in Diverse Populations. School of Biology (Director of the Center for Integrative Genomics: Greg Gibson), Georgia Tech University, Atlanta, GA, December 5, 2013.
32. Approaches to Gene-Nutrient Studies Based on Experiences from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Study. 3<sup>rd</sup> International Vitamin Conference, Washington, DC, May 12-15, 2014.
33. Leveraging Epidemiologic and Clinical Collections for Genomic Studies of Complex Traits. Integrated Systems Biology Analytical Methods for Epidemiological Studies of Complex Traits, 2014 Mid-Atlantic Genetic Epidemiology and Statistics (MAGES) Conference, Philadelphia, PA, May 30, 2014.
34. Genome-wide Association Studies. Big Data Analysis and Translation in Disease Biology (Big Data and Disease), Jawaharlal Nehru University, New Delhi, India, January 19, 2015.
35. All In! Cleveland and Precision Medicine. Center for Systems Genomics, The Pennsylvania State University, August 26, 2015.
36. All In! Cleveland and Precision Medicine. Program in Personalized and Genomic Medicine, University of Maryland, November 18, 2015

37. Phenome-wide Association Studies. Understanding the Function of Human Genome Variation, Keystone Symposia, Uppsala, Sweden, June 1, 2016.
38. All In! Cleveland and Precision Medicine. Single Nucleotide Polymorphisms and Human Disease, Gordon Research Conference, Mount Holyoke, South Hampton, MA, June 16, 2016.
39. All In! Cleveland and Precision Medicine. Computational Challenges for Precision Medicine, MidAtlantic Bioinformatics Conference, Philadelphia, PA, October 26, 2016.
40. Diversity in Precision Medicine Research: An example in Cleveland. Keynote Speaker. Translational Bioinformatics Conference, Long Beach, CA, September 29-October 1, 2017.
41. Extracting Meaningful Clinical Outcomes from Large Biobanks. GpGx Computational Methods for Target Identification and Validation Scientific Input Engagement, Merck Research Labs, Boston, MA, December 12, 2017.
42. What You Need to Know about Precision Medicine Research. Precision Genomics Midwest, Cincinnati, OH, May 11, 2018.
43. Covering All the Bases: A Primer on Today's Sequencing Technologies and Their Applications in Precision Medicine Research. Total Exposure Health, Washington, DC, September 6-7, 2018.
44. Diversity as an Imperative in Precision Medicine. Personalizing CKD Care and Prevention: Lessons from Genomics of Chronic Disease, Kidney Week, American Society of Nephrology, San Diego, CA, October 23-28, 2018.
45. The Importance of Diversity in Big Genomic Data. Keynote speaker. Big Data and the Future of Research Symposia, Sigma Xi, San Francisco, CA, October 26-28, 2018.
46. Challenges in Precision Medicine Research: The Cleveland Experience. HudsonAlpha, Huntsville, AL, February 13, 2019.
47. Challenges in Precision Medicine Research: The Cleveland Experience. Department of Pharmacotherapy and Translational Research, University of Florida, Gainesville, FL, April 12, 2019.
48. Challenges in Precision Medicine Research: The Cleveland Experience. 3<sup>rd</sup> Personalized Medicine Conference, Puerto Vallarta, Mexico, May 30-June 2, 2019.
49. Precision Medicine Research and Issues Related to Return of Results. Center for Public Health Genomics, University of Virginia, Charlottesville, VA, November 20, 2019.
50. Making Precision Medicine Mainstream with Health Data: Challenges to Acceleration, Research Participation and Diversity, Precision Medicine World Conference, Santa Clara,



CA, January 21-24, 2020.

51. Electronic health records and computable phenotyping strategies. Precision Medicine meeting track, 27<sup>th</sup> International Molecular Medicine Tri-Conference, San Francisco, CA, March 2-4, 2020.
52. Medication-dependent computable phenotypes: mapping prescription records within the electronic health record across institutions. Big Drug Data: A Guide to Utilizing Electronic Health Records for Clinical Pharmacology Research, American Society for Clinical Pharmacology & Therapeutics, Houston, TX, March 18-21, 2020 (cancelled due to SARS-CoV-2/COVID-19).
53. Biobanks in diabetes and obesity research and treatment. Biobanks and Electronic Health Records in Diabetes Care and Research, American Diabetes Association, virtual, June 12-16, 2020.
54. Medication-dependent computable phenotypes: mapping prescription records within the electronic health record across institutions. Big Drug Data: A Guide to Utilizing Electronic Health Records for Clinical Pharmacology Research, American Society for Clinical Pharmacology & Therapeutics, virtual, March 8-12 and 15-17, 2021.
55. Electronic health records and genomic discovery: precision medicine research opportunities where Cleveland could really rock. Institute of Precision Medicine (IPM), Mount Sinai Hospital School of Medicine, virtual, May 19, 2021.
56. This Academic's Transition from Promotion to Promoting in Human Genetics and Genomics. Human Genetics Scholars Initiative (HGSI) Chat Session, American Society of Human Genetics, virtual, March 15, 2022.

### **TRAINEES/MENTEES**

#### **VANDERBILT UNIVERSITY**

### **Past Medical Fellows**

Daniel Johnson, MD (2010-2014) Fellow mentoring committee

Sara Van Driest, MD, PhD (2010-2014) Fellow mentoring committee

Quinn Wells, MD, PharmD, MSCI, MS (2014) Masters advisor in genetic epidemiology

### **Past Graduate Students**

PhD Program in Human Genetics:

Dapo Akingbade (2007) Rotation student

Chelsea (Cupp) Sullivan, PhD (2009) Rotation student

Kirsten Diggins, PhD (2012) Rotation student

Haley Eidem, PhD (2013) Rotation student  
Rachel (Hoffmann) Ashley, PhD (2013) Rotation student  
Lindsay (Gordon) Sausville, PhD (2010) Rotation student  
Gunnar Kwakye, PhD (2006) Rotation student  
Carrie Shaffer, PhD (2007) Rotation student  
Corinne Simonti, PhD (2013) Rotation student  
Clare Spielman (2013) Rotation student  
Krystal Tsosie, PhD, MPH (2012) Rotation student  
Olivia Veatch, PhD, MS (2009) Rotation student  
Amy Wotawa, MS, CG (ASCP), (2008) Rotation student  
Victoria Youngblood, PhD (2011) Rotation student

Carrie (Buchanan) Moore, MD, MS, PhD (2011-2013) Masters committee member  
Anna (Davis) Cummings, PhD, MS (2006-2012) Rotation student; Chair of thesis committee  
Laura D'Aoust, MD, PhD (2010-2014) Rotation student; Chair of thesis committee  
Todd Edwards, PhD, MS (2006-2008) Thesis committee  
Jake Hall, PhD, MS (2010-2014) Rotation student; Masters committee member  
Emily Holzinger, PhD, MS (2008-2013) Rotation student; Masters committee member  
Nuri Kodaman, PhD, MS (2009-2014) Masters committee member  
Mary Ellen Koran, MD, PhD (2012-2014) Thesis committee  
Jude McElroy, MD, PhD (2010-2012) Chair of thesis committee  
Sabrina Mitchell, PhD (2007-2010) Thesis committee  
Kelli Ryckman, PhD, MS (2007-2008) Thesis committee  
Rafal Sabota, MD, MS, PhD (2012-2015) Masters committee member; Chair of thesis committee  
Stephen Turner, PhD, MS (2007-2011) Chair of thesis committee; Masters committee member  
Marquitta White, PhD, MS (2009-2014) Rotation student; Thesis committee  
Laura Wiley, PhD, MS (2013-2014) Chair of thesis committee  
Rebecca (Zuvich) Essner, PhD, MS (2007-2009) Thesis committee

Logan Dumitrescu, PhD, MS (2006-2011) PhD thesis and Masters advisor, IDENTIFICATION AND CHARACTERIZATION OF GENETIC VARIANTS ASSOCIATED WITH LIPID AND LIPOPROTEIN LEVELS

- Awards
  - Supported by Training Program on Genetic Variation and Human Phenotype (T32 GM080178) as part of the Center for Human Genetics Research Human Genetics Training Program, 2007-2009
  - Summer Institute in Statistical Genetics Travel Award, Seattle, WA, June 11-29, 2007
  - Vanderbilt University Travel Grant Award, American Society of Human Genetics, Philadelphia, PA, November 11-15, 2008
  - Vanderbilt University Travel Grant Award, American Society of Human Genetics, Honolulu, HI, October 20-24, 2009
  - Teaching Fellowship Award, Vanderbilt University, 2009
  - Charles R. Park Student Travel Award, Human Genome Organisation Meeting, Montpellier, France, May 18-21, 2010
- Positions

- Post-doctoral fellow, Vanderbilt University Medical Center (2011-2013)
- Regulatory writing expert, Synchrogenix (2013-2016)
- Neuroimaging Analyst, Vanderbilt Memory & Alzheimer's Center, Vanderbilt University Medical Center (2016-2018)
- Research Assistant Professor, Vanderbilt Memory & Alzheimer's Center, Vanderbilt University Medical Center (2018-present)

Janina M. Jeff, PhD, MS (2007-2012) PhD thesis and Masters advisor, THE GENETICS OF QUANTITATIVE TRAITS ASSOCIATED WITH CARDIOVASCULAR DISEASE IN AFRICAN AMERICANS

- Awards
  - Supported by Training Program on Genetic Variation and Human Phenotype (T32 GM080178) as part of the Center for Human Genetics Research Human Genetics Training Program, 2008-2010
  - Summer Institute in Statistical Genetics Travel Award, Seattle, WA, June 16–July 2, 2008
  - Carl Storm Fellowship for Gordon Scientific Conferences, The Biology of Post-Transcriptional Gene Regulation, Salve Regina University, Newport, RI, July 18-23, 2010
  - FASEB MARC travel award, American Society of Human Genetics, Washington, DC, November 2-6, 2010
  - Vanderbilt University Travel Grant Award, African Society of Human Genetics, Cape Town, South Africa, March 6-9, 2011
  - Vanderbilt University Graduate School Dissertation Enhancement Grant, March 2011
  - Scientist in the Classroom Teaching Fellowship, Vanderbilt Center for Scientific Outreach, May 2011
  - FASEB MARC travel award, American Society of Human Genetics, Montreal, Canada, October 11-15, 2011
  - Dr. Levi Watkins Jr. Student Award for commitment to diversity, Vanderbilt School of Medicine, October 2011
  - National Graduate Student Symposium, St. Jude Children's Research Hospital, Memphis, TN, (one of the 45 invitees selected from 1,500 applications), March 20-24, 2012
- Positions
  - Post-doctoral fellow, Mount Sinai (2013-2015)
  - Global Bioinformatics Specialist, Illumina (2015-present)
  - In Those Genes podcast, founder (2018-present) and recipient of the American Society of Human Genetics Advocacy Award (2020)

Matt T. Oetjens, PhD, MS (2009-2014) PhD thesis and Masters advisor, PHARMACOGENETIC DISCOVERY IN AN EMR-BIOREPOSITORY

- Awards
  - Supported by Training Program on Genetic Variation and Human Phenotype (T32 GM080178) as part of the Center for Human Genetics Research Human Genetics Training Program, 2010-2012

- Vanderbilt University Travel Grant Award, European Society of Human Genetics, Amsterdam RAI, the Netherlands, May 28-31, 2011
- Positions
  - Post-doctoral fellow, Department of Human Genetics, University of Michigan (2014-2017)
  - Bioinformatics staff scientist, Autism & Developmental Medicine Institute, Geisinger Health System (2017-2019)
  - Assistant Professor, Geisinger Medical Center (2020-present)

Jennifer R. Malinowski, PhD, MS (2010-2014) PhD thesis and Masters advisor, WOMEN'S HEALTH: GENETIC VARIATION IN COMPLEX TRAITS

- Awards
  - Vanderbilt University Travel Grant Award, American Society of Human Genetics, Montreal, Canada, October 11-15, 2011
  - Why We Can't Wait: Conference to Eliminate Health Disparities in Genomic Medicine, travel award, San Francisco, CA, May 29-31, 2013
  - Pacific Symposium on Biocomputing, NLM/NIH travel award, Big Island, HI, January 3-7, 2014
- Positions
  - Associate Research Scientist, Department of Surgery, Section of Endocrine Surgery, Yale University School of Medicine (2014-2015)
  - Associate Analyst, Genetic Test Evaluation Program, Hayes, Inc (2015-2016)
  - Medical Research Analyst, Genetics, Hayes, Inc (2016)
  - Freelance writer (2015-present) and President of Write InSciTe (2017-present)

Nicole A. Restrepo, PhD (2010-2015), MS (2016) PhD thesis and Masters advisor, INVESTIGATION OF THE GENETIC EPIDEMIOLOGY OF AGE-RELATED MACULAR DEGENERATION, PRIMARY OPEN-ANGLE GLAUCOMA, AND DIABETIC RETINOPATHY IN DIVERSE POPULATIONS

- Awards
  - FASEB MARC travel award, American Society for Human Genetics, San Francisco, CA, November 6-10, 2012
  - Why We Can't Wait: Conference to Eliminate Health Disparities in Genomic Medicine, travel award, San Francisco, CA, May 29-31, 2013
  - FASEB MARC travel award, American Society for Human Genetics, Boston, MA, October 22-26, 2013
  - Pacific Symposium on Biocomputing, NSF travel award, Big Island, HI, January 4-8, 2016
- Positions
  - Research Scientist, Case Western Reserve University (2015-2017)
  - Bioinformatics staff scientist, Geisinger Health System (2017-2018)
  - Statistical genetics consultant, Decibel Therapeutics (2019-2020)
  - Genomics scientist, Seven Bridges Genomics (2020-present)

Brittany M. Hollister, PhD (2012-2017), PhD thesis co-advisor, EXAMINING THE ROLE OF SOCIOECONOMIC STATUS ON BLOOD PRESSURE IN AFRICAN AMERICANS

- Awards
  - 2015 Outstanding Student Presentation in Anthropological Genetics, American Association of Anthropological Genetics
  - Pacific Symposium on Biocomputing, NLM/NIH travel award, Big Island, HI, January 3-7, 2017
- Positions
  - Post-doctoral fellow, National Human Genome Research Institute, National Institutes of Health (2017-2019)
  - Academic Program Specialist III, University of Florida Genetics Institute (2019-present)

### **Past Postdoctoral Students**

Sarah A. Pendergrass, PhD, MS (2009-2011)

- Awards
  - Named one of Genome Technology's PIs of Tomorrow 2014
- Positions
  - Research Associate, Penn State University (2011-2015)
  - Assistant Professor, Geisinger Biomedical and Translational Informatics Program (2015-2019)
  - Scientific Manager, Genentech (2019-present)

Janina M. Jeff, PhD, MS (2012-2013)

- Awards
  - FASEB MARC travel award, American Society for Human Genetics, San Francisco, CA, November 6-10, 2012
  - Keystone Symposia Underrepresented Minority Scholarship, New Frontiers in Cardiovascular Genetics Beyond GWAS, Tahoe City, CA, January 13-18, 2013
- Positions
  - Post-doctoral fellow, Mount Sinai (2013-2015)
  - Global Bioinformatics Specialist, Illumina (2015-present)
  - In Those Genes podcast, founder (2018-present) and recipient of the American Society of Human Genetics Advocacy Award (2020)

Logan Dumitrescu, PhD, MS (2011-2013)

- Awards
  - Pacific Symposium on Biocomputing, NSF travel award, Big Island, HI, January 4-8, 2016
- Positions
  - Regulatory writing expert, Synchronix (2013-2016)
  - Neuroimaging Analyst, Vanderbilt Memory & Alzheimer's Center, Vanderbilt University Medical Center (2016-2018)
  - Research Assistant Professor, Vanderbilt Memory & Alzheimer's Center, Vanderbilt University Medical Center (2018-present)

Sabrina L. Mitchell, PhD (2010-2015)

- Awards
  - Pacific Symposium on Biocomputing, NLM/NIH travel award, Big Island, HI, January 3-7, 2014
- Positions
  - Post-doctoral fellow, Vanderbilt University Medical Center (2015-2017)
  - Staff Scientist, Division of Genetic Medicine, Vanderbilt University Medical Center (2017)
  - Staff Scientist, Department of Ophthalmology and Visual Sciences, Vanderbilt University Medical Center (2017-2018)
  - Staff Scientist, Division of Genetic Medicine, Vanderbilt University Medical Center (2018-present)

### **Past Other Students/Mentees**

Roberto Reyes, MS, University of Arizona undergraduate (2011) Minority Summer Research Program, Vanderbilt University Summer Science Academy

- Genetic architecture of triglyceride levels in children over the course of treatment for acute lymphoblastic leukemia (Oral presentation and FASEB MARC Program travel award). Molecular and Computational Biology session, Annual Biomedical Research Conference for Minority Students (ABRCMS), St. Louis, MO, November 9-12, 2011.

### **CASE WESTERN RESERVE UNIVERSITY**

#### **Current Graduate Students**

Jasmine Olvany (2019-present) Genetics and Genome Sciences PhD thesis committee member  
Anna Miller (2019-present) Genetics and Genome Sciences PhD thesis committee chair  
Shiyong Liu (2020-present) Epidemiology and Biostatistics PhD mentor  
Michael Osterman (2020-present) Epidemiology and Biostatistics PhD thesis committee chair  
Lauren Cruz, MPH (2021-present) Epidemiology and Biostatistics PhD co-mentor with Jessica Cooke Bailey, PhD  
Carly Rose (2022-present) Biomedical and Health Informatics PhD mentor

#### **Current Postdoctoral Students**

Andrea Waksmunski, PhD (2021-present) TL1 mentoring committee member.

#### **Current Other Students/Mentees**

Katherine Dobbs, MD (2018-present) K23 Research Mentor for Case Western Reserve University School of Medicine Instructor, Pediatrics (1K23 AI132644-01A1 Epigenetic Reprogramming of Monocyte Functions during Acute Uncomplicated Malaria in Kenyan Children)

#### **Past Graduate Students**

Elina Misicka (2018) Rotation student, Epidemiology and Biostatistics PhD program

Shiying Liu, MS (2019) Rotation student, Epidemiology and Biostatistics PhD program  
Lauren Cruz, MPH (2020) Rotation student, Epidemiology and Biostatistics PhD program  
Carly Rose (2022) Rotation student, Biomedical Health Informatics PhD program

Mike Fang (2018) Ad hoc committee member, Epidemiology and Biostatistics PhD program  
Abby Statler, PhD (2017-2018) Epidemiology and Biostatistics PhD thesis committee chair  
Ruzica Conic, PhD (2017-2019) Clinical Research Scholars Program PhD thesis committee member

Andrea Waksmunski, PhD (2017-2020) Genetics and Genome Sciences PhD thesis committee chair

Xinyuan (Blair) Zhang, PhD (2019-2020) Genomics and Computational Biology, University of Pennsylvania, thesis committee member

Elina Misicka, PhD (2018-2022) Epidemiology and Biostatistics PhD thesis committee chair

Lauren Cruz, MPH (2020) MPH Capstone Committee Chair GENETIC RISK FOR ALZHEIMER'S DISEASE IN AN AMISH COHORT

- Current Position: Graduate student, CWRU Epidemiology and Biostatistics PhD program (2020-present)

### **Past Other Students/Mentees**

Sarah M. Laper, Eastern Virginia Medical School student (2015) CWRU summer volunteer research

- 9th Annual National Conference on Health Disparities and 2016 National Environmental Justice Conference and Training Program (Poster presentation and travel scholarship (declined due to conflict in schedule), Washington, DC, March 9, 2016.
- Current position: MetroHealth Resident Physician (2018-present)

Julia Cuva, Mentor High School senior in Mentor, OH (2016-2017) Academic year research

- The impact of genetic ancestry on the risk of developing chronic kidney disease, Northeastern Ohio Science and Engineering Fair, John Carroll University, University Heights, OH, March 6-9, 2017.
  - Second place overall
  - Special Awards
    - CWRU - Frances Payne Bolton School of Nursing
    - Cleveland Clinic, Department of Pathobiology
    - Cleveland Clinic, Department of Immunology

Kimberly Heath Borrero, University of Puerto Rico Ponce undergraduate (2017) Case Western Reserve University Heart, Lung, and Blood (HLB) Summer Research Program

- Characterization of genetic ancestry among chronic kidney disease patients, Annual Biomedical Research Conference for Minority Students (ABRCMS) (Poster presentation and travel award), Phoenix, AZ, November 1-4, 2017.

Gabriela DeFurio, Case Western Reserve University undergraduate (388S, Fall 2018) SAGES Capstone and independent research project research sponsor. This 3-credit hour research project

spanned the fall semester and required reading from the primary scientific literature, weekly meetings, and data analysis of genetic data linked to electronic health records.

- The project culminated in a short research paper and a poster presentation titled “Genetic Variation and Chronic Kidney Disease” as part of the CWRU Support of Undergraduate Research and Creative Endeavors (SOURCE) in Cleveland, OH on December 7, 2018.

Jessica Cooke Bailey, PhD, MA (2016-2020) KL2 scholar Research Mentor for Case Western Reserve University School of Medicine Instructor, Population and Quantitative Health Sciences

- Current position: CWRU PQHS Assistant Professor (January 2018-present)

Domenica Drouet, Case Western Reserve University medical school student (2020), Case Western Reserve University Heart, Lung, and Blood (HLB) Summer Research Program; Case Western Reserve University School of Medicine MD thesis advisor (2020-2022)

Caitrin W. McDonough, PhD (2018-2022) K01 Research Mentor for University of Florida College of Pharmacy Research Assistant Professor, Pharmacotherapy and Translational Research (1K01 HL41690-01 Integrative data approaches for resistant hypertension identification and prediction)

## **COURSEWORK**

### **Previous Classes and Lectures**

Spring 1997	Human and Molecular Genetics. MEDI 545/IBS 505. Emory University, Atlanta, GA. Small-group seminar facilitator teaching assistant. (Teaching requirement for PhD program; audience: medical school students and graduate students)
Spring 1999	Human and Molecular Genetics. MEDI 545/IBS505. Emory University, Atlanta, GA. Small-group seminar facilitator substitute teaching assistant (audience: medical school students and graduate students).
October 25, 2006	American Society of Human Genetics Outreach to Teach. Honors Biology...Only the Beginning. Vanderbilt University, Nashville, TN. Lecturer (audience: high school students).
September 19, 2007	Epidemiology 1: Research Design. Genome-wide association studies--why all the excitement? Vanderbilt University, Nashville, TN. Lecturer (audience: graduate students and MPH students).
February 27, 2008	Capstone Course. Genome-wide association studies. Rheumatoid arthritis. Vanderbilt University, Nashville, TN. Lecturer (audience: medical school students).
April 14, 2008	GWAS: The Future. Center for Human Genetics Research workshop series Making Sense of the Human Genome (Genome-wide Association



- Studies), Vanderbilt University, Nashville, TN. Lecturer (audience: graduate students, post-doctoral fellows, staff scientists).
- Spring 2008-2009      Tutorials in Statistical and Population Genetics. Vanderbilt University graduate course MPB/HGEN 371. One-hour journal-club style presentations by graduate students from current literature. Co-course director with Dr. Chun Li.
- November 16, 2009      Bioregulation I. Vanderbilt University Integrated Graduate Program graduate course. The Hunt for Human Genes, Part I. Vanderbilt University, Nashville, TN. Lecturer (audience: graduate students).
- November 12, 2010      Master of Science in Clinical Investigation (MSCI) Program. More of the Molecular Toolbox - Types of Genetic Markers, Methods of Genotyping and Microarrays. Vanderbilt University, Nashville, TN. Lecturer (audience: Masters students).
- Fall 2010-2013          Personalize This! Direct-to-Consumer Genetic Products. Biological Sciences 105, Vanderbilt University, Nashville, TN. Lecturer (audience: undergraduates).
- Spring 2007-2010      Human Genetics II. Vanderbilt University graduate course MPB/HGEN 341. Three to five 1 1/2 hour lectures covering various topics in human genetics including epidemiology in genetics, determining the genetic component of a trait, polymorphisms in the Human Genome, and applications of methods using cardiovascular disease as an example.
- Spring 2010-2014      Genetic epidemiology, course director. Vanderbilt University graduate course MPB/HGEN 390. One and a half hour upper-level class covering various topics in human genetic epidemiology. Co-course director with Drs. Scott Williams (2010-2012) and Will Bush (2014).
- Spring 2012-2014      Human Genetics II, course director. Vanderbilt University graduate course. MPB/HGEN 341. One and a half hour upper-level class covering various fundamental topics in human genetics and genetic epidemiology. The course is required of all PhD students in the Program in Human Genetics.
- 2011-2014              Center for Human Genetic Research Journal club, co-director. Vanderbilt University. Non-credit, informal gathering of students, faculty, and staff to discuss current articles relevant to human genetics and ocular genomics. Journal club meets twice a month during the academic year and once a month during the summer. Topics include scientific articles in the literature as well as articles in the literature and lay media related to ethics, responsible conduct in research, effective scientific communication, diversity in the sciences, equal pay, work/life balance, etc.

November 16, 2015 Personalize This! Direct-to-Consumer Genetic Testing. EPBI 501, Case Western Reserve University, Cleveland OH. Lecturer (audience: graduate students and faculty).

Fall 2015, 2017, 2018 Introduction to Population Health, guest lecturer (human genetics and health disparities). Case Western Reserve University graduate source. PQHS 440 (formerly EPBI440). A three-hour graduate-level course that introduces students to the emerging and complex field of population health, which looks beyond individual outcomes and singular determinants of health and disease. This course is required of all Masters and PhD students in Epidemiology and Biostatistics.

Fall 2015-2020 Health Care Analytics (formerly known as Secondary Analysis of Large Health Care Data Bases), course director of electronic health records one credit hour. Case Western Reserve University graduate course. PQHS 515 (formerly EPBI515). A three-hour graduate-level class covering common large-scale secondary data bases generated for research, health care, administration/billing, or other purposes. This course is required for the Health Behavior and Prevention PhD Program Concentration in Epidemiology and Biostatistics and is an elective for other Masters and PhD students.

November 28, 2018 Genome-wide association studies 2. PQHS 451, Case Western Reserve University Cleveland, OH. Lecturer (audience: graduate students).

Fall 2019 Integrated Thinking in Population and Quantitative Health Sciences, co-facilitator for phenome-wide association studies and pleiotropy. Case Western Reserve University graduate course. PQHS 472. A two-hour graduate-level class based on the scientific literature where a specific disease is used each semester as a test case of integration of different domains of knowledge for improved understanding of disease etiology and development of prevention and treatments. This course is required all PhD students in Epidemiology and Biostatistics.

Spring 2021, 2022 Genome-wide association studies. Population structure. PQHS 452, Case Western Reserve University Cleveland, OH. Lecturer (audience: graduate students).

### **Current Classes and Lectures**

Spring 2015-present Communicating in Population Health Science Research, course director. Case Western Reserve University graduate course. PQHS 444 (formerly EPBI 444). A one-hour graduate-level class covering various forms of scientific communication including writing (Spring) and oral presentations (Fall). This course (for a total of two credit hours) is required of all PhD

students in Population and Quantitative Health Sciences (formerly Epidemiology and Biostatistics).

Spring 2015, 2017-2019, 2021, 2022

On Being A Professional Scientist, faculty participant. Case Western Reserve University graduate course. IBMS 500. A mandatory zero credit hour weekly ethics course for first year graduate students. This course offers a 30-40-minute lecture on a specific ethics topic followed by a 45-minute faculty-led small group discussion. Topics covered include defining scientific integrity, mentorship, live animal subjects, data management, research misconduct and policies, commercialization and intellectual property, safe laboratory practices, responsible authorship (publication and peer review), conflicts of interests (personal, professional, and financial), human subjects (IRBs, tissue and databank research), collaborative research, self-promotion in science and social media, and the scientist as a responsible member of society.

2015-present

Case Western Reserve University School of Medicine MD Thesis Reviewer. All CWRU medical school students are required to complete a thesis based on research performed in the Research Block (four months). The thesis is submitted in the fourth year of medical school and reviewed by faculty. Typically, faculty review one to three theses per year.

2017-present

Case Western Reserve University School of Medicine Portfolio Reviewer. All CWRU medical students are required to complete Summative ePortfolio essays at three points of time during the Western Reserve (WR)<sub>2</sub> Curriculum: at the end of Year 1, at the end of Year 2, and after core clerkship rotations. The narrative essays are written by the students with accompanying evidence to demonstrate how a student is progressing with respect to meeting the milestones aligned to the Educational Program Objective of the CWRU SOM curriculum. The essays are reviewed by faculty, and faculty typically review one to three essays per round.

2021-present

PREP-aring for Success in a Biomedical PhD Program, course director. Case Western Reserve University post-baccalaureate course. MGRD 401 (fall) and MGRD 402 (spring). This two-semester series (1 credit unit per semester) designed to prepare CasePREP Scholars for the biomedical PhD program application and admissions processes, improve their application credentials, and prepare them for success in top biomedical PhD programs throughout the nation. Students receive scientific research training, instruction, and experience in reading the primary literature, develop oral and written communication skills, and participate in professional development activities. Students will prepare a professional scientific abstract, submit it to a national meeting, prepare a scientific poster presentation on their research and present that research poster at a national meeting. The course is required for CasePREP Scholars.

**Workshops**

- July 23-24, 2003 From Genome to Disease. Identifying Haplotypes for Genotype-Phenotype Analysis. NHLBI/NIH, Bethesda, MD. Lecturer.
- Sept 8-10, 2003 Variation Discovery Workshop. Applying Data from the PGA-Haplotypes. University of Washington, Seattle, WA. Lecturer.
- July 12-14, 2004 Variation Discovery Workshop. Applying Data from the PGA - Haplotypes. University of Washington, Seattle, WA. Lecturer.
- April 25-26, 2005 SeattleSNPs Variation Workshop. SNP Selection. Washington University, St. Louis, MO. Lecturer.
- May 2, 2005 Genomic Applications in Heart, Lung, Blood, and Sleep Disorders Research. SNP Discovery and Analysis: Application to Association Studies. Morehouse School of Medicine, Atlanta, GA. Lecturer
- July 19-20, 2005 From Genome to Disease II. SNP Discovery and Analysis: Application to Association Studies. NHLBI/NIH, Bethesda, MD Lecturer.
- Sept 12-13, 2005 Variation Discovery Workshop. Picking SNPs: Application to Association Studies. University of Washington, Seattle, WA. Lecturer.
- January 30-31, 2006 SNP Workshop: Bioinformatics and genotyping. Picking SNPs: Application to Association Studies. NIEHS, Research Triangle Park, NC. Lecturer.
- March 20-21, 2006 Variation Discovery Workshop. SNP Selection. University of Washington, Seattle, WA. Lecturer.
- May 15-16, 2006 Program for Genomic Applications Traveling Tutorials. Tools for Association Studies: Candidate genes and quantitative phenotypes. Washington University, St. Louis, MO. Lecturer.
- October 2-3, 2006 Program from Genomic Applications Traveling Tutorials. Tools for Association Studies: Candidate genes and quantitative phenotypes. University of Alabama at Birmingham, Birmingham, AL. Lecturer.
- January 10-11, 2008 NIEHS SNPs Workshop. SNP Selection. Association Analysis. University of Louisville, Louisville, KY. Lecturer.
- Apr/May 2008-2013 Genetic Analysis of Complex Human Diseases. Gene-Gene and Gene-

Environment Interactions. Miami Institute for Human Genomics,  
University of Miami, FL. Lecturer.

February 18-19, 2009 Variation Discovery Workshop. SNP Selection and Association Analysis.  
Centers for Disease Control and Prevention, Atlanta, GA. Lecturer.

March 25, 2011 Direct-to-Consumer Testing: The Promotions and the Products. Center for  
Human Genetics Research workshop series Making Sense of the Human  
Genome (DNA Testing and You), Vanderbilt University, Nashville, TN.  
Lecturer.

April 2011-2012 Personalized Medicine. Vanderbilt Medical School II (VMS II),  
Vanderbilt University School of Medicine, Nashville, TN. Lecturer.

May 2011-2013 Genetic Analysis of Complex Human Diseases. Genome and Variation  
Databases. Miami Institute for Human Genomics, University of Miami,  
FL. Lecturer.

## **RESEARCH SUPPORT**

---

### **ACTIVE**

**2 U01 DK114908-06 (Poggio, Sedor, O'Toole)** 07/01/2022-06/30/2027  
NIH/NIDDK

Cleveland Precision Medicine Chronic Kidney Disease Cohort

The Cleveland KPMP Recruitment Network Site proposes to recruit patients with chronic kidney  
disease for the larger Kidney Precision Medicine Project (KPMP).

Role: Co-investigator

**1UL1 TR002548-01 (Konstan)** 05/15/2018-03/31/2023  
NIH/NCATS

Clinical and Translational Science Collaborative of Cleveland

The Clinical and Translational Science Collaborative (CTSC) of Cleveland is a collaborative  
venture among five Cleveland health institutions - Case Western Reserve University, the  
Cleveland Clinic, University Hospitals, MetroHealth Medical Center, and the Veterans  
Administration Medical Center, as well as community partners.

Role: Co-investigator for the Informatics Component (Lead: Jonathan Haines)

**I01 BX004557-01 (Peachey)** 04/01/2019-03/31/2023  
VA

Deciphering Genetic and Environmental Influences on Visual Disorders in the Million Veteran  
Program

The proposal aims to perform single variant analysis for ocular phenotypes representing the most  
common ocular diseases, to identify common and rare variants in the multi-ethnic MVP  
population and perform cross-trait analyses and PheWAS for various ocular and physiologic  
phenotypes to identify shared (and private) genetic and environmental risk factors.

Role: Co-investigator

**1R13 HG011436 (Crawford)**

12/01/2020-08/31/2023

NIH/NHGRI

Data Lakes Meet the Great Lakes: Deep Dives into Diversity in Genomics

We aim to host an annual symposium every fall focused on precision medicine, big data genomics, and diversity. This proposal aims to support trainees and early career scientists for travel to the symposium.

Role: PI

**2R25 GM075207 (Crawford)**

07/01/2020-06/30/2025

NIH/NIGMS

Case Postbaccalaureate Research Education Program

The overall goal of CasePREP is to develop recent baccalaureate science graduates from diverse backgrounds under-represented in biomedical sciences so that they have the necessary knowledge and skills to pursue PhD or MD-PhD degrees in these fields.

Role: PI

**COMPLETED**

**1UH3 DK114908-05 (Poggio, Sedor, O'Toole)**

07/01/2019-06/30/2022

NIH/NIDDK

Cleveland Precision Medicine Chronic Kidney Disease Cohort

The Cleveland KPMP Recruitment Network Site proposes to recruit patients with chronic kidney disease for the larger Kidney Precision Medicine Project (KPMP).

Role: Co-investigator

**1R01 GM126249-02 (Bush and Crawford)**

09/30/2018-06/30/2021 NCE

NIH/NIGMS

An Atlas of Clinical Associations Mapping to Variants within Protein Structures

This proposal aims to develop and refine methodology for grouping variants within protein structural space for functional association studies and to construct a mapping between three-dimensional protein regions and clinical outcomes using a two-stage Phenome-Wide Association Study in whole-exome sequencing data linked to electronic health records.

Role: MPI

**CTSC Large Pilot Grants (Bush)**

08/01/2020 – 06/30/2021

NIH/NCATS

Glycemic Control and COVID-19 Disease Severity among Patients with Chronic Kidney Disease

We aim to investigate the effect of T2D control on COVID-19 disease severity among CKD patients at the Cleveland Clinic in Cleveland, OH using electronic health records and an existing CKD registry.

Role: Co-investigator

**1R03 AG063229-02 (Crawford)**

05/01/2019-02/28/2021 NCE

NIH/NIA

T-cell Receptor Repertoires and Alzheimer's disease

We aim to characterize T-cell receptor profiles among cases and controls of Alzheimer's disease in Amish living in Ohio and Indiana.

Role: PI

**1R13 HG010286-01 (Crawford)**

08/17/2018-07/31/2020

NIH/NHGRI

Sequencing and Genotyping in Diverse Populations: Who Wants What Back (and When)?

This proposal supports travel scholarships for trainees and early investigators to attend the annual North Coast Conference on Precision Medicine held in Cleveland, OH every fall.

Role: PI

**DiaComp Pilot and Feasibility Program (O'Toole, Crawford)** 11/01/2018-10/31/2019 NCE

NIH/NIDDK

Automated Identification of Diabetic Individuals with Renal Complications

This study will use rule-based algorithms to identify subjects with diabetic kidney diseases from an EHR-derived research database and assess the precision and accuracy of key phenotypic variables and outcomes by comparing EHR data to curated kidney disease databases.

Role: Co-PI

**CTSC Large Pilot Grants (Crawford)**

08/03/2018-04/30/2019

NIH/NCATS

T-cell receptor diversity as a marker of chronic kidney disease (CKD) progression among hypertensive non-diabetic African American patients with CKD stages 3-5

The proposal pilot study will characterize the immune profiles of African American CKD patients using TCR diversity as proxy. The main goal is to assess TCR diversity as a marker for CKD stage and possible predictor of progression to end stage renal disease (ESRD).

Role: PI

**I01 BX003364A1 (Konicki/Peachey)**

10/01/2016-09/30/2018

VA

Genetic Risk for AMD in Diverse Veteran Populations

The goals of this project are to determine whether AMD risk alleles are shared across different ethnic populations, whether the identified genes will be replicated in an independent population, and to determine whether a relationship exists between AMD genes and biomarkers related to blood lipid chemistry.

Role: Co-investigator

**1R13 HG009481-01 (Crawford)**

09/20/2016-07/31/2018

NIH/NHGRI

Precision Medicine for All

This proposal supports travel scholarships for trainees and early investigators to attend the annual North Coast Conference on Precision Medicine held in Cleveland, OH every fall.

Role: PI

**Nord Grant (Crawford)** 07/01/2016-06/30/2017

CWRU/UCITE

The Lacks Family on Consent and Community Engagement in the Era of Precision Medicine  
The Nord Grants, offered through CWRU's University Center for Innovation in Teaching and Education (UCITE), fund projects that directly benefit student learning or indirectly benefit students through faculty development. This grant will support, in part, the invitation of the Lacks Family to speak at CWRU about their family's collective experience in biomedical research projected onto today's environment of precision medicine research. The Lacks Family will speak at CWRU's Institute for Computational Biology (ICB) annual symposium or the equivalent organized by ICB and Dr. Crawford.

Role: PI

**5UL1 TR000439-09 (Konstan)** 09/17/2007-05/31/2017

NIH/NCATS

Clinical and Translational Science Collaborative of Cleveland

The Clinical and Translational Science Collaborative (CTSC) of Cleveland is a collaborative venture among five Cleveland health institutions - Case Western Reserve University, the Cleveland Clinic, University Hospitals, MetroHealth Medical Center, and the Veterans Administration Medical Center, as well as community partners. The CTSC Core Resources, including the CTSC Office of Comparative Effectiveness Research (CER) Core, are organized into twelve groups by area of expertise. Collectively these Cores help in the development of clinical and translational research studies and tools, facilitate clinical-investigator interfaces and community outreach, provide education, and administer and track CTSC activities.

Role: Co-investigator

**Institute for Computational Biology Pilot Grant (Crawford)** 03/01/2016-02/28/2017

CWRU/ICB

MetroHealth-Institute for Computational Biology Pilot study (MIPs)

This pilot study funds the collection of biospecimens from consented MetroHealth patients for precision medicine research. Participants are also surveyed on their attitudes towards biobanking as envisioned by the larger Precision Medicine Initiative Cohort Program and return of research results.

Role: PI

**T32 GM80178-07 (Haines)** 07/01/2012-11/12/2013

(Crawford) 11/13/2013-6/30/2014

(Samuels) 07/01/2014-06/30/2017

NIH/NIGMS

Training Program on Genetic Variation and Human Phenotypes

This training grant provides five slots for graduate-level training towards a PhD in human genetics.

Role: PI

**5U01 HG006385-03 (Haines)** 08/15/2011-01/06/2014

(Harris and Crawford) 01/07/2014-05/18/2014

(Harris) 05/19/2014-07/31/2015



NIH/NHGRI

eMERGE Coordinating Center

The goal of this proposal is to coordinate the efforts and activities of the individual sites within the eMERGE network.

Role: Multiple-PI

**5U91 HL065962-13 (Roden)**

04/01/2000-06/30/2015

NIH/NHLBI

Pharmacogenomics of Arrhythmia Therapy

The goal of this study is to identify genetic variation important for arrhythmias such as drug-induced Long QT syndrome, atrial fibrillation and complications on warfarin therapy. As co-investigator, I lead candidate gene and genome-wide association studies to identify genetic variants that impact risk for drug-induced Long QT syndrome. I also lead BioVU and NHANES genetic analyses as part of the larger International Warfarin Pharmacogenomics Consortium (IWPC). I am also a member of P-STAR, a group within PGRN that has the goal of providing statistical resources and guidance for projects related to pharmacogenomics as part of the Pharmacogenetics Research Network (PGRN).

Role: Co-investigator

**5U01 HG006378-03 (Roden)**

08/15/2011-07/31/2015

NIH/NHGRI

Vanderbilt Genome-Electronic Records Project

The primary goal of this project is to assess the usefulness of biobanks in performing genome-wide association studies. This grant will fund the study design of a genome-wide association study. This grant will also support work towards developing tools to mine the electronic medical records and tools to de-identify these data for use in human genetics. As co-investigator, I lead the BioVU genomic analyses as part of the larger electronic Medical Records & Genomics (eMERGE) Network. I will also design studies to assess the contribution genetic variants, alone or in combination, contribute risk to clinically relevant outcomes to identify “actionable variants” for the network.

Role: Co-investigator

**5R01 LM010685-03 (Denny)**

09/1/2011-08/31/2014

NIH/NLM

From GWAS to PheWAS: Scanning the EMR phenome for gene-disease associations The overall goal of this proposal is to systematically identify pleiotropic associations using DNA samples linked to electronic health records.

Role: Co-investigator

**5R01 CA092447-12 (Blot)**

09/26/2011-06/30/2016

National Cancer Institute

Southern Community Cohort Study

The Southern Community Cohort Study is a large, prospective epidemiology cohort study designed to investigate the environmental and genetic causes for racial disparities in cancer and other health outcomes.

Role: Co-investigator

**W81XWH-12-1-0547 (Aldrich)** 09/15/2012-09/14/2014

DoD

Prognosis of Lung Cancer: Heredity or Environment?

The goal of this project is to identify genetic risk factors in lung cancer, and to determine the potential role of environmental factors and how they interact with the genetic risk factors.

Role: Co-investigator

**VUMC42613 5R01 DK078616-05S1 (Meigs/Kabagambe)** 12/01/2013-11/31/2014

NIH/NIDDK

Meta-analysis of Type 2 Diabetes in African Americans - the MEDIA Consortium The primary goal of this proposal is to identify genetic variants associated with risk of type 2 diabetes in African Americans. This supplement will support the addition of data from the Southern Community Cohort Study and/or BioVU, the Vanderbilt biorepository linked to de-identified electronic medical records to the parent grant, *Common Genetic Variation and Quantitative Diabetes Traits*.

Role: Co-investigator

**(Villegas)** 04/01/2014–01/31/2015

Vanderbilt Diabetes Research and Training Center

Insulin resistance genes and type 2 diabetes in African Americans

In this pilot study, we aim to identify common and rare variants as associated with type 2 diabetes in African Americans. The scope of inquiry will be limited to genes known to be involved in insulin resistance. We will also characterize the potential modifying effects of body mass index on these genetic associations.

Role: Co-investigator

**VR4427 (Crawford)** 2012-2013

Vanderbilt Institute for Clinical and Translational Research (VICTR)

*APOC3* R19X and very low triglyceride levels in European Americans

This VICTR voucher provided the funds to genotype 184 individuals in BioVU (Vanderbilt's biorepository linked to de-identified electronic medical records) with very low triglyceride levels on the Illumina ExomeChip.

Role: PI

**VR3288 (Dumitrescu)** 2012-2013

Vanderbilt Institute for Clinical and Translational Research (VICTR)

Replication of MI Associations in African American BioVU Samples

This VICTR voucher provided the funds to genotype individuals in BioVU (Vanderbilt's biorepository linked to de-identified electronic medical records) with and without myocardial infarction (MI) to replicate an association identified in NHANES III between MI and *LPA* variants.

Role: Co-investigator

**3U01 HG004798 (Crawford)** 07/01/2008-12/31/2013

NIH /NHGRI

**Epidemiologic Architecture for Genes Linked to Environment (EAGLE)**

The primary goal of this project is to describe the epidemiologic architecture of genetic variations identified through genome-wide association studies (GWAS) using a population-based, diverse cross-sectional survey known as the National Health and Nutrition Examination Survey (NHANES). We will also replicate previously published GWAS and identified potential mitochondrial and/or environmental modifiers. ARRA supplement provided funds for genotyping ancestry informative markers in NHANES III and NHANES 1999-2002. ARRA supplement provided funds to identify and genotype cases and controls for eight major cancers in BioVU, the Vanderbilt DNA Databank, for eventual meta-analysis in the Population Architecture using Genomics and Epidemiology (PAGE) Study.

Role: PI

**5RC2 GM092618-02 (Denny/Roden)**

09/30/2009-01/31/2012

NIH/NIGMS

VESPA: Vanderbilt Electronic Systems for Pharmacogenomic Assessment

The overall goal of this project is to use the Vanderbilt DNA Databank (BioVU) to identify cases of adverse reactions to medication and controls for pharmacogenomic studies using the ADME developed by Illumina. As co-investigator, I lead the genomic study design and analysis of outcomes and traits related to pharmacogenomics. I also lead the quality control efforts for these large datasets in BioVU.

Role: Co-investigator

**CRC1599 (Edwards)**

2009-2010

Vanderbilt Institute for Clinical and Translational Research (VICTR)

INF 15.06 Pilot Study of the Genotypic Analysis of Patients Infected with Influenza Virus Compared with Matched Uninfected Controls (DMID 06-0092)

This VICTR voucher provided the funds to collect and extract DNA from blood and mouthwash samples from children exposed to the influenza vaccine for an eventual genome-wide association study of adverse reactions (wheezing) following vaccination.

Role: Co-investigator

**200-2002-00732 (Edwards)**

10/01/2002-09/30/2008

CDC

Vaccine Safety Surveillance and Assessment

The overall goal of this multi-center study is to examine clinical immunization safety assessment of children.

Role: Co-investigator

**VICTR PN\_1829 (Crawford)**

2008-2009

Vanderbilt Institute for Clinical and Translational Research (VICTR)

Genetic determinants of lipids among nonfasting children

This VICTR voucher provided the funds for targeted genotyping NHANES III participants (n=7,159) to replicate a genome-wide association study performed in non-fasting children ascertained by St. Jude Children's Hospital.

Role: PI

**VICTR PN\_1860 (Ritchie)**

2008-2009

Vanderbilt Institute for Clinical and Translational Research (VICTR)

Ancestry informative markers in the Vanderbilt DNA databank

This VICTR voucher provided the funds for genotyping the Illumina DNA Test Panel (360 SNPs) in BioVU, the biorepository linked to electronic medical records, for ancestry informative markers and other quality control metrics. The pilot phase genotyped almost 2,000 samples and the full project included the first 9,000 DNA samples in BioVU.

Role: Co-investigator

**RSnG G78 (Crawford)**

09/13/06-10/01/07

NIH/NHLBI

Defining the role of candidate gene variation in the quantitative phenotypes related to heart disease

This Re-sequencing and Genotyping (RSnG) award provided genotyping support for 384 SNPs on 7,159 samples from NHANES III. The SNPs will be genotyped on a set of 12 candidate genes whose intermediate phenotypes are associated with increased risk for coronary artery disease.

Role: PI

**RSnG G62 (Lingappa)**

09/13/2006-10/01/2007

NIH/NHLBI

Genetic factors in invasive pneumococcal disease

This Re-sequencing and Genotyping (RSnG) award provided genotyping support for 384 SNPs on approximately 1,000 DNA samples of cases with pneumococcal disease and population-based controls.

Role: Co-investigator

**5P30 ES007033-12 (Crawford)**

10/01/2006-03/31/2007

Univ. of Washington NIH/NIEHS

Center for Ecogenetics and Environmental Health

The primary goal of this project is to identify associations between triglycerides measured in the National Health and Nutrition Examination Survey (n=7,159) and SNPs in the candidate gene *APOA4*. This grant supports the genotyping of *APOA4*.

Role: PI

**1 F32 HL079864-01 (Crawford)**

(Awarded 12/22/2004; declined)

NRSA Post-Doctoral Fellowship NIH-NHLBI

Genetic determinants of baseline CRP from NHANES III

Role: PI

**5 F31 HD08443-02 (Crawford)**

07/01/1998 – 05/15/2000

National Research Service Award NIH-NICHHD

Minority Predoctoral Fellowship Program

Role: PI

**BIBLIOGRAPHY**

---

ORCID: 0000-0002-6437-6248

Underlined authors represent Crawford lab trainees.

### PEER REVIEWED ARTICLES

1997

1. Qu S, Perlaky SE, Organ EL, **Crawford D**, and Cavener DR. Mutations at the Ser50 residue of translation factor eIF-2 $\alpha$  dominantly affect developmental rate, body weight, and viability of *Drosophila melanogaster*. *Gene Expression*, 6:349-360 (1997). [PMID: 9495316](#)
2. Savage A, Sun F, **Crawford D**, Ashley A, Yang Q, and Sherman SL. Sequential sibpair and association studies to detect genes in quantitative traits. *Genetic Epidemiology*, 14:885-890 (1997). [PMID: 9433595](#)  
\*\*\*This article was selected for an oral presentation (Savage) at the Genetic Analysis Workshop 10 (GAW10) in Watsonville, CA, October 26-29, 1996\*\*\*

1998

3. Gunter C, Paradee W, **Crawford DC**, Meadows KL, Newman J, Kunst CB, Nelson DL, Schwartz C, Murray A, Macpherson JN, Sherman SL, and Warren ST. Reexamination of factors associated with expansion of CGG repeats using a single nucleotide polymorphism in *FMR1*. *Human Molecular Genetics*, 7(12):1935-1946 (1998). [PMID: 9811938](#)

1999

4. **Crawford DC**, Meadows KL, Newman JL, Taft LF, Pettay DL, Gold LB, Hersey SJ, Hinkle EF, Stanfield ML, Holmgren P, Yeargin-Allsopp M, Boyle C, and Sherman SL. Prevalence and phenotype consequence of FRAXA and FRAXE alleles in a large, ethnically diverse special education needs population. *American Journal of Human Genetics*, 64(2):495-507 (1999). [PMC1377758](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the 6<sup>th</sup> International Fragile X Syndrome Conference, Asheville, NC, July 26-29, 1998\*\*\*

2000

5. **Crawford DC**, Schwartz CE, Meadows KL, Newman JL, Taft LF, Gunter C, Brown WT, Carpenter NJ, Howard-Peebles PN, Monaghan KG, Nolin SL, Reiss AL, Feldman GL, Rohlfs EM, Warren ST, and Sherman SL. Survey of the fragile X syndrome CGG repeat and STR- and SNP- haplotypes in an African-American population. *American Journal of Human Genetics*, 66(2):480-493 (2000). [PMC1288101](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the European Molecular Biology Organization Workshop, London, England, April 1-3, 1998, the 6<sup>th</sup> International Fragile X Syndrome Conference, Asheville, NC, July 26-29, 1998, and the American Society of Human Genetics, Denver, CO, October 27-31, 1998\*\*\*
6. **Crawford DC**, Zhang F, Wilson B, Warren ST, and Sherman SL. Fragile X CGG repeat structures among African-Americans: Identification of a novel factor responsible for repeat instability. *Human Molecular Genetics*, 9(12):1759-1769 (2000). [PMID: 10915764](#)
7. **Crawford DC**, Wilson B, and Sherman SL. Factors involved in the initial mutation of the fragile X CGG repeat as determined by sperm small pool PCR. *Human Molecular Genetics*, 9(19):2909-2918 (2000). [PMID: 11092767](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the American Society

of Human Genetics, Philadelphia, PA, October 3-7, 2000\*\*\*

2002

8. Sullivan AK, **Crawford DC**, Scott EH, Leslie MS, and Sherman SL. Paternally-transmitted FMR1 alleles are less stable than maternally-transmitted alleles in the common and intermediate size range. *American Journal of Human Genetics*, 70(6):1532-1544 (2002). [PMC379140](#)
9. **Crawford DC**, Meadows KL, Newman JL, Taft LF, Scott E, Leslie M, Shubeck L, Holmgren P, Yeargin-Allsopp M, Boyle C, and Sherman SL. Prevalence of the fragile X syndrome in African Americans. *American Journal of Medical Genetics*, 110(3):226-233 (2002). [PMID: 12116230](#)
10. **Crawford DC**, Bailey DB, Skinner D, Sparkman K, Moore CA, and Olney RS. Delayed diagnosis of fragile X syndrome - United States, 1990-1999. *Morbidity and Mortality Weekly Report (MMWR)*, 51(33):740-742 (2002). [PMID: 12201607](#)
11. **Crawford DC**, Caggana M, Harris KB, Lorey F, Nash C, Pass K, Tempelis C, and Olney RS. Characterization of  $\beta$ -globin haplotypes using blood spots from a population-based cohort of newborns with homozygous HbS. *Genetics in Medicine* 4(5):328-335 (2002). [PMID: 12394345](#)
12. Tan C, Sandhu H, **Crawford DC**, the Regional Anthrax Surveillance Team, Redd S, Beach M, Buehler J, Bresnitz E, Pinner R, Bell B, and the CDC New Jersey Anthrax Surveillance Team. Surveillance for anthrax cases associated with anthrax-contaminated letters—New Jersey, Delaware and Pennsylvania, 2001. *Emerging Infectious Diseases* 8(10):1073-1077 (2002). [PMC2730289](#)

2004

1. **Crawford DC**, Carlson CS, Rieder MJ, Carrington DP, Yi Q, Smith JD, Eberle MA, Kruglyak L, and Nickerson DA. Haplotype diversity across 100 candidate genes for inflammation, lipid metabolism, and blood pressure regulation in two populations. *American Journal of Human Genetics* 74(4):610-622 (2004). [PMC1181939](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the American Society of Human Genetics, Los Angeles, CA, November 4-8, 2003 and was selected as winner of the 2004 American Society of Human Genetics C.W. Cotterman Award\*\*\*
13. **Crawford DC**, Bhangale T, Li N, Hellenthal G, Rieder MJ, Nickerson DA, and Stephens M. Evidence for substantial fine-scale variation in recombination rates across the human genome. *Nature Genetics* 36(7):700-706 (2004). [PMID: 15184900](#)
14. Livingston RJ, von Niederhausern A, Jegga A, **Crawford DC**, Carlson CS, Rieder MJ, Aronow BJ, Weiss RB, and Nickerson DA. Pattern of sequence variation across 213 environmental response genes. *Genome Research* 14(10a):1821-1831 (2004). [PMC524406](#)

2006

15. **Crawford DC**, Yi Q, Smith JD, Shephard C, Wong M, Witrak L, Livingston RJ, Rieder MJ, Nickerson DA. Allelic spectrum of the natural variation in *CRP*. *Human Genetics* 119(5):496-504 (2006). [PMC1449912](#)
16. **Crawford DC**, Sanders CL, Qin X, Smith JD, Shephard C, Wong M, Witrak L, Rieder MJ, Nickerson DA. Genetic variation is associated with C-reactive protein levels in the Third National Health and Nutrition Examination Survey. *Circulation* 114(23):2458-2465 (2006). [PMID: 17101857](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the American Society

of Human Genetics, Salt Lake City, UT, October 25-29, 2005 and the Keystone Symposia on Genome Sequence Variation and the Inherited Basis of Common Disease and Complex Traits, Big Sky, MT, January 8-13, 2006. This article was also featured in the 2007 Genome Technology's "Tomorrow's PIs" issue\*\*\*

2008

17. **Crawford DC**, Nord AS, Badzioch MD, Ranchalis J, McKinstry LA Ahearn M, Bertucci C, Shephard C, Wong M, Rieder MJ, Nickerson DA, Heagerty P, Wijsman EM, and Jarvik GP. *VLDLR* common genetic variation and interaction with *APOE* is associated with carotid artery disease. *Journal of Lipid Research* 49(3):588-596 (2008). [PMID: 18056683](#)  
\*\*\* This article was selected for an oral presentation (Crawford) in the session titled "Cardiovascular Genetics" at the American Society of Human Genetics, New Orleans, LA, October 9-13, 2006\*\*\*
18. **Crawford DC**, Zimmer SM, Morin CA, Messonnier NE, Lynfield R, Yi Q, Shephard C, Wong M, Rieder MJ, Livingston RJ, Nickerson DA, Whitney C, and Lingappa J. Integrating host genomics with surveillance for invasive bacterial diseases. *Emerging Infectious Diseases* 14(7):1138-1140 (2008). [PMC2600343](#)
19. **Crawford DC**, Peng Z, Cheng J-F, Boffelli D, Ahearn M, Nguyen D, Shaffer T, Yi Q, Livingston RJ, Rieder MJ, and Nickerson DA. *LPA* and *PLG* sequence variation and kringle IV-2 copy number in two populations. *Human Heredity* 66(4):199-209 (2008). [PMC2861532](#)

2009

20. Bush WS, **Crawford DC**, Alexander C, George AL, Roden DM, Ritchie MD. Genetic variation in the rhythmome: ethnic variation and haplotype structure in candidate genes for arrhythmias. *Pharmacogenomics* 10(6): 1043-1053 (2009). [PMC2746955](#)
21. **Crawford DC**, Zheng N, Rieder MJ, Stanaway I, Speelman EC, Nickerson DA, McElrath MJ, Lingappa J. An excess of rare genetic variation in *ABCE1* among Yorubans and African-Americans with HIV-1. *Genes and Immunity* 10(8)715-721 (2009). [PMC2829431](#)

2010

22. Heike CL, Starr JR, Rieder MJ, Cunningham ML, Edwards KL, Stanaway I, **Crawford DC**. Single nucleotide polymorphism discovery in *TBX1* in individuals with and without 22q11.2 deletion syndrome. *Birth Defects Research Part A: Clinical and Molecular Teratology* 88(1):54-63 (2010). [PMC4535433](#)
23. Hung AM, **Crawford DC**, Griffin MR, Brown-Gentry K, Lipkowitz MS, Siew ED, Cavanaugh K, Lewis JB, Ikizler TA, AASK Study Group. *CRP* polymorphisms and progression of chronic kidney disease in African Americans. *Clinical Journal of the American Society of Nephrology* 5(1):24-33 (2010). [PMC2801650](#)
24. Ritchie MD\*, Denny JC\*, **Crawford DC\***, Havens AK, Weiner JB, Pulley JM, Basford MA, Balser JR, Masys DR, Haines JL, Roden DM. Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. *American Journal of Human Genetics* 86(4):560-572 (2010). [PMC2850440](#)  
\*\*\*This article was featured in the *J Am Med Inform Assoc*'s "2010 Translational bioinformatics year in review" ([PMC3128418](#))\*\*\*
25. Denny JC, Ritchie MD, Basford MA, Pulley JM, Bastarache L, Brown-Gentry K, Wang D, Masys DR, Roden DM, **Crawford DC**. PheWAS: Demonstrating the feasibility of a

- phenome-wide scan to discover gene-disease associations. *Bioinformatics* 26(9):1205-1210 (2010). [PMC2859132](#)
- \*\*\*This work was featured in *Nature Biotechnology*'s "Discovery from data repositories" (doi: 10.1038/nbt0111-46), in the *Journal of American Medical Informatics Association* "2010 Translational bioinformatics year in review" ([PMC3128418](#)), and as a "trailblazing idea" in the Nashville Scene (8/12/2010).\*\*\*
26. Limdi NA, Wadelius M, Cavallari L, Eriksson N, **Crawford DC**, Lee M-T M, Chen C-H, Motsinger-Reif A, Sagreiya H, Liu N, Wu AHB, Gage BF, Jorgensen A, Pirmohamed M, Shin J-G, Suarez-Kurtz G, Kimmel SE, Johnson JA, Klein TE and Wagner MJ on behalf of the IWPC. Warfarin Pharmacogenetics: *VKORC1* genotype as predictive as haplotype across three racial groups. *Blood* 115(18):3827-3834 (2010). [PMC2865873](#)
  27. Dumitrescu L, Ritchie MD, Brown-Gentry K, Pulley JJ, Basford M, Denny J, Oksenberg JR, Roden DM, Haines JL, **Crawford DC**. Assessing the accuracy of ancestry reported in a biorepository linked to electronic medical records for genetic association studies. *Genetics in Medicine* 12(10):648-650 (2010). [PMC2952033](#)
  28. Denny JC, Ritchie MD, **Crawford DC**, Schildcrout J, Havens A, Pulley J, Basford M, Mays DR, Haines J, Roden DM. Identification of genomic predictors of atrioventricular conduction. *Circulation* 122(20):2016-21 (2010). [PMC2991609](#)
  29. **Crawford DC**, Brown-Gentry K, Rieder MJ. *VKORC1* common variation and bone mineral density in the Third National Health and Nutrition Examination Survey. *PLoS One* 5(12):e15088 (2010). [PMC3001474](#)
  30. Pendergrass SA, Dudek SM, **Crawford DC**, Ritchie MD. Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. *BioData Mining* 3:10 (2010). [PMC3012023](#)
- 2011
31. Pendergrass S, Dudek S, Roden DM, **Crawford DC**, Ritchie MD. Visual integration of results from BioVU using Synthesis View. *Pacific Symposium on Biocomputing* 265-275 (2011). [PMC3065108](#)
- \*\*\*This article was selected for an oral presentation (Pendergrass) at the Pacific Symposium on Biocomputing, Big Island, Hawaii, January 3-7, 2011\*\*\*
32. Dumitrescu L, Glenn K, Brown-Gentry K, Shephard C, Wong M, Rieder MJ, Smith JD, Nickerson DA, **Crawford DC**. Variation in *LPA* is associated with Lp(a) levels in three populations from the Third National Health and Nutrition Examination Survey. *PLoS One* 6(1):e16604 (2011). [PMC3030597](#)
  33. Jeff JM, Brown-Gentry K, Buxbaum SG, Sarpong DF, Taylor HA, George Jr AL, Roden DM, **Crawford DC**. *SCN5A* variation is associated with electrocardiographic traits in the Jackson Heart Study. *Circulation: Cardiovascular Genetics* 4(2):139-144 (2011). [PMC3080430](#)
  34. Miller EK, Dumitrescu L, Cupp C, Dorris S, Taylor S, Sparks R, Fawkes D, Frontiero V, Rezendes AM, Marchant C, Edwards KM, **Crawford DC**. Atopy history and the genomics of wheezing and lack of vaccine efficacy after influenza vaccination in children 6-59 months of age. *Vaccine* 29(18):3431-3437 (2011). [PMC3334304](#)
  35. Hung AM, Ikizler A, Griffin MR, Glenn K, Greevy R, Grijalva CG, **Crawford DC**. *CRP* polymorphisms and CKD in the Third National Health and Nutrition Examination Survey. *BMC Medical Genetics* 12(1):65 (2011). [PMC3119179](#)
  36. Turner SD, Berg RL, Linneman JG, Peissig PL, **Crawford DC**, Denny JC, Roden DM,



- McCarty CA, Ritchie MD, Wilke RA. Knowledge-driven multi-locus analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent EMR-linked biobanks. *PLoS One* 6(5):e19586 (2011). [PMC3092760](#)
37. Pendergrass SA, Brown-Gentry K, Dudek S, Ambite JL, Avery CL, Buyske S, Cai C, Heiss G, Hindorff LA, Kooperberg C, Lin Y, Jackson RD, Wallace R, Reiner AL, Moreland L, Manolio TA, Matise TC, Wilkens LR, Fesinmeyer MD, Hsu C-N, **Crawford DC**, Ritchie MD. Phenome-wide association study (PheWAS) for exploration of novel genotype-phenotype relationships within the PAGE network. *Genetic Epidemiology* 35(5):410-422 (2011). [PMC3116446](#)
38. Xu H, Jiang M, Oetjens M, Bowton EA, Ramirez AH, Jeff JM, Basford MA, Pulley JM, Cowan JD, Wang X, Ritchie MD, Masys DR, Roden DM, **Crawford DC**, Denny JC. Facilitating pharmacogenetic studies using electronic health records and natural language processing: a case study of warfarin. *Journal of American Medical Informatics Association* 18(4):387-391 (2011). [PMC3128409](#)
39. Dumitrescu L, Carty CL, Taylor K, Schumacher FR, Hindorff LA, Ambite JL, Anderson G, Best LG, Brown-Gentry K, Bůžková P, Carlson CS, Cochran B, Cole SA, Devereux RB, Duggan D, Eaton CB, Fornage M, Franceschini N, Haessler H, Howard BV, Johnson KC, Laston S, Kolonel LN, Lee ET, MacCluer JW, Manolio TA, Pendergrass SA, Quibrera M, Shohet RV, Wilkens LR, Haiman CA, Le Marchand L, Buyske S, Kooperberg C, North KE, **Crawford DC**. Genetic determinants of lipid traits in diverse populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *PLoS Genetics* 7(6): e1002138 (2011). [PMC3128106](#)  
\*\*\*This work was selected for an oral presentation (North) at the Joint Conference - 50th Cardiovascular Disease Epidemiology and Prevention - and - Nutrition, Physical Activity, and Metabolism, San Francisco, CA, March 2-5, 2010. This article was voted "Top 10 Paper" in the Vanderbilt Epidemiology Center for 2011\*\*\*
40. Clark WB, Brown-Gentry KD, **Crawford DC**, Snavely J, Fan K-H, Savani BN, Kassim A, Schuening FG, Engelhardt BG, Jagasia MH. Genetic variation in recipient B-cell activating factor (BFF) modulates phenotype of graft versus host disease. *Blood* 118(4):1140-1144 (2011). [PMID: 21628416](#)
41. Dumitrescu L, Brown-Gentry K, Goodloe R, Glenn K, Yang, W, Kornegay N, Pui C-H, Relling M, **Crawford DC**. Evidence for age as a modifier of genetic associations for lipids levels. *Annals of Human Genetics* 75(5):589-597 (2011). [PMC3155612](#)  
\*\*\*This article was featured on the cover of the journal's issue\*\*\*
42. Lingappa JR\*, Dumitrescu L\*, Zimmer SM, Lynfield R, McNicholl J, Messonnier NE, Whitney CG, **Crawford DC**. Identifying host genetic risk factors in the context of public health surveillance for invasive Pneumococcal disease. *PLoS One* 6(8):e23413 (2011). [PMC3156135](#)
43. Matise T, Ambite JL, Buyske S, Cole SA, **Crawford DC**, Haiman C, Heiss H, Kooperberg C, Le Marchand L, Manolio TA, North K, Peters R, Ritchie MD, Hindorff L, Haines JL, for PAGE. The next PAGE in understanding complex traits: study design for analysis of Population Architecture using Genomics and Epidemiology. *American Journal of Epidemiology* 174(7):849-859 (2011). [PMC3176830](#)  
\*\*\*This work was selected for an oral presentation (Crawford) for the session titled "Opportunities and obstacles with genome-wide association studies (GWAS)" at the American Public Health Association, Denver, CO, November 6-10, 2010\*\*\*

44. Denny JC\*, **Crawford DC\***, Ritchie MD, Basford MA, Bradford Y, Zuvich R, Bastarache L, Wilke RA, Peissig P, Pathak J, Rasmussen L, Carrell D, Wang X, Bielinski SJ, Pacheco J, Kho A, Weston N, Newton K, Li R, Manolio T, Chute C, Chisolm R, Larson E, McCarty C, Masys DR, Roden DM, de Andrade M. Variants near *FOXE1* are associated with hypothyroidism and other thyroid conditions: using electronic medical records for genome- and phenome-wide studies. *American Journal of Human Genetics* 89(4):529-542 (2011). [PMC3188836](#)  
\*\*\* This article was selected for an oral presentation (Crawford) for the session titled “Statistical Genetics II: Expanding Genome-Wide Association Studies” at the International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011 and was featured by Medscape Medical News (10/17/2011)\*\*\*
45. Zuvich RL, Armstrong LL, Bielinski S, Bradford Y, Carlson CS, Clayton E, **Crawford DC**, Crenshaw AT, de Andrade M, Doheny KF, Haines JL, Hayes G, Jarvik G, Jiang L, Kullo I, Li R, Ling H, Matsumoto ME, McCarty CA, McDavid AN, Mirel DB, Olson L, Paschall JE, Pugh EW, Rasmussen LV, Rasmussen-Torvik L, Turner SD, Wilke RA, Ritchie MD. Pitfalls of merging GWAS data: lessons learned in the eMERGE Network and quality control procedures to maintain high data quality. *Genetic Epidemiology* 35(8):887-898 (2011). [PMC3592376](#)
- 2012
46. Spencer KL, Glenn K, Brown-Gentry K, Haines JL, **Crawford DC**. Population differences in genetic risk for age-related macular degeneration and implications for genetic testing. *Archives in Ophthalmology* 130(1):116-117 (2012). [PMC3326353](#)
47. Delaney JT, Ramirez AH, Bowton E, Pulley JM, Basford MA, Schildcrout JS, Shi Y, Zink R, Oetjens M, Xu H, Cleator JH, Jahangir E, Ritchie MD, Masys DR, Roden DM, **Crawford DC\***, Denny JC\*. Predicting clopidogrel response using DNA samples linked to an electronic health record. *Clinical Pharmacology & Therapeutics* 91(2):257-263 (2012). [PMC3621954](#)
48. Käåb S\*, **Crawford DC\***, Sinner MF\*, Behr E\*, Kannankeril PJ, Wilde AAM, Bezzina CR, Schulze-Bahr E, Guicheney P, Bishopric N, Myerburg R, Schott J-J, Pfeufer A, Beckmann B-M, Martens E, Steinbeck G, Perz S, Lichtner P, Meitinger T, Peters A, H.-Wichmann H-E, Ingram C, Bradford Y, Carter S, Norris K, Ritchie MD, George Jr AL, Roden DM. A large candidate gene survey identifies the *KCNE1* D85N polymorphism as a modulator of drug-induced torsades de pointes. *Circulation: Cardiovascular Genetics* 5(1):91-99 (2012). [PMC3288202](#)  
\*\*\*This article was selected for an oral presentation at the American Society of Human Genetics, Honolulu, HI, October 20-24, 2009 (Roden)\*\*\*
49. Murabito JM\*, White C\*, Kavousi M\*, Sun YV\*, Feitosa MF\*, Nambi V\*, Lamina C\*, Schillert A\*, Coassin S, Bis JC, Broer L, **Crawford DC**, Franceschini N, Frikke-Schmidt R, Haun M, Holewijn S, Huffman JE, Hwang SJ, Kiechl S, Kollerits B, Montasser ME, Nolte IM, Ruddock ME, Senft A, Teumer A, van der Harst P, Vitart V, Waite LL, Wood AR, Wassel CL, Absher DM, Allison MA, Amin N, Arnold A, Asselbergs FW, Aulchenko Y, Bandinelli S, Barbalic M, Boban M, Brown-Gentry K, Couper D, Criqui MH, Dehghan A, den Heijer M, Dieplinger B, Ding J, Dörr M, Espinola-Klein C, Felix SB, Ferrucci L, Folsom A, Fraedrich G, Gibson Q, Goodloe R, Gunjaca G, Haltmayer M, Heiss G, Hofman A, Kieback A, Kiemeny LA, Kolcic I, Kullo IJ, Kritschewsky SB, Lackner KJ, Li X, Lieb W, Lohman K, Meisinger C, Melzer D, Mohler ER, Mudnic I,

- Mueller T, Navis G, Oberhollenzer F, Olin JW, O'Connell J, O'Donnell CJ, Palmas W, Penninx BW, Petersmann A, Polasek O, Psaty BM, Rantner B, Rice K, Rivadeneira F, Rotter JI, Seldenrijk A, Stadler M, Summerer M, Tanaka T, Tybjaerg-Hansen A, Uitterlinden A, van Gilst WH, Vermeulen S, Wild SH, Wild PS, Willeit J, Zeller T, Zemunik T, Zgaga L, Assimes TL, Blankenberg S, Boerwinkle E, Campbell H, Cooke JP, de Graaf J, Herrington D, Kardia SLR, Mitchell BD, Murray A, Munzel T, Newman AB, Oostra BA, Rudan I, Shuldiner AR, Snieder H, van Duijn CM, Völker U, Wright AF, Wichmann HE, Wilson JF, Witteman J, Liu Y\*, Hayward C\* Borecki IB\*, Ziegler A\*, North KE\*, Cupples LA\*, Kronenberg F\*. Association between chromosome 9p21 variants and the Ankle-Brachial Index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics* 5(1):100-112 (2012). [PMC3303225](#)
50. Crosslin DR, McDavid A, Weston N, Nelson SC, Zheng X, Hart E, de Andrade M, Kullo IJ, McCarty CA, Doheny KF, Pugh E, Kho A, Hayes MG, Pretel S, Saip A, Ritchie MD, **Crawford DC**, Crane PK, Newton K, Li R, Mirel D, Crenshaw A, Larson EB, Carlson C, Jarvik GP, the electronic Medical Records and Genomics (eMERGE) Network. Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. *Human Genetics* 131(4):639-652 (2012). [PMC3640990](#)
51. Jeff JM, Brown-Gentry K, **Crawford DC**. Replication and characterization of genetic variants in the fibrinogen gene cluster with fibrinogen levels and haematological traits in the Third National Health and Nutrition Examination Survey. *Thrombosis and Haemostasis* 107(3):458-467 (2012). [PMC3989929](#)
52. Ramirez AH, Shi Y, Schildcrout JS, Delaney JT, Xu H, Oetjens MT, Zuvich R, Basford MA, Bowton E, Zink R, Cowan J, Pulley JM, Ritchie MD, Masys DR, Roden DM, **Crawford DC**, Denny JC. Predicting warfarin dosage in European and African Americans using DNA samples linked to an electronic health record *Pharmacogenomics* 13(4):407-418 (2012). [PMC3361510](#)  
 \*\*\*This article was selected for an oral presentation at the American Society of Human Genetics, Washington, DC, November 2-6, 2010 (Oetjens); the American Heart Association Scientific Sessions, Chicago, IL, November 13-17, 2010 (Ramirez); and the International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011 (Ramirez)\*\*\*
53. Wassel CL\*, Lamina C\*, Nambi V\*, Cossain S\*, Mukamal KJ\*, Ganesh S, Jacobs DJ, Franceschini N, Gibson Q, Yanek LR, van der Harst P, Ferguson J, **Crawford DC**, Waite LI, Allison MA, Criqui MH, McDermott MM, Mehra R, Cupples LA, Hwang SJ, Redline S, Kaplan RC, Heiss G, Rotter JI, Taylor HA, Boerwinkle E, Eraso LH, Haun M, Li M, Meisinger C, O'Connell J, Shuldiner AR, Tybjaerg-Hansen A, Frikke-Schmidt R, Kollerits B, Rantner B, Dieplinger B, Stadler M, Mueller T, Haltmayer M, Klein-Weigel P, Summerer M, Wichmann HE, Asselbers FW, Navis G, Mateo Leach I, Brown-Gentry K, Goodloe R, Assimes TL, Cooke JP, Absher DM, Olin JW, Mitchell BD, Reilly M, Mohler E\*, North KE\*, Reiner AP\*, Kronenberg F\*, Murabito JM\*. Genetic determinants of the ankle-brachial index: a meta-analysis of a cardiovascular candidate gene 50K SNP panel in the candidate gene association resource (CARE) consortium. *Atherosclerosis* 222(1):138-147 (2012). [PMC3596171](#)
54. Fullerton SM, Wolf WA, Brothers KB, Wright Clayton E, **Crawford DC**, Denny JC, Greenland P, Koenig BA, Leppig KA, Lindor NM, McCarty CA, McGuire AL, McPeck-

- Hinz ER, Mirel DB, Ramos EM, Ritchie MD, Smith ME, Waudby CJ, Burke W, Jarvik GP. Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records & Genomics (eMERGE) Network. *Genetics in Medicine* 14(4):424-431 (2012). [PMC3723451](#)
55. Delaney JT, **Jeff JM**, Brown NJ, Pretorius M, Okafor HE, Darbar D, Roden DM, **Crawford DC**. Characterization of genome-wide association-identified variants for atrial fibrillation in African Americans. *PLoS One* 7(2):e32338 (2012). [PMC3285683](#)
56. Buyske S, Wu Y, Carty CL, Cheng I, Assimes TL, Dumitrescu L, Hindorff L, Mitchell S, Ambite JL, Boerwinkle E, Bůžková 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 T, Robinson JG, Rodriguez C, Schumacher FR, Voight BF, Young A, Manolio TA, Mohlke KL, Haiman CA, Peters U, **Crawford DC**, North KE. Evaluation of the MetaboChip genotyping array in African Americans and implications for fine mapping of GWAS-identified loci: the PAGE study. *PLoS One* 7(4):e35651 (2012). [PMC3335090](#)  
\*\*\*This article was selected for an oral presentation (Buyske) at the International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011\*\*\*
57. Mitchell S, Welch-Burke T, Dumitrescu L, Lomenick JP, Murdock D, **Crawford DC**, The Urea Cycle Disorders Consortium, Summar M. Peptide tyrosine levels are increased in patients with urea cycle disorders. *Molecular Genetics and Metabolism* 106(1):39-42 (2012). [PMC3336020](#)
58. Haiman CA, Fesinmeyer M, Spencer KL, Bůžková P, Voruganti VS, Wan P, Haessler J, Franceschini N, Monroe K, Howard BV, Jackson RD, Florez JC, Kolonel LN, Buyske S, Goodloe RJ, Liu S, Manson JE, Meigs JB, Waters K, Mukamal KJ, Pendergrass SA, Shrader P, Wilkens LR, Hindorff LA, Ambite JL, North KE, Peters U, **Crawford DC**, Le Marchand L, Pankow JS. Consistent direction of effect for established T2D risk variants across populations: The Population Architecture using Genomics and Epidemiology (PAGE) Consortium. *Diabetes* 61(6): 1642-1647 (2012). [PMC3357304](#)
59. Pendergrass SA, Dudek SM, **Crawford DC**, Ritchie MD. Visually integrating and exploring high throughput phenome-wide association (PheWAS) results using PheWAS-View. *BioData Mining* 5(1):5 (2012). [PMC3476448](#)  
\*\*\*This article was selected for an oral presentation (Pendergrass) at the American Society of Human Genetics, San Francisco, California, November 6-10, 2012\*\*\*
60. Liu Y, Boerwinkle E, Peters U, Kooperberg C, Carlson C, Le Marchand L, Haiman C, **Crawford DC**, Buyske S, Matise T, Manolio T, Hindorff L, Haessler J, Aragaki A, Wang W, North KE, Li Y. Genotype imputation of MetaboChip SNPs using study specific reference panel of ~4,000 haplotypes in African Americans. *Genetic Epidemiology* 36(2):107-117 (2012). [PMC3410659](#)
61. Jagasia M, Clark WB, Brown-Gentry KD, **Crawford DC**, Fan KH, Chen H, Kassim A, Greer JP, Engelhardt BG, Savani BN. Genetic variation in donor *CTLA-4* regulatory region is a strong predictor of outcome after allogeneic hematopoietic cell transplantation for hematological malignancies. *Biology of Blood and Marrow Transplantation* 18(7):1069-1075 (2012). [PMID: 22178694](#).
62. Pulley JM, Denny JC, Peterson JF, Bernard GR, Vnencak-Jones CL, Ramirez AH, Delaney JT, Bowton E, Brothers K, Johnson K, **Crawford DC**, Schildcrout J, Masys DR, Dilks HH, Wright-Clayton E, Shultz E, Laposata M, McPherson J, Jirjis JN, Roden DM.

- Operational implementation of prospective genotyping for personalized medicine: the design of the Vanderbilt PREDICT project. *Clinical Pharmacology & Therapeutics* 92(1):87-95 (2012). [PMC3581305](#)
63. Schildcrout JS, Denny JC, Bowton E, Gregg W, Pulley JM, Basford MA, Cowan J, Ramirez AH, **Crawford DC**, Ritchie MD, Peterson JF, Masys DR, Wilke R, Roden DM. Optimizing drug outcomes with pharmacogenomics: a case for preemptive genotyping *Clinical Pharmacology & Therapeutics* 92(2):235-242 (2012). [PMC3785311](#)  
\*\*\*This article was selected for an oral presentation (Schildcrout) at the International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011\*\*\*
64. Dumitrescu L, Goodloe R, Brown-Gentry K, Mayo P, Allen M, Jin H, Gillani NB, Schnetz-Boutaud N, Dilks HH, **Crawford DC**. Serum vitamins A and E as modifiers of lipid trait genetics in the National Health and Nutrition Examination Surveys as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. *Human Genetics* 131(11):1699-1708 (2012). [PMC3472117](#)  
\*\*\*This article was selected for an oral presentation (Dumitrescu) in the session titled “Statistical Genetics II: Expanding Genome-Wide Association Studies” at the 2011 International Congress of Human Genetics meeting in Montreal, Canada, October 11-15, 2011\*\*\*
65. Rasmussen-Torvik LJ, Pacheco JA, Hayes MG, Kho AN, Muthalagu A, Armstrong LL, Sheftner DA, Thompson WK, Wilkins JT, Bielinski SJ, **Crawford DC**, Crosslin D, Denny JC, Jarvik GP, Kullo IJ, Li R, Manolio TA, McCarty CA, Ritchie MD, Roden DM, Wilke RA, Zuvich RL, Carlson CS, Chisholm RL. High density GWAS for LDL cholesterol in African Americans using electronic medical records reveals a strong predictive variant in *APOE*. *Clinical and Translational Science* 5(5):394-399 (2012). [PMC3521536](#)
- 2013
66. Bush WS\*, Boston J\*, Pendergrass SA, Dumitrescu L, Goodloe R, Brown-Gentry K, Wilson S, McClellan Jr B, Torstenson E, Basford MA, Spencer KL, Ritchie MD, **Crawford DC**. Enabling high-throughput genotype-phenotype associations in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. *Pacific Symposium on Biocomputing* 18:373-384 (2013). [PMC3579641](#)
67. **Crawford DC**, Goodloe R, Brown-Gentry K, Wilson S, Roberson J, Gillani NB, Ritchie MD, Dilks HH, Bush WS. Characterization of the MetaboChip in diverse populations from the International HapMap Project in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project. *Pacific Symposium on Biocomputing* 18: 188-199 (2013). [PMC3584704](#)  
\*\*\*This article was selected for an oral presentation (Bush) at the Pacific Symposium on Biocomputing, Big Island, HI, January 3-7, 2013\*\*\*
68. Peters U, North KE, Sethupathy P, Buyske S, Haessler J, Fesinmeyer MD, Jackson RD, Kuller LH, Rajkovic A, Lim U, Cheng I, Schumacher F, Wilkens L, Li R, Monda K, Ehret G, Ngyuen KD, Cooper R, Lewis CE, Leppert M, Irvin MR, Gu CC, Houston D, Bůžková P, Ritchie M, Matisse TC, Le Marchand L, Hindorff LA, **Crawford DC**, Haiman CA, Kooperberg C. A systematic mapping approach of 16q12.2/*FTO* and BMI in over 20,000 African Americans narrows in on the underlying functional variation. *PLoS Genetics* 9(1):e1003171 (2013). [PMC3547789](#)

69. Fesinmeyer MD, North KE, Ritchie MD, Lim U, Franceschini N, Wilkens L, Gross M, Bůžková P, Glenn K, Quibrera M, Fernández-Rhodes L, Li Q, Fowke JH, Li R, Carlson CS, Prentice RL, Kuller LH, Manson JE, Matisse TC, Cole SA, Chen CTL, Howard BV, Kolonel LN, Henderson BE, Monroe KR, **Crawford DC**, Hindorff LA, Buyske S, Haiman CA, LeMarchand L, Peters U. Genetic risk factors for body mass index and obesity in an ethnically diverse population: results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *Obesity* 21(4):835-846 (2013). [PMC3482415](#)  
 \*\*\*This article was selected for an oral presentation (Fesinmeyer) at the Obesity Society Scientific Meeting, San Diego, CA, October 8-12, 2010 and the Obesity Society Annual Scientific Meeting, Orlando, Florida, October 1-5, 2011\*\*\*
70. Pendergrass SA, Brown-Gentry K, Dudek S, Frase A, Torstenson ES, Goodloe R, Ambite JL, Avery CL, Buyske S, Bůžková P, Deelman E, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Jackson RD, Kooperberg C, LeMarchand L, Park L, Lin Y, Matisse TC, Monroe KR, Moreland L, Reiner A, Wallace R, Wilkens LR, **Crawford DC**, Ritchie MD. Phenome-wide association study (PheWAS) for detection of pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. *PLoS Genetics* 9(1):e1003087 (2013). [PMC3561060](#)  
 \*\*\*This article was selected for oral presentations (Pendergrass) at the International Genetic Epidemiology Society, Boston, MA, October 10-12, 2010, the American Society of Human Genetics, Washington, DC, November 2-6, 2010, and the Translational Bioinformatics Conference, Seoul, Korea, October 2-4, 2013\*\*\*
71. Spencer KL\*, Malinowski J\*, Carty CL, Franceschini N, Fernández-Rhodes L, Young A, Cheng I, Ritchie MD, Haiman CA, Wilkens L, Wu C, Matisse TC, Carlson CS, Brennan K, Park P, Rajkovic A, Hindorff LA, Buyske S, **Crawford DC**. Genetic variation and the reproductive timing: African American women from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *PLoS One* 8(2):e55258 (2013). [PMC3570525](#)
72. Fesinmeyer M, North KE, Lim U, Bůžková P, **Crawford DC**, Haessler J, Gross MD, Fowke JH, Goodloe R, Love S, Graff M, Carlson CS, Kuller LH, Matisse TC, Hong CP, Henderson BE, Allen M, Rohde RR, Mayo P, Schnetz-Boutaud N, Monroe KR, Ritchie MD, Prentice RL, Kolonel LN, Manson JE, Pankow J, Hindorff LA, Franceschini N, Wilkens LR, Haiman CA, LeMarchand L, Peters U. Effects of smoking on the genetic risk of obesity: the Population Architecture using Genomics and Epidemiology (PAGE) Study. *BMC Med Genet* 14:6 (2013). [PMC3564691](#)
73. Wu Y, Waite LL, Jackson AU, Sheu WH-H, Buyske S, Absher D, Arnett DK, Boerwinkle E, Bonnycastle LL, Carty CL, Cheng I, Croteau-Chonka DC, Cochran B, Dumitrescu L, Eaton CB, Franceschini N, Guo X, Henderson BE, LeMarchand L, Hindorff LA, Kim E, Kinnunen L, Komulainen P, Lee W-J, Lin Y, Lindström J, Lingaas-Holmen O, Mitchell SL, Narisu N, Robinson JG, Schumacher F, Stančáková A, Sundvall J, Sung Y-J, Swift AJ, Wang W-C, Wilkens L, Wilsgaard T, Young AM, Adair LS, Ballantyne C, Bůžková P, Chakravarti A, Collins FS, Duggan D, Feranil AB, Ho L-T, Hung Y-J, Hunt SC, Hveem K, Juang J-MJ, Kesäniemi AY, Kuusisto J, Laakso M, Lakka TA, Lee I-T, Leppert MF, Matisse TC, Moilanen L, Njølstad I, Peters U, Quertermous T, Rauramaa R, Rotter JI, Saramies J, Tuomilehto J, Uusitupa M, Wang T-D, Boehnke M\*, Haiman C\*, Chen Y-D I\*, Kooperberg C\*, Assimes TL\*, **Crawford**

- DC\***, Hsiung CA\*, North KE\*, Mohlke KL\*. Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PLoS Genetics* 9(3): e1003379 (2013). [PMC3605054](#)  
\*\*\*This article was selected for an oral presentation (Wu) at the American Heart Association Epidemiology and Prevention/Nutrition, Physical Activity and Metabolism 2012 Scientific Sessions, San Diego, CA, March 13-16, 2012\*\*\*
74. Ritchie MD\*, Denny JC\*, Zuvich RL\*, **Crawford DC**, Schildcrout JS, Bastarache L, Ramirez AH, Mosley JD, Pulley JM, Basford MA, Bradford Y, Rasmussen LV, Pathak J, Chute CG, Kullo IJ, McCarty C, Chisholm R, Kho AN, Carlson CS, Larson EB, Jarvik GP, Sotoodehnia N on behalf of the CHARGE QRS Group, Manolio TA, Li R, Masys DR, Haines JL, Roden DM. Genome- and phenome-wide analysis of cardiac conduction identified markers of arrhythmia risk. *Circulation* 127(13):1377-1385 (2013). [PMC3713791](#)
75. Graff M, Gordon-Larsen P, Lim U, Fowke JH, Love S, Fesinmeyer M, Wilkens LR, Vertilus S, Ritchie MD, Prentice RL, Pankow J, Monroe K, Manson JE, Le Marchand L, Kuller LH, Kolonel LN, Hong CP, Henderson BE, Haessler J, Gross MD, Goodloe R, Franceschini N, Carlson CS, Buyske S, Bůžková P, Hindorff LA, Matisse TC, **Crawford DC**, Haiman CA, Peters U, North KE. The influence of obesity related SNPs on BMI across the life course: the PAGE Study. *Diabetes* 62(5):1763-1767 (2013). [PMC3636619](#)  
\*\*\*This work was selected for an oral presentation (Graff) at the American Heart Association Nutrition, Physical Activity and Metabolism/Cardiovascular Disease Epidemiology and Prevention 2013 Scientific Sessions, New Orleans, March 19-22, 2013\*\*\*
76. Crosslin DR, McDavid A, Weston N, Nelson S, Zheng X, Hart E, de Andrade M, Kullo IJ, McCarty CA, Doheny KF, Pugh E, Kho A, Hayes MG, Pretel S, Saip A, Ritchie MD, **Crawford DC**, Crane PK, Newton K, Li R, Mirel D, Crenshaw A, Larson EB, Carlson CS, Jarvik GP, The electronic Medical Records and Genomics (eMERGE) Network. Genetic variation associated with circulating monocyte count in the eMERGE Network. *Human Molecular Genetics* 22(10):2119-27 (2013). [PMC3633369](#)
77. Carty CL, Spencer KL, Setiawan VW, Fernandez-Rhodes L, Malinowski J, Buyske S, Young A, Jorgensen NW, Cheng I, Carlson CS, Brown-Gentry K, Goodloe R, Park A, Henderson B, Le Marchand L, Kooperberg C, Wactawski-Wende J, Fornage M, Matisse TC, Hindorff LA, Arnold AM, Haiman CA, Franceschini N, Peters U, **Crawford DC**. Replication of GWAS loci for ages at menarche and menopause in women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study. *Human Reproduction* 28(6):1695-1706 (2013). [PMC3657124](#)
78. Oetjens MT, Denny JC, Ritchie MD, Gillani NB, Richardson DM, Restrepo NA, Pulley JM, Dilks HH, Basford MA, Bowton E, Masys DR, Wilke RA, Roden DM, **Crawford DC**. Assessment of a pharmacogenomic marker panel in a polypharmacy population identified from electronic medical records. *Pharmacogenomics* 14(7):735-744 (2013). [PMC3725600](#)
79. Taylor KC, Carty CL, Dumitrescu L, Bůžková P, Cole SA, Hindorff LA, Schumacher FR, Wilkens LR, Shohet RV, Quibrera M, Johnson KC, Henderson BE, Haessler J, Franceschini N, Eaton CB, Duggan DJ, Cochran B, Cheng I, Carlson CS, Brown-Gentry K, Anderson G, Ambite JL, Haiman CA, Le Marchand L, Kooperberg C, **Crawford DC**, Buyske S, North KE, Fornage M, for the PAGE Study. Investigation of gene-by-sex

- interactions for lipid traits in diverse populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *BMC Genetics* 14(1):33 (2013). [PMC3669109](#)
80. Zhang L, Bůžková P, Wassel CL, Roman MJ, North KE, **Crawford DC**, Boston J, Brown-Gentry KD, Cole SA, Deelman E, Goodloe R, Wilson S, Heiss G, Jenny NS, Jorgensen NW, Matisse TC, McClellan Jr. BE, Nato Jr AQ, Ritchie, MD, Franceschini N, Kao WHL. Lack of Associations of Coronary Heart Disease Risk Genetic Variants and Subclinical Atherosclerosis in Four U.S. Populations: The Population Architecture using Genomics and Epidemiology (PAGE) Study. *Atherosclerosis* 228(2):390-399 (2013). [PMC3717342](#)  
\*\*\*This article was featured in a commentary by Vogel U in *Atherosclerosis* 228(2):324 (2013)(doi: [10.1016/j.atherosclerosis.2012.11.014](#))\*\*
81. Zhang L, Spencer KL, Voruganti VS, Jorgensen NW, Fornage M, Best LG, Brown-Gentry KD, Cole SA, **Crawford DC**, Deelman E, Franceschini N, Gaffo AL, Glenn KR, Heiss G, Jenny NS, Kottgen A, Li Q, Liu K, Matisse TC, North KE, Umans JG, Kao WHL. Association of functional polymorphism rs2231142 (Q141K) in *ABCG2* gene with serum uric acid and gout in four US populations: The Population Architecture using Genomics and Epidemiology (PAGE) Study. *American Journal of Epidemiology* 177(9):923-932 (2013). [PMC4023295](#)
82. Ding K, de Andrade M, Manolio T, **Crawford DC**, Rasmussen-Torvik LJ, Ritchie MD, Denny JC, Masys DR, Jouni H, Pacheco JA, Kho AN, Roden DM, Chisholm R, Kullo IJ. Genetic variants that confer resistance to malaria are associated with red blood cell traits in African Americans: an electronic medical record-based genome wide association study. *G3: Genes, Genomes, Genetics* 3(7):1061-1068 (2013). [PMC3704235](#)
83. Perera MA, Cavallari LH, Limdi NA, Gamazon ER, Konkashbaev A, Daneshjou R, Pluzhnikov A, **Crawford DC**, Wang J, Liu N, Tatonetti NJ, Bourgeois S, Takahashi H, Bradford Y, Burkley BM, Desnick RJ, Halperin JL, Khalifa SI, Langae TY, Lubitz SA, Nutescu EA, Oetjens M, Shahin MH, Shitalben RP, Tector M, Rieder MJ, Scott SA, Wu AHB, Burmester JK, Deloukis P, Wagner MJ, Mushiroda T, Kubo M, Roden DM, Cox NJ, Altman RB, Klein TE, Nakamura Y, Johnson JA. Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. *Lancet* 382(9894):790-796 (2013). [PMC3759580](#)  
\*\*\*This article was selected for an oral presentation (Perera) at the American Heart Association 83<sup>rd</sup> Scientific Sessions, Orlando, Florida, November 12-16, 2011\*\*\*
84. Park SL, Cheng I, Pendergrass SA, Kucharska-Newton AM, Lim U, Ambite JL, Caberto CP, Monroe KR, Schumacher F, Hindorff LA, Oetjens M, Wilson S, Goodloe RJ, Love S-A, Henderson BE, Kolonel LN, Haiman CA, **Crawford DC**, North KE, Heiss G, Ritchie MD, Wilkens LR, Le Marchand L. *FTO* obesity risk variant rs8050136 is associated with percentage of energy intake from fat in older adults: The PAGE Study. *American Journal of Epidemiology* 178(5):780-790 (2013). [PMC3755639](#)  
\*\*\*This article was selected as one of the 10 best articles for 2013 published in the *American Journal of Epidemiology*\*\*\*
85. Fesinmeyer MD, Meigs JB, North KE, Schumacher FR, Bůžková P, Franceschini N, Haessler J, Goodloe R, Spencer KL, Voruganti VS, Howard BV, Jackson R, Kolonel LN, Liu S, Manson JE, Monroe KR, Mukamal K, Dilks HH, Pendergrass SA, Nato A, Wan P, Wilkens LR, Le Marchand L, Ambite JL, Buyske S, Florez JC, **Crawford DC**, Hindorff



- LA, Haiman CA, Peters U, Pankow JS. Genetic variants associated with fasting glucose and insulin concentrations in an ethnically diverse population: results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. *BMC Medical Genetics* 14(1):98 (2013). [PMC3870971](#)
86. Carlson CS, Matise TC, North KE, Haiman CA, Fesinmeyer MD, Buyske S, Schumacher F, Peters U, Franceschini N, Ritchie MD, Duggan DJ, Spencer KL, Dumitrescu L, Eaton CB, Thomas F, Young A, Carty C, Manolio TA, Heiss G, Le Marchand L, **Crawford DC**, Hindorff LA, Kooperberg C, for the PAGE Study. Generalization and dilution of association results from European GWAS in populations of non-European ancestry: the PAGE Study. *PLoS Biology* 11(9):e1001661 (2013). [PMC3775722](#)
87. Gong J, Schumacher F, Lim U, Hindorff LA, Haessler J, Buyske S, Carlson CS, Rosee S, Bůžková P, Fornage M, Gross M, Pankratz N, Pankow JS, Schreiner PJ, Cooper R, Ehret G, Gu CC, Houston D, Irvin MR, Jackson R, Kuller L, Henderson B, Cheng I, Wilkens L, Leppert M, Lewis CE, Li R, Nguyen K-DH, Goodloe R, Farber-Eger E, Boston J, Dilks HH, Ritchie MD, Fowke J, Pooler L, Graff M, Fernandez-Rhodes L, Cochrane B, Boerwinkle E, Kooperberg C, Matise TC, Le Marchand L, **Crawford DC**, Haiman CA, North KE, Peters U. Fine mapping and identification of BMI loci in African Americans. *American Journal of Human Genetics* 93(4):661-671 (2013). [PMC3791273](#)  
\*\*\*This article was featured in a Research Highlight in a 2013 issue of *Genome Medicine* (5:102) by Dr. Scott M. Williams (doi: <https://doi.org/10.1186/gm506>)\*\*\*
88. Duan Q, Liu, EY, Auer P, Zhang G, Lange E, Jun G, Bizon C, Jiao S, Buyske S, Franceschini N, Carlson CS, Hsu L, Reiner AP, Peters U, Haessler J, Curtis K, Wassel CL, Robinson JG, Martin LW, Haiman CA, Le Marchand L, Matise TC, Hindorff LA, **Crawford DC**, Assimes TL, Kang HM, Heiss G, Jackson RD, Kooperberg C, Wilson JG, Abecasis GR, North KE, Nickerson DA, Lange LA, Li Y. Imputation of Coding Variants in African Americans: Better Performance using Data from the Exome Sequencing Project. *Bioinformatics* 29(21):2744-2749 (2013). [PMC3799474](#)
89. Dumitrescu L, Carty CL, Franceschini N, Hindorff LA, Cole SA, Bůžková P, Schumacher FR, Eaton CB, Goodloe RJ, Duggan DJ, Haessler J, Cochran B, Henderson BE, Cheng I, Johnson KC, Carlson CS, Love S-A, Brown-Gentry K, Nato AQ, Quibrera M, Shohet R, Ambite JL, Wilkens LR, Le Marchand L, Haiman CA, Buyske S, Kooperberg C, North KE, Fornage M, **Crawford DC**. No evidence of interaction between known lipid-associated genetic variants and smoking in the multi-ethnic PAGE population. *Human Genetics* 132(12):1427-1431 (2013). [PMC3895337](#)
90. Behr ER, Ritchie MD, Tanaka T, Kaab S, **Crawford DC**, Nicoletti P, Floratos A, Sinner MF, Kannankeril PJ, Wilde AAM, Bezzina CR, Schulze-Bahr E, Zumhagen S, Guicheney P, Bishopric NH, Marshall V, Shakir S, Dalageorgou C, Bevan S, Jamshidi Y, Bastiaenen R, Myerburg RJ, Schott J-J, Camm AJ, Steinbeck G, Norris K, Altman RB, Tatonetti N, Jeffery S, Kubo M, Nakamura Y, Shen Y, George Jr AL, Roden DM. Genomewide analysis of drug-induced Torsades de Pointes: lack of common variants with large effect sizes. *PLoS One* 8(11):e78511 (2013). [PMC3819377](#)  
\*\*\*This work was selected for an oral presentation (Crawford) at the Pharmacogenetics Research Network (PGRN) Statistical Analysis Workshop V, Rochester, MN, April 15, 2009\*\*\*
91. Dumitrescu L, Carty CL, Franceschini N, Hindorff LA, Cole SA, Bůžková P, Schumacher FR, Eaton CB, Goodloe RJ, Duggan DJ, Haessler J, Cochran B, Henderson

- BE, Cheng I, Johnson KC, Carlson CS, Love S-A, Brown-Gentry K, Quibrera M, Anderson G, Shohet R, Ambite JL, Wilkens LR, Le Marchand L, Haiman CA, Buyske B, Kooperberg C, North KE, Fornage M, **Crawford DC**. Post genome-wide association study challenges for lipid traits: describing age as a genetic modifier in the Population Architecture using Genomics and Epidemiology (PAGE) study. *Annals of Human Genetics* 77(5):416-425 (2013). [PMC3796061](#)
92. **Jeff JM**, Ritchie MD, Denny JC, Kho AN, Ramirez AH, Crosslin D, Armstrong L, Basford MA, Wolf WA, Pacheco JA, Chisholm RL, Roden DM, Hayes MG, **Crawford DC**. Generalization of variants identified by genome-wide association studies for ECG traits in African Americans. *Annals of Human Genetics* 77:321-332 (2013). [PMC3743946](#)
93. Denny JC, Bastarache L, Ritchie MD, Carroll RJ, Zink R, Mosley JD, Field JR, Pulley JM, Ramirez AH, Bowton E, Basford MA, Carrell D, Peissig PL, Kho AN, Pacheco JA, Rasmussen LV, Crosslin DR, Crane PK, Pathak J, Bielinski SJ, Pendergrass SA, Xu H, Hindorff LA, Li R, Manolio TA, Chute CG, Chisholm RL, Larson EB, Jarvik GP, Brilliant MH, McCarty CA, Kullo IJ, Haines JL, **Crawford DC**, Masys DR, Roden DM. Using electronic medical records to elucidate the genetic architecture of the clinical disease phenome. *Nature Biotechnology* 31(12):1102-1111 (2013). [PMC3969265](#)  
\*\*\*This article was featured in The New York Times article titled “Linking Genes to Diseases by Sifting Through Electronic Medical Records” (November 28, 2013)\*\*\*
94. Goodloe R, Brown-Gentry K, Gillani NB, Jin H, Mayo P, Allen M, McClellan Jr B, Boston J, Sutcliffe C, Schnetz-Boutaud N, Dilks HH, **Crawford DC**. Lipid-trait associated genetic variation is associated with gallstone disease in the diverse Third National Health and Nutritional Examination Survey (NHANES III). *BMC Med Genetics* 14(1):120 (2013). [PMC3870971](#)
- 2014
95. **Malinowski J**, Farber-Eger E, **Crawford DC**. Development of a data-mining algorithm to identify ages at reproductive milestones in electronic medical records. *Pacific Symposium on Biocomputing* 19:376-387 (2014). [PMC3905575](#)  
\*\*This article was selected for an oral presentation (Malinowski) at the Pacific Symposium on Biocomputing, Big Island, HI, January 3-7, 2014\*\*\*
96. **Oetjens M**, Bush WS, Birdwell KA, Dilks HH, Bowton EA, Denny JC, Wilke RA, Roden DM, **Crawford DC**. Utilization of an EMR-biorepository to identify the genetic predictors of calcineurin-inhibitor toxicity in heart transplant recipients. *Pacific Symposium on Biocomputing* 19:253-264 (2014). [PMC3923429](#)  
\*\*\*This article was selected for an oral presentation (Oetjens) at the Pacific Symposium on Biocomputing, Big Island, HI, January 3-7, 2014\*\*\*
97. Hall MA, Dudek SM, Goodloe R, **Crawford DC**, Pendergrass SA, Peissig P, Brilliant M, McCarty CA, Ritchie MD. Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. *Pacific Symposium on Biocomputing* 19:200-211 (2014). [PMC4037237](#)  
\*\*\*This article was selected for an oral presentation (Hall) at the Pacific Symposium on Biocomputing, Big Island, HI, January 3-7, 2014\*\*\*
98. **Jeff JM**, Donahue BS, Brown-Gentry K, Roden DM, **Crawford DC**, Stein CM, Kurnik D. Genetic variation in the beta-1 adrenergic receptor is associated with the risk of atrial fibrillation after cardiac surgery. *American Heart Journal* 167(1):101-108 (2014).

- [PMC3868008](#)
99. Jeff JM, Armstrong L, Ritchie MD, Denny JC, Kho AN, Basford M, Wolfe WA, Pacheco JA, Li R, Chisholm RL, Roden DM, Hayes MG, **Crawford DC**. Admixture mapping and subsequent fine mapping suggests a biologically relevant and novel association on chromosome 11 for type 2 diabetes in African Americans. *PLoS One* 9(3):e86931 (2014). [PMC3940426](#)  
\*\*\*This work was selected for an oral presentation (Jeff) at the African Society of Human Genetics, Cape Town, South Africa, March 6-9, 2011\*\*\*
100. Cheng I\*, Kocarnik JM\*, Dumitrescu L, Lindor N, Chang-Claude J, Avery C, Caberto C, Love S-A, Slattery M, Chan AT, Baron J, Hindorff LA, Park SL, Schumacher FR, Hoffmeister M, Kraft P, Butler A, Junkins HA, Duggan D, Hou L, Carlson CS, Monroe K, Lin Y, Carty CL, Mann S, Ma J, Giovannucci E, Fuchs C, Newcomb P, Jenkins M, Hopper J, Haile R, Conti D, Campbell P, Potter J, Caan B, Schoen R, Hayes R, Chanock S, Berndt S, Kury S, Bezieau S, Richardson D, Goodloe RJ, Dilks HH, Baker P, Zanke B, Lemire M, Gallinger S, Hsu L, Jiao S, Harrison T, Seminara D, Matise TC, Haiman CA, Kooperberg C, Wilkens LR, Hutter C, White E, **Crawford DC**, Heiss G, Hudson T, Bush WS, Brenner H, Casey G, Le Marchand L\*, Peters U\* Pleiotropic effects of genetic risk variants for other cancer malignancies on colorectal cancer: PAGE, GECCO, and CCFR Consortia. *Gut* 63(5):800-807 (2014). [PMC3918490](#)
101. Kocarnik JM, Park SL, Han J, Dumitrescu L, Cheng I, Wilkens LR, Schumacher FR, Kolonel L, Carlson CS, **Crawford DC**, Goodloe RJ, Dilks H, Baker P, Richardson D, Ambite JL, Song F, Quresch AA, Zhang M, Duggan D, Hutter C, Hindorff LA, Bush WS, Kooperberg C, LeMarchand L, and Peters U. Replication of associations between GWAS SNPs and melanoma risk in the Population Architecture using Genomics and Epidemiology (PAGE) study. *Journal of Investigative Dermatology* 134(7):2049-2052 (2014). [PMC4057959](#)
102. Mitchell SL, Goodloe R, Brown-Gentry K, Pendergrass SA, Murdock DG, **Crawford DC**. Characterization of mitochondrial haplogroups in a large US population-based sample from the United States. *Human Genetics* 133(7):861-868 (2014). [PMC4113317](#)
103. Park SL, Fesinmeyer MD, Timofeeva M, Caberto CP, Kocarnik JM, Han Y, Love SA, Young A, Dumitrescu L, Lin Y, Goodloe R, Wilkens LR, Hindorff L, Fowke J, Carty C, Buyske S, Schumacher FR, Butler A, Dilks H, Deelman E, Cote ML, Chen W, Pande M, Christiani DC, Field JK, Bickeboller H, Risch A, Heinrich J, Brennan P, Wang Y, Eisen T, Houlston RS, Thun M, Albanes D, Caporaso N, Peters U, North KE, Heiss G, **Crawford DC**, Bush WS, Haiman CA, Landi MT, Hung RJ, Kooperberg C, Amos CI, Le Marchand L, Cheng I. Pleiotropic associations of risk variants identified for other cancers with lung cancer risk: The PAGE and TRICL consortia. *J Natl Cancer Inst* 106(4): (2014). [PMC3982896](#)
104. Kocarnik JM, Pendergrass SA, Carty CL, Pankow JS, Schumacher FR, Cheng I, Durda P, Ambite JL, Deelman E, Cook NR, Liu S, Wactawski-Wende J, Hutter C, Brown-Gentry K, Wilson S, Pankratz N, Hong C-P, Cole SA, Voruganti S, Bůžková P, Jorgensen NW, Jenny NS, Wilkens LR, Haiman CA, Kolonel LN, LaCroix A, North K, Jackson R, Le Marchand L, Hindorff LA, **Crawford DC**, Gross M, Peters U. Multi-ancestral analysis of inflammation-related genetic variants and C-reactive protein in the Population Architecture using Genomics and Epidemiology (PAGE) Study. *Circulation: Cardiovascular Genetics* 7(2):178-188 (2014). [PMC4104750](#)

105. Mitchell SL\*, Hall JB\*, Goodloe R, Boston J, Farber-Eger E, Pendergrass SA, Bush WS, **Crawford DC**. Investigating the relationship between mitochondrial genetic variation and cardiovascular-related traits to develop a framework for mitochondrial phenome-wide association studies. *BioData Mining* 7(1):6 (2014). [PMC4021623](#)
106. Hall JB, Dumitrescu L, Dilks HH, **Crawford DC**, Bush WS. Accuracy of observer-reported ancestry for diverse populations in an electronic medical record-linked biobank. *PLoS One* 9(6):e99161 (2014). [PMC4045967](#)
107. Villegas R, Goodloe RJ, McClellan B, Boston J, **Crawford DC**. Gene-carbohydrate and gene-fiber interactions and type 2 diabetes in diverse populations from the National Health and Nutrition Examination Surveys (NHANES) as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. *BMC Genetics* 15(1):69 (2014). [PMC4094781](#)
108. Ng MCY, Shriner D, Chen BH, Li J, Chen, W-M, Guo, X, Liu J, Bielinski SJ, Yanek LR, Nalls MA, Comeau ME, Rasmussen-Torvik LJ, Jensen RA, Evans DS, Sun YV, An P, Patel SR, Lu Y, Long J, Armstrong LL, Wagenknecht L, Yang L, Snively BM, Palmer ND, Mudgal P, Langefeld CD, Keene KL, Breedman BI, Mychaleckyj JC, Nayak U, Raffel L, Goddarzi MO, Chen Y-D I, Taylor HA, Correa A, Sims M, Couper D, Pankow JS, Boerwinkle E, Adeyemo A, Doumatey A, Chen G, Mathias RA, Vaidya D, Singleton AB, Zonderman AB, Igo RP, Sedor JR, Kabagambe E, Siscovick DS, McKnight B, Rice K, Liu Y, Hsueh W-C, Zhao W, Bielak LF, Kraja A, Province MA, Bottinger EP, Gottesman O, Cai Q, Zheng W, Blot WJ, Lowe WL, Pacheco JA, **Crawford DC**, Gundberg E, Rich SS, Hayes MG, Shu Z-O, Loos RJF, Borecki IB, Peyser PA, Cummings SR, Psaty BM, Fornage M, Iyengar SK, Evans MK, Becker MD, Kao WHL, Wilson JG, Rotter JI, Sale MM, Liu S, Rotimi CN, Bowden DWW. Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. *PLoS Genetics* 10(8):e1004517 (2014). [PMC4125087](#)
109. Cronin RM, Field J, Bastarache L, Mosley J, Edward TL, Carroll R, Lin S, Hebring SJ, Hindorff LA, Crane PK, Pendergrass SA, Ritchie MD, **Crawford DC**, Bradford Y, Shaffer C, Pathak J, Bielinski SJ, Carrel DS, Crosslin DR, Carey DJ, Tromp G, Williams MS, Larson EB, Jarvik GP, Peissig PL, Brilliant MH, McCarty CA, Chute C, Kullo IJ, Bottinger E, Chisholm R, Smith M, Roden DM, Denny JC. Phenome wide association studies demonstrating pleiotropy of genetic variants within *FTO* with and without adjustment for body mass index. *Frontiers in Genetics* 5:250 (2014). [PMC4134007](#)
110. Setiawan VW, Schumacher F, Prescott J, Haessler J, Malinowski J, Wentzensen N, Yang H, Chanock S, Brinton L, Hartge P, Lissowska J, Park SL, Cheng I, Bush WS, **Crawford DC**, Ursin G, Horn-Ross P, Bernstein L, Lu L, Risch H, Yu H, Sakoda LC, Doherty J, Chen C, Jackson R, Yasmineen S, Cote M, Kocarnik JM, Peters U, Kraft P, De Vivo I, Haiman C, Kooperberg C, Le Marchand L. Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 Consortia. *Carcinogenesis* 35(9):2068-73 (2014). [PMC4146418](#)
111. Restrepo NA\*, Spencer KL\*, Goodloe R, Garrett T, Heiss G, Bůžková P, Jorgensen N, Jensen RA, Matise TC, Hindorff LA, Klein BEK, Klein R, Yin WT, Cheng CY, Cornes, B, Tai ES, Ritchie MD, Haines JL, **Crawford DC**. Genetic determinants of age-related macular degeneration in diverse populations: The Population Architecture using Genomics and Epidemiology (PAGE) Study. *Investigative Ophthalmology and Visual Science* 55(10):6839-6850 (2014). [PMC4214207](#)

112. Park SL, Caberto C, Lin Y, Goodloe R, Dumitrescu L, Love S-A, Matisse T, Hindorff LA, Fowke J, Schumacher FR, Beebe-Dimmer J, Chen C, Hou L, Thomas F, Deelman E, Han Y, Peters U, North KE, Heiss G, **Crawford DC**, Haiman CA, Wilkens LR, Bush WS, Kooperberg C, Cheng I, Le Marchand L. Association of cancer susceptibility variants with risk of multiple primary cancers: The Population Architecture using Genomics and Epidemiology Study. *Cancer Epidemiology, Biomarkers & Prevention* 23(11):2568-2578 (2014). [PMC4221293](#)
113. Wells QS, Farber-Eger E, **Crawford DC**. Extraction of echocardiographic data from the electronic medical record is a rapid and efficient method for study of cardiac structure and function. *Journal of Clinical Bioinformatics* 4:12 (2014). [PMC4177384](#)
114. Wood AR, Esko T, Yang J, Vedantam S, Pers TH, Gustafsson S, Chu AY, Estrada K, Luan J, Kutalik Z, Amin N, Buchkovich ML, Croteau-Chonka DC, Day FR, Duan Y, Fall T, Fehrmann R, Ferreira T, Jackson AU, Karjalainen J, Lo KS, Locke AE, Mägi R, Mihailov E, Porcu E, Randall JC, Scherag A, Vinkhuyzen AA, Westra HJ, Winkler TW, Workalemahu T, Zhao JH, Absher D, Albrecht E, Anderson D, Baron J, Beekman M, Demirkan A, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Fraser RM, Goel A, Gong J, Justice AE, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Lui JC, Mangino M, Leach IM, Medina-Gomez C, Nalls MA, Nyholt DR, Palmer CD, Pasko D, Pechlivanis S, Prokopenko I, Ried JS, Ripke S, Shungin D, Stancáková A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Afzal U, Arnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Bolton JL, Böttcher Y, Boyd HA, Bruinenberg M, Buckley BM, Buyske S, Caspersen IH, Chines PS, Clarke R, Claudi-Boehm S, Cooper M, Daw EW, De Jong PA, Deelen J, Delgado G, Denny JC, Dhonukshe-Rutten R, Dimitriou M, Doney AS, Dörr M, Eklund N, Eury E, Folkersen L, Garcia ME, Geller F, Giedraitis V, Go AS, Grallert H, Grammer TB, Gräßler J, Grönberg H, de Groot LC, Groves CJ, Haessler J, Hall P, Haller T, Hallmans G, Hannemann A, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hemani G, Henders AK, Hillege HL, Hlatky MA, Hoffmann W, Hoffmann P, Holmen O, Houwing-Duistermaat JJ, Illig T, Isaacs A, James AL, Jeff J, Johansen B, Johansson A, Jolley J, Juliusdottir T, Junttila J, Kho AN, Kinnunen L, Klopp N, Kocher T, Kratzer W, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Lu Y, Lyssenko V, Magnusson PK, Mahajan A, Maillard M, McArdle WL, McKenzie CA, McLachlan S, McLaren PJ, Menni C, Merger S, Milani L, Moayyeri A, Monda KL, Morken MA, Müller G, Müller-Nurasyid M, Musk AW, Narisu N, Nauck M, Nolte IM, Nöthen MM, Oozageer L, Pilz S, Rayner NW, Renstrom F, Robertson NR, Rose LM, Roussel R, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Schunkert H, Scott RA, Sehmi J, Seufferlein T, Shi J, Silventoinen K, Smit JH, Smith AV, Smolonska J, Stanton AV, Stirrups K, Stott DJ, Stringham HM, Sundström J, Swertz MA, Syvänen AC, Tayo BO, Thorleifsson G, Tyrer JP, van Dijk S, van Schoor NM, van der Velde N, van Heemst D, van Oort FV, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Waldenberger M, Wennauer R, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Bergmann S, Biffar R, Blangero J, Boomsma DI, Bornstein SR, Bovet P, Brambilla P, Brown MJ, Campbell H, Caulfield MJ, Chakravarti A, Collins R, Collins FS, **Crawford DC**, Cupples LA, Danesh J, de Faire U, den Ruijter HM, Erbel R, Erdmann J, Eriksson JG, Farrall M, Ferrannini E,

- Ferrières J, Ford I, Forouhi NG, Forrester T, Gansevoort RT, Gejman PV, Gieger C, Golay A, Gottesman O, Gudnason V, Gyllensten U, Haas DW, Hall AS, Harris TB, Hattersley AT, Heath AC, Hengstenberg C, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Hovingh GK, Humphries SE, Hunt SC, Hypponen E, Jacobs KB, Jarvelin MR, Jousilahti P, Jula AM, Kaprio J, Kastelein JJ, Kayser M, Kee F, Keinanen-Kiukaanniemi SM, Kiemeny LA, Kooner JS, Kooperberg C, Koskinen S, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lupoli S, Madden PA, Männistö S, Manunta P, Marette A, Matisse TC, McKnight B, Meitinger T, Moll FL, Montgomery GW, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Ouwehand WH, Pasterkamp G, Peters A, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ritchie M, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Sebert S, Sever P, Shuldiner AR, Sinisalo J, Steinthorsdottir V, Stolk RP, Tardif JC, Tönjes A, Tremblay A, Tremoli E, Virtamo J, Vohl MC; The Electronic Medical Records and Genomics (eMERGE) Consortium; The MIGen Consortium; The PAGE Consortium; The LifeLines Cohort Study, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hayes MG, Hui J, Hunter DJ, Hveem K, Jukema JW, Kaplan RC, Kivimäki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Powell JE, Power C, Quertermous T, Rauramaa R, Reinmaa E, Ridker PM, Rivadeneira F, Rotter JI, Saaristo TE, Saleheen D, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Strauch K, Stumvoll M, Tuomilehto J, Uusitupa M, van der Harst P, Völzke H, Walker M, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Zanen P, Deloukas P, Heid IM, Lindgren CM, Mohlke KL, Speliotes EK, Thorsteinsdottir U, Barroso I, Fox CS, North KE, Strachan DP, Beckmann JS, Berndt SI, Boehnke M, Borecki IB, McCarthy MI, Metspalu A, Stefansson K, Uitterlinden AG, van Duijn CM, Franke L, Willer CJ, Price AL, Lettre G, Loos RJ, Weedon MN, Ingelsson E, O'Connell JR, Abecasis GR, Chasman DI, Goddard ME, Visscher PM, Hirschhorn JN, Frayling TM. Defining the role of common variation in the genomic and biologic architecture of adult human height. *Nature Genetics* 46(11):1173-1186 (2014). [PMC4250049](#)
115. Crosslin DR, Tromp G, Burt A, Kim DS, Verma SS, Lucas AM, Bradford Y, **Crawford DC**, Armasu SM, Heit JA, Hayes MG, Kuivaniemi H, Ritchie MD, Jarvik GP, de Andrade M, The electronic Medical Records and Genomics (eMERGE) Network. Controlling for population structure and genotyping platform bias in the eMERGE multi-institutional biobank linked to electronic health records. *Frontiers in Genetics* 5:352 (2014). [PMC4220165](#)
116. Xie W, Kantarcioglu M, Bush WS, **Crawford D**, Denny JC, Heatherly R, Malin BA. Multi-site genotyping-phenotype association studies without revealing research participant identities. *Bioinformatics* 30(23):3334-3341 (2014). [PMC4296153](#)
117. Malinowski JR, Denny JC, Bielinski SJ, Basford MA, Bradford Y, Peissig PL, Carrel D, Crosslin DR, Pathak I, Rasmussen L, Pacheco J, Kho A, Newton KM, Li R, Kullo IJ, Chute CG, Chisholm RL, Jarvik GP, Larson EB, McCarty CA, Masys DR, Roden DM, de Andrade M, Ritchie MD, **Crawford DC**, on behalf of the eMERGE Network. Genetic

- variants associated with serum thyroid stimulating hormone (TSH) levels in European Americans and African Americans from the eMERGE Network. *PLoS One* 9(12):e111301 (2014). [PMC4249871](#)
118. Hall MA, Verma A, Brown-Gentry KD, Goodloe R, Boston J, Wilson S, McClellan B, Sutcliffe C, Dilks HH, Gillani NB, Jin H, Mayo P, Allen M, Schnetz-Boutaud N, Pendergrass SA, **Crawford DC**, Ritchie MD. A phenome-wide association study (PheWAS) using multiple National Health and Nutrition Examination Surveys (NHANES) to identify pleiotropy. *PLoS Genetics* 10(12):e1004678 (2014). [PMC4256091](#)  
 \*\*\*This article was selected for an oral presentation (Pendergrass) at the Translational Bioinformatics Conference, Jeju Island, Korea, October 13-16, 2012\*\*\*
119. **Crawford DC**, Dumitrescu L, Goodloe R, Brown-Gentry K, Boston J, McClellan B, Sutcliffe C, Wiseman R, Baker P, Pericak-Vance MA, Scott WK, Allen M, Mayo P, Schnetz-Boutaud N, Dilks HH, Haines JL, Pollin TI. Rare variant *APOC3* R19X is associated with cardio-protective profiles in a diverse population-based survey as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. *Circulation: Cardiovascular Genetics* 7(6):848-853 (2014). [PMC4305446](#)
120. Jeff JM, Brown-Gentry K, Goodloe R, Ritchie MD, Denny JC, Kho AN, Armstrong L, McClellan B, Mayo P, Allen M, Jin H, Gillani NB, Schnetz-Boutaud N, Dilks HH, Basford MA, Pacheco JA, Chisholm RL, Roden DM, Hayes MG, **Crawford DC**. Replication of *SCN5A* associations with electrocardiographic traits in African Americans from clinical and epidemiologic studies. *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics Lecture Notes in Computer Science* Volume 7833 2014: 939-951 (2014). [PMC4290789](#)
121. Verma SS, De Andrade M, Tromp G, Kuivaniemi H, Pugh E, Namjou B, Mukherjee JS, Jarvik GP, Kottyan LC, Burt A, Bradford Y, Armstrong GD, Derr K, **Crawford DC**, Haines JL, Li R, Crosslin D, Ritchie MD. Imputation and quality control steps for combining multiple genome-wide datasets. *Frontiers in Genetics* 5:370 (2014). [PMC4263197](#)
- 2015
122. Crosslin DR, Carrell DS, Burt A, Kim DS, Underwood J, Hanna DS, Comstock B, Baldwin E, de Andrade M, Kullo IJ, Tromp G, Kuivaniemi H, Borthwick KM, McCarty CA, Peissig PL, Doheny KF, Pugh E, Kho A, Pacheco J, Hayes MG, Ritchie MD, Verma SS, Armstrong G, Saip A, Stallings S, Denny JC, Carroll RJ, **Crawford DC**, Crane PK, Mukherjee S, Bottinger E, Manolio T, Li R, Beating B, Mirel DB, Carlson CS, Harley JB, Larson EB, Jarvik GP, the electronic MEDical Records and Genomics (eMERGE) Network. Genetic variation in the *HLA* region is associated with susceptibility to herpes zoster. *Genes and Immunity* 16(1):1-7 (2015). [PMC4308645](#)
123. Jeff JM, Brown-Gentry K, **Crawford DC**. Identification of genetic modifiers within the fibrinogen gene cluster for fibrinogen levels in three ethnically diverse populations. *Pacific Symposium on Biocomputing* 20:219-230 (2015). [PMC4357227](#)  
 \*\*\*This article was selected for an oral presentation (Jeff) at the Pacific Symposium on Biocomputing, Big Island, HI, January 4-8, 2015\*\*\*
124. Restrepo N, Mitchell SL, Goodloe RJ, Murdock DG, Haines JL, **Crawford DC**. Mitochondrial variation and the risk of age-related macular degeneration across diverse populations. *Pacific Symposium on Biocomputing* 20:243-254 (2015). [PMC4299880](#)

125. **Crawford DC**, Brown-Gentry K, Rieder MJ. Measures of exposure impact genetic association studies: an example in vitamin K levels and *VKORC1*. *Pacific Symposium on Biocomputing* 20:161-170 (2015). [PMC4299921](#)
126. Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, Strawbridge RJ, Pers TH, Fischer K, Justice AE, Workalemahu T, Wu JM, Buchkovich ML, Heard-Costa NL, Roman TS, Drong AW, Song C, Gustafsson S, Day FR, Esko T, Fall T, Kutalik Z, Luan J, Randall JC, Scherag A, Vedantam S, Wood AR, Chen J, Fehrmann R, Karjalainen J, Kahali B, Liu CT, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bragg-Gresham JL, Buyske S, Demirkan A, Ehret GB, Feitosa MF, Goel A, Jackson AU, Johnson T, Kleber ME, Kristiansson K, Mangino M, Mateo Leach I, Medina-Gomez C, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Stančáková A, Ju Sung Y, Tanaka T, Teumer A, Van Vliet-Ostaptchouk JV, Yengo L, Zhang W, Albrecht E, Ärnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Böhringer S, Bonnet F, Böttcher Y, Bruinenberg M, Carba DB, Caspersen IH, Clarke R, Daw EW, Deelen J, Deelman E, Delgado G, Doney AS, Eklund N, Erdos MR, Estrada K, Eury E, Friedrich N, Garcia ME, Giedraitis V, Gigante B, Go AS, Golay A, Grallert H, Grammer TB, Gräßler J, Grewal J, Groves CJ, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heikkilä K, Herzig KH, Helmer Q, Hillege HL, Holmen O, Hunt SC, Isaacs A, Itermann T, James AL, Johansson I, Juliusdottir T, Kalafati IP, Kinnunen L, Koenig W, Kooner IK, Kratzer W, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Mach F, Magnusson PK, Mahajan A, McArdle WL, Menni C, Merger S, Mihailov E, Milani L, Mills R, Moayyeri A, Monda KL, Mooijaart SP, Mühleisen TW, Mulas A, Müller G, Müller-Nurasyid M, Nagaraja R, Nalls MA, Narisu N, Glorioso N, Nolte IM, Olden M, Rayner NW, Renstrom F, Ried JS, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Sennblad B, Seufferlein T, Sitlani CM, Vernon Smith A, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tayo BO, Thorand B, Thorleifsson G, Tomaschitz A, Troffa C, van Oort FV, Verweij N, Vonk JM, Waite LL, Wennauer R, Wilsgaard T, Wojczynski MK, Wong A, Zhang Q, Hua Zhao J, Brennan EP, Choi M, Eriksson P, Folkersen L, Franco-Cereceda A, Gharavi AG, Hedman ÅK, Hivert MF, Huang J, Kanoni S, Karpe F, Keildson S, Kiryluk K, Liang L, Lifton RP, Ma B, McKnight AJ, McPherson R, Metspalu A, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Olsson C, Perry JR, Reinmaa E, Salem RM, Sandholm N, Schadt EE, Scott RA, Stolk L, Vallejo EE, Westra HJ, Zondervan KT; ADIPOGen Consortium; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GEFOS Consortium; GENIE Consortium; GLGC; ICBP; International Endogene Consortium; LifeLines Cohort Study; MAGIC Investigators; MuTHER Consortium; PAGE Consortium; ReproGen Consortium, Amouyel P, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Brown MJ, Burnier M, Campbell H, Chakravarti A, Chines PS, Claudi-Boehm S, Collins FS, **Crawford DC**, Danesh J, de Faire U, de Geus EJ, Dörr M, Erbel R, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gieger C, Gudnason V, Haiman CA, Harris TB, Hattersley AT, Heliövaara M, Hicks AA, Hingorani AD, Hoffmann W, Hofman A, Homuth G, Humphries SE, Hyppönen E, Illig T, Jarvelin MR, Johansen B, Jousilahti P, Jula AM, Kaprio J, Kee F, Keinanen-Kiukkaanniemi SM, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Lakka TA, Langenberg C, Le Marchand



- L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Musk AW, Möhlenkamp S, Morris AD, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Palmer LJ, Penninx BW, Peters A, Pramstaller PP, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Shuldiner AR, Staessen JA, Steinthorsdottir V, Stolk RP, Strauch K, Tönjes A, Tremblay A, Tremoli E, Vohl MC, Völker U, Vollenweider P, Wilson JF, Witteman JC, Adair LS, Bochud M, Boehm BO, Bornstein SR, Bouchard C, Cauchi S, Caulfield MJ, Chambers JC, Chasman DI, Cooper RS, Dedoussis G, Ferrucci L, Froguel P, Grabe HJ, Hamsten A, Hui J, Hveem K, Jöckel KH, Kivimäki M, Kuh D, Laakso M, Liu Y, März W, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sinisalo J, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Veronesi G, Walker M, Wareham NJ, Watkins H, Wichmann HE, Abecasis GR, Assimes TL, Berndt SI, Boehnke M, Borecki IB, Deloukas P, Franke L, Frayling TM, Groop LC, Hunter DJ, Kaplan RC, O'Connell JR, Qi L, Schlessinger D, Strachan DP, Stefansson K, van Duijn CM, Willer CJ, Visscher PM, Yang J, Hirschhorn JN, Zillikens MC, McCarthy MI, Speliotes EK, North KE, Fox CS, Barroso I, Franks PW, Ingelsson E, Heid IM, Loos RJ, Cupples LA, Morris AP, Lindgren CM, Mohlke KL. New genetic loci link adipose and insulin biology to body fat distribution. *Nature* 518 (7538):187-196 (2015). [PMC4338562](https://pubmed.ncbi.nlm.nih.gov/25765034/)
127. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR, Powell C, Vedantam S, Buchkovich ML, Yang J, Croteau-Chonka DC, Esko T, Fall T, Ferreira T, Gustafsson S, Kutalik Z, Luan J, Mägi R, Randall JC, Winkler TW, Wood AR, Workalemahu T, Faul JD, Smith JA, Hua Zhao J, Zhao W, Chen J, Fehrmann R, Hedman ÅK, Karjalainen J, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bolton JL, Bragg-Gresham JL, Buyske S, Demirkan A, Deng G, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Goel A, Gong J, Jackson AU, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Mangino M, Mateo Leach I, Medina-Gomez C, Medland SE, Nalls MA, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Shungin D, Stančáková A, Strawbridge RJ, Ju Sung Y, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Isaacs A, Albrecht E, Ärnlöv J, Arscott GM, Attwood AP, Bandinelli S, Barrett A, Bas IN, Bellis C, Bennett AJ, Berne C, Blagieva R, Blüher M, Böhringer S, Bonnycastle LL, Böttcher Y, Boyd HA, Bruinenberg M, Caspersen IH, Ida Chen YD, Clarke R, Warwick Daw E, de Craen AJ, Delgado G, Dimitriou M, Doney AS, Eklund N, Estrada K, Eury E, Folkersen L, Fraser RM, Garcia ME, Geller F, Giedraitis V, Gigante B, Go AS, Golay A, Goodall AH, Gordon SD, Gorski M, Grabe HJ, Grallert H, Grammer TB, Gräßler J, Grönberg H, Groves CJ, Gusto G, Haessler J, Hall P, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hengstenberg C, Holmen O, Hottenga JJ, James AL, Jeff JM, Johansson Å, Jolley J, Juliusdottir T, Kinnunen L, Koenig W, Koskenvuo M, Kratzer W, Laitinen J, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Sin Lo K, Lobbens S, Lorbeer R, Lu Y, Mach F, Magnusson PK, Mahajan A, McArdle WL, McLachlan S, Menni C, Merger S, Mihailov E, Milani L, Moayyeri A, Monda KL, Morcken MA, Mulas A, Müller G, Müller-Nurasyid M, Musk AW, Nagaraja R, Nöthen MM, Nolte IM, Pilz S, Rayner NW, Renstrom F, Rettig R, Ried JS, Ripke S,

Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Scott WR, Seufferlein T, Shi J, Vernon Smith A, Smolonska J, Stanton AV, Steinthorsdottir V, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tan ST, Tayo BO, Thorand B, Thorleifsson G, Tyrer JP, Uh HW, Vandenput L, Verhulst FC, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Warren HR, Waterworth D, Weedon MN, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q; LifeLines Cohort Study, Brennan EP, Choi M, Dastani Z, Drong AW, Eriksson P, Franco-Cereceda A, Gådin JR, Gharavi AG, Goddard ME, Handsaker RE, Huang J, Karpe F, Kathiresan S, Keildson S, Kiryluk K, Kubo M, Lee JY, Liang L, Lifton RP, Ma B, McCarroll SA, McKnight AJ, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Okada Y, Perry JR, Dorajoo R, Reinmaa E, Salem RM, Sandholm N, Scott RA, Stolk L, Takahashi A, Tanaka T, Van't Hooft FM, Vinkhuyzen AA, Westra HJ, Zheng W, Zondervan KT; ADIPOGen Consortium; AGEN-BMI Working Group; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GLGC; ICBP; MAGIC Investigators; MuTHER Consortium; MIGen Consortium; PAGE Consortium; ReproGen Consortium; GENIE Consortium; International Endogene Consortium, Heath AC, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Bovet P, Campbell H, Caulfield MJ, Cesana G, Chakravarti A, Chasman DI, Chines PS, Collins FS, **Crawford DC**, Adrienne Cupples L, Cusi D, Danesh J, de Faire U, den Ruijter HM, Dominiczak AF, Erbel R, Erdmann J, Eriksson JG, Farrall M, Felix SB, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gejman PV, Gieger C, Gottesman O, Gudnason V, Gyllensten U, Hall AS, Harris TB, Hattersley AT, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Homuth G, Kees Hovingh G, Humphries SE, Hunt SC, Hyppönen E, Illig T, Jacobs KB, Jarvelin MR, Jöckel KH, Johansen B, Jousilahti P, Wouter Jukema J, Jula AM, Kaprio J, Kastelein JJ, Keinanen-Kiukaanniemi SM, Kiemeny LA, Knekt P, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Moll FL, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Madden PA, Pasterkamp G, Peden JF, Peters A, Postma DS, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Rioux JD, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schunkert H, Schwarz PE, Sever P, Shuldiner AR, Sinisalo J, Stolk RP, Strauch K, Tönjes A, Trégouët DA, Tremblay A, Tremoli E, Virtamo J, Vohl MC, Völker U, Waeber G, Willemsen G, Wittteman JC, Zillikens MC, Adair LS, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bornstein SR, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hui J, Hunter DJ, Hveem K, Kaplan RC, Kivimaki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Metspalu A, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sattar N, Schadt EE, Schlessinger D, Eline Slagboom P, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Walker M, Wallaschofski H, Wareham NJ, Watkins H, Weir DR, Wichmann HE, Wilson JF, Zanen P, Borecki IB, Deloukas P, Fox CS, Heid IM, O'Connell JR, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, Franke L, Frayling TM,

- McCarthy MI, Visscher PM, Scherag A, Willer CJ, Boehnke M, Mohlke KL, Lindgren CM, Beckmann JS, Barroso I, North KE, Ingelsson E, Hirschhorn JN, Loos RJ, Speliotes EK. Genetic studies of body mass index yield new insights for obesity biology. *Nature* 518 (7538):197-206 (2015). [PMC4382211](#)
128. Kocarnik JM, Park SL, Han J, Dumitrescu L, Cheng I, Wilkens LR, Schumacher FR, Kolonel L, Carlson CS, **Crawford DC**, Goodloe RJ, Dilks HH, Baker P, Richardson D, Matisse TC, Ambite JL, Song F, Qureshi AA, Zhang M, Duggan D, Hutter C, Hindorff L, Bush WS, Kooperberg C, Le Marchand L, Peters U. Pleiotropic and sex-specific effects of cancer GWAS SNPs on melanoma risk in the Population Architecture using Genomics and Epidemiology (PAGE) study. *PLoS One* 10(3):e0120491 (2015). [PMC4366224](#)
129. Freitag DF, Butterworth AS, Willeit P, Howson JM, Burgess S, Kaptoge S, Young R, Ho WK, Wood AM, Sweeting M, Spackman S, Staley JR, Ramond A, Harshfield E, Nielsen SF, Grande P, Lange LA, Bown MJ, Jones GT, Scott RA, Bevan S, Porcu E, Thorleifsson G, Zeng L, Kessler T, Do R, Nikpay M, Zhang W, Hopewell JC, Kleber M, Delgado GE, Nelson CP, Goel A, Bis JC, Dehghan A, Ligthart S, Smith AV, Qu L, van 't Hof FN, de Bakker PI, Baas AF, van Rij A, Tromp G, Kuivaniemi H, Ritchie MD, Verma SS, **Crawford DC**, Malinowski J, de Andrade M, Kullo IJ, Peissig PL, McCarty CA, Böttlinger EP, Gottesman O, Crosslin DR, Carrell DS, Rasmussen-Torvik LJ, Pacheco JA, Huang J, Timpson NJ, Kettunen J, Ala-Korpela M, Mitchell GF, Parsa A, Wilkinson IB, Gorski M, Li Y, Franceschini N, Keller MF, Ganesh SK, Langefeld CD, Bruijn L, Brown MA, Evans DM, Baltic S, Ferreira MA, Baurecht H, Weidinger S, Franke A, Lubitz SA, Müller-Nurasyid M, Felix JF, Smith NL, Sudman M, Thompson SD, Zeggini E, Panoutsopoulou K, Nalls MA, Singleton A, Polychronakos C, Bradfield JP, Hakonarson H, Easton DF, Thompson D, Tomlinson IP, Dunlop M, Hemminki K, Morgan G, Eisen T, Goldschmidt H, Allan JM, Henrion M, Whiffin N, Wang Y, Chubb D, Houlston RS, Iles MM, Bishop DT, Law MH, Hayward NK, Luo Y, Nejentsev S, Barbalic M, Crossman D, Sanna S, Soranzo N, Markus HS, Wareham NJ, Rader DJ, Reilly M, Assimes T, Harris TB, Hofman A, Franco OH, Gudnason V, Tracy R, Psaty BM, Farrall M, Watkins H, Hall AS, Samani NJ, März W, Clarke R, Collins R, Kooner JS, Chambers JC, Kathiresan S, McPherson R, Erdmann J, Kastrati A, Schunkert H, Stefánsson K, Walston JD, Tybjærg-Hansen A, Alam DS, Majumder AA, Di Angelantonio E, Chowdhury R, Nordestgaard BG, Saleheen D, Thompson SG, Danesh J. Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomization analysis. *Lancet Diabetes Endocrinology* 3(4):242-253 (2015). [PMC4648058](#)
130. Dumitrescu L, Goodloe R, Farber-Eger E, Boston J, **Crawford DC**. The effects of electronic medical record phenotyping details on genetic association studies: HDL-C as a case study. *BioData Mining* 8:15 (2015). [PMC4428098](#)
131. Van Driest SL, McGregor TL, Velez Edwards DR, Lu Z, Saville BR, Kitchner TE, Hebring SJ, Brilliant M, Jouni H, Kullo IJ, Creech CB, Kannankeril PJ, Vear S, Brother KB, Bowton EA, Shaffer CM, Patel N, Delaney JT, Bradford Y, Wilson S, Olson L, **Crawford DC**, Potts AL, Ho RH, Roden DM, Denny JC. Genome-wide association study of serum creatinine levels during vancomycin therapy. *PLoS One* 10(6):e0127791 (2015). [PMC4452656](#)
- \*\*\*This article was selected for an oral presentation (Van Driest) at the American Society of Human Genetics, San Francisco, California, November 6-10, 2012\*\*\*

132. Restrepo NA, Farber-Eger E, Goodloe R, Haines JL, **Crawford DC**. Extracting primary open-angle glaucoma from electronic medical records for genetic association studies. *PLoS One* 10(6):e0127817 (2015). [PMC4465698](#)
133. Hall MA, Verma SS, Berg R, Connolly J, **Crawford DC**, Crosslin DR, de Andrade M, Doheny KF, Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Tromp G, Pendergrass SA, McCarty CA, Ritchie MD. Biology-driven gene-gene interaction analysis of age-related cataract in the eMERGE Network. *Genetic Epidemiology* 39(5):376-384 (2015). [PMC4550090](#)
134. Malinowski J, Goodloe R, Brown-Gentry K, **Crawford DC**. Cryptic relatedness in epidemiologic collections accessed for genetic association studies: experiences from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study and the National Health and Nutrition Examination Surveys (NHANES). *Frontiers in Genetics* 6:317 (2015). [PMC4620157](#)
135. Dumitrescu L, Restrepo NA, Goodloe R, Boston J, Farber-Eger E, Pendergrass SA, Bush WS, **Crawford DC**. Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. *BioData Mining* 8:35 (2015). [PMC4642611](#)
- 2016
136. Mosley JD, Shaffer CM, Van Driest SL, Weeke PE, Quinn S, Wells QS, Karnes JH, Velez Edwards DR, Wei W-Q, Teixeira PL, Bastarache L, **Crawford DC**, Li R, Manolio TA, Bottinger EP, McCarty CA, Linneman J, Brilliant MH, Pacheco JA, Thompson W, Chisholm RL, Jarvik GP, Crosslin DR, Carrell DS, Baldwin E, Ralston J, Larson EB, Grafton J, Scrol A, Jouni H, Kullo IJ, Tromp G, Borthwick KM, Kuivaniemi H, Carey DJ, Ritchie MD, Chute CG, Veluchamy A, Siddiqui MK, Palmer CNA, Morris AD, Doney A, Mahmoudpour SH, Maitland-van der Zee AH, Denny JC, Roden DM. A genome wide association study identifies variants in *KCNIP4* associated with ACE inhibitor induced cough. *The Pharmacogenomics Journal* 16(3):231-237 (2016). [PMC4713364](#)
137. Dumitrescu L, Diggins KE, Goodloe R, **Crawford DC**. Testing population-specific quantitative trait associations for clinical outcome relevance in a biorepository linked to electronic health records: *LPA* and myocardial infarction in African Americans. *Pacific Symposium on Biocomputing* 21:96-107 (2016). [PMC4720978](#)
138. Laper SM, Restrepo NA, **Crawford DC**. The challenges in using electronic health records for pharmacogenomics and precision medicine research. *Pacific Symposium on Biocomputing* 21:369-380 (2016). [PMC4720980](#)  
\*\*\*This article was selected for an oral presentation (Restrepo) at the Pacific Symposium on Biocomputing, Big Island, HI, January 4-8, 2016\*\*\*
139. Cooke Bailey JN, Wilson S, Brown-Gentry K, Goodloe R, **Crawford DC**. Kidney disease genetics and the importance of diversity in precision medicine. *Pacific Symposium on Biocomputing* 21:285-296 (2016). [PMC4720994](#)  
\*\*\*This article was selected for an oral presentation (Cooke Bailey) at the Pacific Symposium on Biocomputing, Big Island, HI, January 4-8, 2016\*\*\*
140. Oetjens MT, Brown-Gentry K, Goodloe R, Dilks HH, **Crawford DC**. Population stratification in the context of diverse epidemiologic surveys sans genome-wide data. *Frontiers in Genetics* 7:76 (2016). [PMC4858524](#)
141. Oetjens MT, Bush WS, Denny JC, Birdwell K, Dilks HH, Pendergrass SA, Ritchie MD, **Crawford DC**. Evidence for extensive pleiotropy among pharmacogenes.

*Pharmacogenomics* 17(8):853-866 (2016). [PMC5352965](#)

\*\*\*This article was selected for an oral presentation (Oetjens) in the session titled “Pharmacogenetics: From Association to Action” at the American Society of Human Genetics, San Diego, CA, October 18-22, 2014\*\*\*

142. Liu C-T, Raghavan S, Maruthur N, Kabagambe EK, Hong J, Ng MCY, Hivert M-F, Lu Y, An P, Bentley AR, Drolet AM, Gaulton KJ, Guo X, Armstrong LL, Irvin MR, Li M, Lipovich L, Rybin, DV, Taylor, KD, Agyemang C, Palmer ND, Cade BE, Chen W-M, Dauriz M, Delaney JAC, Edwards TL, Evans DS, Evans MK, Lange LA, Leong AS, Liu J, Liu Y, Nayak U, Patel SR, Pormeala BC, Rasmussen-Torvik LJ, Snijder MB, Stallings S, Tanaka T, Yanek LR, Zhao W, Becker BM, Bielak LF, Biggs ML, Bottinger EP, Bowden DW, Chen G, Correa A, Couper DJ, **Crawford DC**, Cushman M, Eicher JD, Fornage M, Franceschini N, Fu Y-P, Goodarzi MO, Gottesman O, Hara K, Harris TB, Jensen RA, Johnson AD, Jhun MA, Karter AJ, Keller MF, Kho AN, Kizer JR, Krauss R, Langfeld CD, Li X, Liang J, Liu S, Lowe Jr WL, Mosley TH, North KE, Pacheco JA, Peyser PA, Patrick AL, Rice KM, Selvin E, Sims M, Smith JA, Tajuddin SM, Vaidya D, Wren MP, Yao J, Zhu X, Ziegler JT, Zmuda JM, Zonderman AB, Zwinderman AH, AAAG Consortium, CARE Consortium, COGENT-BP Consortium, eMERGE Consortium, MEDIA Consortium, Adeyemo A, Boerwinkle E, Ferrucci L, Hayes MG, Kardina SLR, Miljkovic I, Pankow JS, Rotimi CN, Sale MM, Wagenknecht LE, Arnett DK, Chen Y-DI, Nalls MA, Province MA, Kao WHL, Siscovick DS, Psaty BM, Wilson JG, Loos RJF, Dupuis J, Rich SS, Florez JC, Rotter JI, Morris AP, Meigs JB. Trans-ethnic meta-analysis and functional annotation illustrates the genetic architecture of fasting glucose and insulin. *American Journal of Human Genetics* 99(1):56-75 (2016). [PMC5005440](#)
143. Bush WS, Crosslin DR, Obeng AO, Wallace J, Almoguera B, Basford MA, Bielinski SJ, Carrell DS, Connolly JJ, **Crawford D**, Doheny KF, Gallego CJ, Gordon AS, Keating B, Kirby J, Kitchner T, Manzi S, Mejia AR, Pan V, Perry C, Peterson JF, Prows CA, Ralston J, Scott SA, Scrol A, Smith M, Stallings SC, Veldhuizen T, Wolf W, Volpi S, Wiley K, Li R, Manolio T, Bottinger E, Brilliant MH, Carey D, Chisholm RL, Chute CG, Haines JL, Hakonarson H, Harley JB, Holm IA, Kullo IJ, Jarvik GP, Larson EB, McCarty CA, Williams MS, Denny JC, Rasmussen-Torvik LJ, Roden DM, Ritchie MD. Genetic variation among 84 pharmacogenes: the PGRN-Seq data from the eMERGE Network. *Clinical Pharmacology and Therapeutics* 100(2):160-169 (2016). [PMC5010878](#)
144. van 't Hof FNG, Ruigrok YM, Ripke S, Anderson G, de Andrade M, Baas AF, Blankensteijn J, Böttinger EP, Bown MJ, Broderick J, Bijlenga P, Carrell DS, **Crawford DC**, Crosslin DR, Ebeling C, Eriksson JG, Fornage M, Foroud T, von und zu Fraunberg M, Friedrich CM, Gaál EI, Gottesman O, Harrison SC, Hernesniemi J, Hofman A, Inoue I, Jääskeläinen JE, Jones GT, Kiemeny LALM, Kivisaari R, Ko N, Koskinen S, Kubo M, Kullo IJ, Kuivaniemi H, Kurki MI, Laakso A, Lai, D, Leal SM, Lehto H, Low S-K, Malinowski J, McCarty CA, Mosley TH, Nakamura Y, Nakaoka H, Niemelä M, Pacheco J, Peissig PL, Pera J, Ritchie MD, Rivadeneira F, van Rij AM, Santos-Cortez RL, Saratzis A, Slowik A, Takahashi A, Torvik-Rasmussen L, Tromp G, Uitterlinden AG, Verma SS, Vermeulen SH, Wang GT, AAA Consortium; Vascular Research Consortium of New Zealand; Rinkel GJE, de Bakker PIW. Shared genetic risk factors of intracranial, abdominal and thoracic aneurysms. *Journal of the American Heart Association* 5(7)

- (2016). [PMC5015357](#)
145. Verma A, Verma SS, Pendergrass SA, **Crawford DC**, Crosslin DR, Kuivaniemi H, Bush WS, Bradford Y, Kullo I, Bielinski SJ, Li R, Denny JC, Peissig P, Hebring S, de Andrade M, Ritchie MD, Tromp G. eMERGE phenome-wide association study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. *BMC Medical Genomics* 9(Suppl 1):32 (2016). [PMC27535653](#)  
\*\*\*This article was selected for an oral presentation (Verma) at the 5<sup>th</sup> Annual Translational Bioinformatics Conference, Tokyo, Japan, November 7-9, 2015\*\*\*
146. Restrepo NA, Farber-Eger E, **Crawford DC**. Searching in the dark: phenotyping diabetic retinopathy in a de-identified electronic medical record sample of African Americans. *AMIA Joint Summits Translational Science Proceedings* 2016:221-230 (2016). [PMC5001772](#)  
\*\*\*This article was selected for an oral presentation (Restrepo) at the AMIA 2016 Joint Summits on Translational Science, San Francisco, CA, March 21-24, 2016\*\*\*
147. Butkiewicz M, Restrepo NA, Haines JL, **Crawford DC**. Drug-drug interaction profiles of medication regimens extracted from a de-identified electronic medical records system. *AMIA Joint Summits Translational Science Proceedings* 2016:33-40 (2016). [PMC5001747](#)  
\*\*\*This article was selected for an oral presentation (Butkiewicz) at the AMIA 2016 Joint Summits on Translational Science, San Francisco, CA, March 21-24, 2016\*\*\*
148. Restrepo NA, Butkiewicz M, McGrath JA, **Crawford DC**. Shared genetic etiology of autoimmune diseases from a biorepository linked to de-identified electronic medical records. *Frontiers in Genetics* 7:185 (2016). [PMC5071319](#)
149. Zubair N, Graff M, Ambite J-L, Bush WS, Kichaev G, Lu Y, Manichaikul A, Sheu W H-H, Absher D, Assimes TL, Bielinski SJ, Bottinger EP, Buzkova P, Chuang L-M, Chung R-H, Cochran B, Dumitrescu L, Gottesman O, Haessler JW, Haiman C, Heiss G, Hsiung CA, Hung Y-J, Hwu C-M, Juang J-M J, Le Marchand L, Lee I-T, Lee W-J, Lin L-A, Lin D, Lin S-Y, Mackey RH, Martin LW, Pasaniuc B, Peters U, Predazzi I, Quertermous T, Reiner AP, Robinson J, Rotter JI, Ryckman KK, Schreiner PJ, Stahl E, Tao R, Tsai MY, Waite LL, Wang T-D, Buyske S, Chen Y-D I, Cheng I, **Crawford DC**, Loos RJF, Rich SS, Fornage M, North KE, Kooperberg C, Carty CL. Fine-mapping of lipid regions in global populations discovers race/ethnicity-specific signals and refines previously identified loci. *Human Molecular Genetics* 25(24):5500-5512 (2016). [PMC5721937](#)  
\*\*\*This work was selected for an oral presentation (Zubair) at the American Heart Association Epidemiology and Prevention/Lifestyle and Cardiometabolic Health 2015 Scientific Sessions, Baltimore, Maryland, March 3-6, 2015\*\*\*
- 2017
150. Hollister BM, Restrepo NA, Farber-Eger E, **Crawford DC**, Aldrich MC, Non A. Development and performance of text-mining algorithms to extract socioeconomic status from de-identified electronic health records. *Pacific Symposium on Biocomputing* 22:230-241 (2017). [PMC5147499](#)  
\*\*\*This work was selected for an oral presentation (Hollister) at the American Association of Physical Anthropologists, St. Louis, MO, March 25-28, 2015 and the Pacific Symposium on Biocomputing, Big Island, HI, January 3-7, 2017\*\*\*
151. Jones GT, Tromp G, Kuivaniemi H, Gretarsdottir S, Baas AF, Giusti B, Strauss E, van 't Hof FN, Webb T, Erdman R, Ritchie MD, Elmore JR, Verma A, Pendergrass S, Kullo IJ,

- Ye Z, Peissig PL, Gottesman O, Verma SS, Malinowski J, Rasmussen-Torvik LJ, Borthwick K, Smelser DT, Crosslin DR, de Andrade M, Ryer EJ, McCarty CA, Bottinger EP, Pacheco JA, **Crawford DC**, Carrell DS, Gerhard GS, Franklin DP, Carey DJ, Phillips VL, Williams MJ, Wei W, Blair R, Hill AA, Vasudevan TM, Lewis DR, Thomson IA, Krysa J, Hill GB, Roake J, Merriman TR, Oszkinis G, Galora S, Saracini C, Abbate R, Pulli R, Pratesi C, Saratzis A, Verissimo A, Bumpstead SJ, Badger SA, Clough RE, Cockerill GW, Hafez H, Scott DJ, Futers TS, Romaine SP, Bridge K, Griffin KJ, Bailey MA, Smith A, Thompson MM, van Bockxmeer F, Matthiasson SE, Thorleifsson G, Thorsteinsdottir U, Blankensteijn JD, Teijink JA, Wijmenga C, de Graaf J, Kiemeny LA, Lindholt JS, Hughes AE, Bradley DT, Stirrups K, Golledge J, Norman PE, Powell JT, Humphries SE, Hamby SE, Goodall AH, Nelson CP, Sakalihasan N, Courtois A, Ferrell RE, Eriksson P, Folkersen L, Franco-Cereceda A, Eicher JD, Johnson AD, Betsholtz C, Ruusalepp A, Franzén O, Schadt E, Björkegren JL, Lipovich L, Drolet AM, Verhoeven E, Zeebregts CJ, Geelkerken RH, van Sambeek MR, van Sterkenburg SM, de Vries JP, Stefansson K, Thompson JR, de Bakker PI, Deloukas P, Sayers RD, Harrison S, van Rij AM, Samani NJ, Bown MJ. Meta-analysis of genome-wide association studies for abdominal aortic aneurysm identified four new disease-specific risk loci. *Circulation Research* 120(2):341-353 (2017). [PMC5253231](#)  
 \*\*\*This article was featured in an editorial titled “Understanding AAA Pathobiology: A GWAS Leads the Way” by Chasman DI and Lawler PR, *Circulation Research* 120(20):259-261 (2017). [PMC5267556](#)\*\*\*
152. Dumitrescu L, Ritchie MD, Denny JC, El Rouby NM, McDonough CW, Bradford Y, Ramirez AH, Bielinski SJ, Basford MA, Chai HS, Peissig P, Carrell D, Pathak J, Rasmussen LV, Wang X, Pacheco JA, Kho AN, Hayes MG, Matsumoto M, Smith ME, Li R, Cooper-DeHoff RM, Kullo IJ, Chute CG, Chisholm RL, Jarvik GP, Larson EB, Carey D, McCarty CA, Williams MS, Roden DM, Bottinger E, Johnson JA, de Andrade M, **Crawford DC**. Genome-wide study of resistant hypertension in African and European Americans identified from electronic health records. *PLoS One* 12(2):e0171745 (2017). [PMC5319785](#)
153. Avery CL, Wassel CL, Richard MA, Highland HM, Bien S, Zubair N, Soliman EZ, Fornage M, Bielinski SJ, Tao R, Seyerle AA, Shah SJ, Lloyd-Jones DM, Buyske S, Rotter JI, Post WS, Rich SS, Hindorff LA, Jeff JM, Shohet RV, Sotoodehnia N, Lin DY, Whitsel EA, Peters U, Haiman CA, **Crawford DC**, Kooperberg C, North KE. Fine-mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. *Heart Rhythm* 14(4):572-580 (2017). [PMC5448160](#)  
 \*\*\*This article was selected for an oral presentation (Avery) at the American Heart Association Nutrition, Physical Activity and Metabolism/Cardiovascular Disease Epidemiology and Prevention 2012 Scientific Sessions, San Diego, CA, March 13-16, 2012\*\*\*
154. Fernández-Rhodes L, Gong J, Haessler J, Franceschini N, Graff M, Nishimura KK, Wang Y, Highland H, Yoneyama S, Bush WS, Goodloe R, Ritchie MD, **Crawford D**, Gross M, Fornage M, Buzkova P, Tao R, Isasi C, Avilés-Santa L, Daviglus M, Mackey RH, Houston D, Gu CC, Ehret G, Nguyen K-DH, Lewis CE, Leppert M, Irvin MR, Lim U, Haiman CA, Le Marchand L, Schumacher F, Wilkens L, Lu Y, Bottinger EP, Loos RJJ, Sheu WH-H, Guo X, Lee W-J, Hai Y, Hung Y-J, Absher D, Wu I-C, Taylor KD, Lee I-TL, Liu Y, Wang

T-D, Quertermous T, Juang J-MJ, Rotter JI, Assimes T, Hsiung CA, Chen Y-DI, Prentice R, Kuller LH, Manson JE, Kooperberg C, Smokowski P, Robinson WR, Gordon-Larsen P, Li R, Hindorff L, Buyske S, Matise TC, Peters U, North KE. Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. *Human Genetics* 136(6):771-800 (2017).

[PMC5485655](#)

\*\*\*This work was selected for an oral presentation (Fernández-Rhodes) at the American Heart Association Nutrition, Physical Activity and Metabolism/Cardiovascular Disease Epidemiology and Prevention 2013 Scientific Sessions, New Orleans, March 19-22, 2013\*\*\*

155. Jones CC, Bush WS, **Crawford DC**, Wenzlaff AS, Schwartz AG, Wiencke JK, Wrensch MR, Blot WJ, Chanock SJ, Grogan EL, Aldrich MC. Germline genetic variants and lung cancer survival in African Americans. *Cancer Epidemiology, Biomarkers & Prevention* 26(8):1288-1295 (2017). [PMC5540773](#)

156. Farber-Eger E, Goodloe R, Boston J, Bush WS, **Crawford DC**. Extracting country of origin from electronic health records for gene-environment studies as part of the Epidemiologic Architecture for Genes Linked to Environment. *AMIA Joint Summits Translational Science Proceedings* 2017:50-57 (2017). [PMC5543359](#)

\*\*\*This article was selected for an oral presentation (Crawford) at the AMIA 2017 Joint Summits on Translational Science, San Francisco, CA, March 27-30, 2017\*\*\*

157. Goodloe R, Farber-Eger E, Boston J, **Crawford DC**, Bush WS. Reducing clinical noise for body mass index measures due to unit and transcription errors in the electronic health record. *AMIA Joint Summits Translational Science Proceedings* 2017:102-111 (2017). [PMC5543370](#)

\*\*\*This article was selected for an oral presentation (Crawford) at the AMIA 2017 Joint Summits on Translational Science, San Francisco, CA, March 27-30, 2017\*\*\*

158. Conti DV, Wang K, Sheng X, Bensen JT, Hazelette DJ, Cook MB, Ingles SA, Kittles RA, Strom SS, Rybicki BA, Nemesure B, Isaacs WB, Stanford JL, Zheng W, Sanderson M, John EM, Park JY, Xu J, Stevens VL, Berndt SI, Huff CD, Wang Z, Yeboah ED, Tettey Y, Biritwum RB, Adjei AA, Tay E, Truelove A, Niwa S, Sellers TA, Yamoah K, Murphy AB, **Crawford DC**, Gapstur SM, Bush WS, Aldrich MC, Cussenot O, Petrovics G, Cullen J, Neslund-Dudas C, Stern MC, Jarai ZK, Goindasami K, Chokkalingam AP, Hsing AW, Goodman PJ, Hoffman T, Drake BF, Hu JJ, Clark PE, Van Den Eeden SK, Blanchet P, Fowke JH, Casey G, Hennis AJM, Han Y, Lubwama A, Thompson IM Jr, Leach R, Easton DF, Schumacher F, Van de Berg DJ, Gundell SM, Stram A, Wan P, Xia L, Menegaux F, Cancel-Tassin G, Lein EA, Brureau L, Stram DO, Watya S, Chanock SJ, Witte JS, Blot WJ, Henderson BE, Haiman CA; for the PRACTICAL/ELLIPSE Consortium. Two novel susceptibility loci for prostate cancer in men of African ancestry. *Journal of the National Cancer Institute* 109(8):(2017). [PMC5448553](#)

2018

159. Fish AE, **Crawford DC**, Capra JA, Bush WS. Local ancestry transitions modify SNP-trait associations. *Pacific Symposium on Biocomputing* 23:424-435 (2018). [PMC5728664](#)

160. Gong J, Nishimura KK, Fernandez-Rhodes L, Haessler J, Bien S, Graff M, Lim U, Lu Y, Gross M, Fornage M, Yoneyama S, Isasi CR, Buzkova P, Daviglus M, Lin DY, Tao R, Goodloe R, Bush WS, Farber-Eger E, Boston J, Dilks HH, Ehret G, Gu CC, Lewis CE,



- Ngyuen KH, Cooper R, Leppert M, Irvin MR, Bottinger EP, Wilkens LR, Haiman CA, Park L, Monroe KR, Cheng I, Carlson CS, Jackson R, Kuller L, Houston D, Kooperberg C, Buyske S, Hindorff LA, **Crawford DC**, Loos RJF, Le Marchand L, Matisse TC, North KE, Peters U. Trans-ethnic analysis of Metabochip data identifies two new loci associated with BMI. *International Journal of Obesity* 42(3):384-390 (2018). [PMC5876082](#)
161. **Crawford DC**, Cooke Bailey JN, Miskimen K, Miron P, McCauley JL, Sedor JR, O'Toole JF, Bush WS. Somatic T-cell receptor diversity in a chronic kidney disease patient population linked to electronic health records. *AMIA Joint Summits Translational Science Proceedings* 2017:63-71 (2018). [PMC5961818](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the AMIA 2018 Joint Summits on Translational Science, San Francisco, CA, March, 12-15, 2018\*\*\*
162. Smieszek S, Mitchell SL, Farber-Eger EH, Veatch OJ, Wheeler NR, Goodloe RJ, Wells QS, Murdock DG, **Crawford DC**. Hi-MC: A novel method for high-throughput mitochondrial haplogroup classification. *PeerJ* 6:e5149 (2018). [PMC6022720](#)
163. Cooke Bailey JN\*, **Crawford DC\***, Goldenberg A, Slaven A, Pencak J, Schachere M, Bush WS, Sedor JR, O'Toole JF. Willingness to participate in a national precision medicine cohort: Attitudes of chronic kidney disease patients at a Cleveland public hospital. *Journal of Personalized Medicine* 8(3):21 (2018). [PMC6164471](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at Keystone Symposia's One Million Genomes: From Discovery to Health, Hannover, Germany, June 4-8, 2018\*\*\*
164. Fernández-Rhodes L\*, Malinowski JR\*, Wang Y\*, Tao R\*, Pankratz N\*, Jeff JM\*, Yoneyama S\*, Carty CL, Setiawan VW, Le Marchand L, Haiman C, Corbett S, Heiss G, Gross M, Buzkova P, **Crawford DC**, Hunt SC, Rao DC, Schwander K, Chakravarti A, Gottesman O, Abul-Husn NS, Bottinger EP, Loos RJF, Raffel LJ, Yao J, Guo X, Bielinski SJ, Rotter JI, Vaidya D, Chen YL, Castaneda SF, Daviglus M, Kaplan R, Talavera GA, Ryckman KK, Peters U, Ambite JL, Buyske S, Hindorff L, Kooperberg C, Matisse T, Franceschini N, North KE. The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. *PLoS One* 13(7):e0200486 (2018). [PMC6059436](#)
165. van Setten J, Brody JA, Jamshidi Y, Swenson BR, Butler AM, Campbell H, Del Greco FM, Evans DS, Gibson Q, Gudbjartsson DF, Kerr KF, Krijthe BP, Lyttikainen L-P, Muller C, Muller-Nurasyid M, Nolte IM, Padmanabhan S, Ritchie MD, Robino A, Smith AV, Steri M, Tanaka T, Teumer A, Trompet S, Ulivi S, Verweij N, Yin X, Arnar DO, Asselbergs FW, Bader JS, Barnard J, Bis J, Blankenberg S, Boerwinkle E, Bradford Y, Buckley BM, Chung MK, **Crawford D**, den Hoed M, Denny J, Dominiczak AF, Ehret GB, Eijgelsheim M, Ellinor PT, Felix SB, Franco OH, Franke L, Harris TB, Holm H, Ilaria G, Iorio A, Kahonen M, Kolcic I, Kors JA, Lakatta EG, Launer LJ, Lin H, Lin HJ, Loos RJF, Lubitz SA, Macfarlane PW, Magnani JW, Leach IM, Meitinger T, Mitchell BD, Munzel T, Papanicolaou GJ, Peters A, Pfeufer A, Pramstaller PP, Raitakari OT, Rotter JI, Rudan I, Samani NJ, Schlessinger D, Silva Aldana CT, Sinner MF, Smith JD, Snieder H, Soliman EZ, Spector TD, Stott DJ, Strauch K, Tarasov KV, Uitterlinden AG, van Wagoner DR, Volker U, Volzke H, Waldenberger M, Westra HJ, Wild PS, Zeller T, Alonso A, Avery CL, Bandinelli S, Benjamin EJ, Cucca F, Dorr M, Ferrucci L, Gasparini

- P, Gudnason V, Hayward C, Heckbert SR, Hicks AA, Jukema JW, Kaab S, Lehtimaki T, Liu Y, Munroe PB, Parsa A, Polasek O, Psaty BM, Roden DM, Schnabel RB, Sinagra G, Stefansson K, Stricker BH, van der Harst P, van Duijn CM, Wilson JF, Gharib S, de Bakker PIW, Isaacs A, Arking DE, Sotoodehnia N. PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications* 9(1):2904 (2018). [PMC6060178](#)
166. **Crawford DC**, **Restrepo NA**, Diggins KE, Farber-Eger E, Wells QS. Frequency and phenotype consequence of *APOC3* rare variants in patients with very low triglyceride levels. *BMC Medical Genomics* 11(Suppl 3):66 (2018). [PMC6156840](#)  
\*\*\*This article was selected for an oral presentation (Crawford) at the 2017 Translational Bioinformatics in Precision Medicine and 7<sup>th</sup> Annual Translational Bioinformatics Conference, Long Beach, CA, September 29-October 1, 2017\*\*\*
167. **Restrepo NA**, **Laper SM**, Farber-Eger E, **Crawford DC**. Local genetic ancestry in *CDKN2B-AS1* is associated with primary open-angle glaucoma in an African American cohort extracted from de-identified electronic health records. *BMC Medical Genomics* 11 (Suppl 3):70 (2018). [PMC6157155](#)  
\*\*\*This article was selected for an oral presentation (Restrepo) at the 2017 Translational Bioinformatics in Precision Medicine and 7<sup>th</sup> Annual Translational Bioinformatics Conference, Long Beach, CA, September 29-October 1, 2017\*\*\*
168. Kocarnik JM, Richard M, Graff M, Haessler J, Carlson C, Carty CL, Reiner AP, Avery CL, Ballantyne CM, LaCroix AZ, Assimes TL, Barbalic M, Pankratz N, Tang W, Chen D, Pereira R, Bien S, Nishimura K, Best LG, Ambite JL, Cheng I, **Crawford DC**, Hindorff LA, Heiss G, North K, Haiman CA, Peters U, Le Marchand L, Kooperberg C. Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the MetaboChip in the Population Architecture using Genomics and Epidemiology (PAGE) study. *Human Molecular Genetics* 27(16):2940-2953 (2018). [PMC6077792](#)
169. Jones CC, Fletcher S, Blume J, Wenzlaff A, Chen H, Deppen SA, Bush WS, **Crawford DC**, Schwartz A, Blot WJ, Grogan EL, Aldrich MC. Racial disparities in lung cancer survival: The contribution of stage, treatment, and ancestry. *Journal of Thoracic Oncology* 13(10):1464-1473 (2018). [PMC6153049](#)
- 2019
170. **Hollister BM**, Farber-Eger E, Aldrich MC, **Crawford DC**. A social determinant of health may modify genetic associations for blood pressure: Evidence from a SNP by education interaction in an African American population. *Frontiers in Genetics* 10:428 (2019). [PMC6523518](#)
171. El Rouby N, McDonough CW, Gong Y, McClure LA, Mitchell BD, Horenstein RB, Talbert RL, **Crawford DC** on behalf of the eMERGE network, Gitzendanner MA, Takahashi A, Tanaka T, Kubo M, Pepine CJ, Cooper-DeHoff RM, Benavente OR, Shuldiner AR, Johnson JA. Genome wide association analysis of common genetic variants of resistant hypertension. *The Pharmacogenomics Journal* 19(3): 295-304 (2019). [PMC6426691](#)
172. Halladay CW, Hadi T, Anger MD, Greenberg PB, Sullivan JM, Konicki PE, Peachey NS, Igo RP, Iyengar SK, Wu W-C, **Crawford DC**, for the VA Million Veteran Program. Genetically-guided algorithm development and sample size optimization for age-related macular degeneration cases and controls in electronic health records from the VA Million

Veteran Program. *AMIA Joint Summits Translational Science Proceedings* 2019: 153-162 (2019). [PMC6568141](#)

\*\*\*This article was selected for an oral presentation (Crawford) at the American Medical Informatics Association (AMIA) Informatics Summit, San Francisco, CA, March 25-28, 2019\*\*\*

173. Pendergrass SA, Buyske S, Jeff JM, Frase A, Dudek S, Bradford Y, Ambite J-L, Avery CL, Bůžková P, Deelman E, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Jackson RD, Lin Y, Le Marchand L, Matisse TC, Monroe KR, Moreland L, North KE, Park SL, Reiner A, Wallace R, Wilkens LR, Kooperberg C, Ritchie MD\*, **Crawford DC\***. A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans *PLoS One* 14(12):e0226771 (2019). [PMC6938343](#)

\*\*\*This article was selected for an oral presentation (Pendergrass) at the International Genetic Epidemiology Society, Heidelberg, Germany, September 18-20, 2011 and the Keystone Symposia on Molecular and Cellular Biology. Complex Traits: Genomics and Computational Approaches, Breckenridge, CO, February 20-25, 2012\*\*\*

2020

174. **Crawford DC**, Lin J, Cooke Bailey JN, Kinzy T, Sedor JR, O'Toole JF, Bush WS. Frequency of ClinVar pathogenic variants in chronic kidney disease patients surveyed for return of research results at a Cleveland public hospital *Pacific Symposium on Biocomputing* 25:575-586 (2020). [PMC6931908](#)

175. Darst BF, Wan P, Sheng X, Bensen JT, Ingles SA, Rybicki BA, Nemesure B, John EM, Fowke JH, Stevens VL, Berndt SI, Huff CD, Strom SS, Park JY, Zhen W, Ostrander EA, Walsh PC, Yeboah ED, Tettey Y, Biritwum RB, Adjei AA, Tay E, Srivastava S, Carpten J, Truelove A, Niwa S, Sellers TA, Yamoah K, Murphy AB, Sanderson M, **Crawford DC**, Gapstur SM, Bush WS, Aldrich MC, Cussenot O, Petrovics G, Cullen J, Neslund-Dudas C, Kittle RA, Xu J, Stern MC, Jarai Z-K, Govindasami K, Chokkalingam AP, Multigner L, Parent M-E, Menegaux F, Cancel-Tassin G, Kibel AS, Klein EA, Goodman PJ, Drake BF, Hu JJ, Clark PE, Planchet P, Casey G, Hennis AJM, Lubwama A, Thompson IM, Leach R, Gundell SM, Pooler L, Xia L, Mohler JL, Fontham ETH, Smith GJ, Taylor JA, Eeles RA, Brureau L, Chanock SJ, Watya S, Stanford JL, Mandal D, Isaacs WB, Cooney K, Blot WJ, Conti DV, Haiman CA. A germline variant at 8q24 contributes to familial clustering of prostate cancer in men of African ancestry *European Urology* 78(3):316-320 (2020). [PMC7805560](#)

176. McDonough CW, Babcock K, Chucru K, **Crawford DC**, Bian J, Modave F, Cooper-DeHoff RM, Hogan WR. Optimizing identification of resistant hypertension: computable phenotype development and validation *Pharmacoepidemiology and Drug Safety* 29(11):1393-1401 (2020). [PMC7754782](#)

2021

177. Karunamuni R, Huynh-Le M-P, Fan CC, Thompson W, Eeles RA, Kote-Jarai Z, Muir K, UKGPCS collaborators, Lophatananon A, Tangen CM, Goodman PJ, Thompson Jr. I, Blot WJ, Zheng W, Kibel AS, Drake BF, Cussenot O, Cancel-Tassin G, Menegaux F, Truong T, Park JY, Lin H-Y, Bensen JT, Fontham ETH, Mohler JL, Taylor JA, Multigner L, Blanchet P, Brureau L, Romana M, Leach RJ, John EM, Fowke J, Bush WS, Aldrich M, **Crawford DC**, Srivastava S, Cullen JC, Petrovics G, Parent M-E, Hu JJ, Sanderson M, Mills IG, Andreassen OA, Dale AM, Seibert TM, PRACTICAL

- Consortium. African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer *International Journal of Cancer* 148(1):99-105 (2021). [PMC8135907](#)
178. Conti DV\*, Darst B\*, Moss L, Saunders EJ, Sheng X, Chou A, Schumacher FR, Amin Al Olama A, Benlloch S, Dadaev T, Brook MN, Sahimi A, Hoffmann TJ, Takahashi A, Matsuda K, Momozawa Y, Fujita M, Muir K, Lophatananon A, Wan P, Le Marchand L, Wilkens L, Stevens VL, Gapstur SM, Carter BD, Schleutker J, Tammela TLJ, Sipeky C, Auvinen A, Giles GG, Southey MC, MacInnis RJ, Cybulski C, Wokolorczyk D, Lubinski J, Neal DE, Donovan JL, Hamdy FC, Martin RM, Nordestgaard BG, Nielsen SF, Weischer M, Bojesen SE, Roder MA, Iversen P, Batra J, Chambers S, Moya L, Horvath L, Clements JA, Tilley W, Risbridger GP, Gronberg H, Aly M, Szulkin R, Eklund M, Norstrom T, Pashayan N, Dunning AM, Ghoussaini M, Travis RC, Key TJ, Riboli E, Park JY, Sellers TA, Lin H-Y, Albanes D, Weinstein S, Mucci LA, Giovannucci E, Lindstrom S, Kraft P, Hunter DJ, Penney KL, Turman C, Tangen CM, Goodman PJ, Thompson IM, Hamilton RJ, Fleshner NE, Finelli A, Parent M-E, Stanford JL, Ostrander EA, Geybels MS, Koutros S, Beane Freeman LE, Stampfer M, Wolk A, Hakansson N, Adriole GL, Hoover RN, Machiela MJ, Sorensen KD, Borre M, Blot WJ, Zheng W, Yeboah ED, Mensah JE, Lu Y-J, Zhang H-W, Feng N, Mao X, Wu Y, Zhao S-C, Sun Z, Thibodeau SN, McDonnell SK, Schaid DJ, West CML, Burnet N, Maier C, Schnoeller T, Luedeke M, Kibel AS, Drake BF, Cussenot O, Cancel-Tassin G, Menegaux F, Truong T, Koudou YA, John EM, Grindedal EM, Maehle L, Khaw K-T, Ingles SA, Stern MC, Vega A, Gomze-Caamno A, Fachal L, Rosentstein BS, Kerns SL, Ostrer H, Teixeira MR, Paulo P, Brandao A, Watya S, Lubwana A, Bensen JT, Fonham ETH, Mohler J, Taylor JA, Kogevinas M, Llorca J, Castano-Vinyals G, Cannon-Albright L, Teerlink CC, Huff C, Strom SS, Multigner L, Blanchet P, Brureau L, Kaneva R, Slavov C, Mitev V, Leach RJ, Weaver B, Brenner H, Cuk K, Holleczeck B, Saum K-U, Klein EA, Hsing AW, Kittles RA, Murphy AB, Logothetis CJ, Kim J, Neuhausen SL, Steele L, Ding YC, Isaacs WB, Nemesure B, Hennis AJM, Carpten J, Pandha H, Michael A, De Ruyck K, De Meerleer G, Ost P, Xu J, Razack A, Lim J, Teo S-H, Newcomb LF, Lin DW, Fowke J, Neslund-Dudas C, Rybicki BA, Gamulin M, Lessel D, Kulis T, Usmani N, Singhal S, Parliament M, Claessens F, Joniau S, Van de Broeck T, Gago-Dominguez M, Castelao JE, Martinez ME, Larkin S, Townsend PA, Aukim-Hastie C, Bush WS, Aldrich MC, **Crawford DC**, Srivastava S, Cullen JC, Petrovics G, Casey G, Roobol MJ, Jenster G, van Schaik RHN, Hu JJ, Sanderson M, Varma R, McKean-Cowdin R, Torres M, Mancuso N, Berndt SI, Van Den Eeden SK, Easton DF, Chanock SJ, Cooke MB, Wiklund F, Nakagawa H, Witte JS, Eeles RA\*, Kote-Jarai Z\*, Haiman CA\*. Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction *Nature Genetics* 53(1):65-75 (2021). [PMC8148035](#)
179. Kaur H, **Crawford DC**, Liang J, Zhu X, Kallianpur AR, Bush WS. Replication of European hypertension associations in a case-control study of 9,534 African Americans *PLoS One* 16(11):e0259962 (2021). [PMC8601554](#)
- 2022
180. Peloso GM, Tcheandjieu C, Wu W-C, Posner DC, Zhou JJ, MVP COVID-19 GWAS Working Group, Joseph J, Efir JT, **Crawford DC**, Sun YV, McGeary JE, Arjomandi M, Assimes TL, Huffman JE, VA Million Veteran Program COVID-19 Science Initiative. Genetic loci associated with COVID-19 positivity and hospitalization in White, Black,

- and Hispanic Veterans of the VA Million Veteran Program. *Frontiers in Genetics* 12:777076 (2022). [PMC8864634](#)
181. Karunamuni R, Huynh-Le M-P, Fan CC, Thompson W, Eeles RA, Kote-Jarai Z, Muir K, UKGPCS collaborators, Lophatananon A, Tangen CM, Goodman PJ, Thompson Jr. I, Blot WJ, Zheng W, Kibel AS, Drake BF, Cussenot O, Cancel-Tassin G, Menegaux F, Truong T, Park JY, Lin H-Y, Bensen JT, Fontham ETH, Mohler JL, Taylor JA, Multigner L, Blanchet P, Brureau L, Romana M, Leach RJ, John EM, Fowke J, Bush WS, Aldrich MC, **Crawford DC**, Srivastava S, Cullen JC, Petrovics G, Parent M-E, Hu JJ, Sanderson M, Mills IG, Andreassen OA, Dale AM, Seibert TM, PRACTICAL Consortium. Performance of African-ancestry-specific polygenic hazard score varies according to local ancestry in 8q24. *Prostate Cancer and Prostatic Diseases* 25(2):229-237 (2022). [PMC8669040](#)
  182. Nealon CL, Halladay CW, Kinzy TG, Simpson P, Simpson P, Canania RL, Anthony SA, Roncone DP, Sawicki Rogers LRS, Leber JN, Dougherty JM, the VA Million Veteran Program, Sullivan JM, Wu W-C, Greenberg PB, Iyengar SK, **Crawford DC**, Peachey NS, Cooke Bailey JN. Development and evaluation of rules-based algorithms for primary open-angle glaucoma in the VA Million Veteran Program. *Ophthalmic Epidemiology* (in press).  
 \*\*\*This article was selected for an oral presentation (Nealon) at the Association for Research in Vision and Ophthalmology (ARVO), virtual, May 1-7, 2021\*\*\*
  183. Verma A, Tsao N, Thomann L, Ho Y-L, Carr R, **Crawford DC**, Efirid JT, Huffman J, Hung A, Ivey K, Iyengar S, Levin M, Luoh S-W, Lynch J, Natarajan P, Pyarajan S, Bick A, Costa L, Genovese G, Hauger R, Madduri R, Pathak G, Polimanti R, Voight B, Vujkovic M, Zekavat M, Zhao H, Ritchie MD, VA Million Veteran Program COVID-19 Science Initiative, Chang K-M, Kelly Cho, Casas JP, Tsao PS, Gaziano JM, O'Donnell C, Damrauer S\*, Liao K\*. A phenome-wide association study of genes associated with COVID-19 severity reveals shared genetics with complex disease in the Million Veteran Program. *PLoS Genetics* 18(4):e1010113 (2022). [PMC9049369](#)  
 \*\*\*This article was selected for an oral presentation (Verma) at the American College of Rheumatology, virtual due to SARS-CoV-2/COVID-19, November 3-4, 2021\*\*\*
  184. Huynh-Le M-P, Karunamuni R, Fan CC, Asona L, Thompson WK, Martinez ME, Eeles RA, Zsofia Kote-Jarai Z, Muir KR, Lophatananon A, Schleutker J, Pashayan N, Batra J, Grönberg H, Neal DE, Nordestgaard BG, Tangen CM, MacInnis RJ, Wolk A, Albanes D, Haiman CA, Travis RC, Blot WJ, Stanford JL, Mucci LA, West CML, Nielsen SF, Kibel AS, Cussenot O, Berndt SI, Koutros S, Dalsgaard Sørensen K, Cybulski C, Grindedal EM, Menegaux F, Park JY, Ingles SA, Maier C, Hamilton RJ, Rosenstein BS, Lu Y-J, Watya S, Vega A, Kogevinas M, Wiklund F, Penney KL, Huff CD, Teixeira MR, Multigner L, Leach RJ, Brenner H, John EM, Kaneva R, Logothetis CJ, Neuhausen SL, De Ruyck K, Ost P, Razack A, Newcomb LF, Fowke JH, Gamulin M, Abraham A, Claessens F, Castela J, Townsend PA, **Crawford DC**, Petrovics G, van Schaik RHN, Parent M-E, Hu JJ, Zheng W, Mills IG, Andreassen OA, Dale AM, Seibert TM. Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. *Prostate Cancer and Prostatic Diseases* (in press).
  185. Darst BF, Hughley R, Pfennig A, Hazra U, Fan C, Wan P, Sheng X, Xia L, Andrews C, Chen F, Berndt SI, Kote-Jarai Z, Govindasami K, Bensen JT, Ingles SA, Rybicki BA, Nemesure B, John EM, Fowke JH, Huff CD, Strom SS, Isaacs WB, Park JY, Zheng W,

- Ostrander EA, Walsh PC, Carpten J, Sellers TA, Yamoah K, Murphy AB, Sanderson M, **Crawford DC**, Gapstur SM, Bush WS, Aldrich MC, Cussenot O, Petrovics G, Cullen J, Neslund-Dudas C, Kittles RA, Xu J, Stern MC, Chokkalingam AP, Multigner L, Parent ME, Menegaux F, Cancel-Tassin G, Kibel AS, Klein EA, Goodman PJ, Stanford JL, Drake BF, Hu JJ, Clark PE, Blanchet P, Casey G, Hennis AJM, Lubwama A, Thompson IM Jr, Leach RJ, Gundell SM, Pooler L, Mohler JL, Fontham ETH, Smith GJ, Taylor JA, Brureau L, Blot WJ, Biritwum R, Tay E, Truelove A, Niwa S, Tettey Y, Varma R, McKean-Cowdin R, Torres M, Jalloh M, Magueye Gueye S, Niang L, Ogunbiyi O, Oladimeji Idowu M, Popoola O, Adebisi AO, Aisuodionoe-Shadrach OI, Nwegbu M, Adusei B, Mante S, Darkwa-Abrahams A, Yeboah ED, Mensah JE, Anthony Adjei A, Diop H, Cook MB, Chanock SJ, Watya S, Eeles RA, Chiang CWK, Lachance J, Rebbeck TR, Conti DV, Haiman CA. A rare germline *HOXB13* variant contributes to risk of prostate cancer in men of African ancestry. *European Urology* 81(5):458-462 (2022). PMC9018520
186. Jin B, Capra JA, Benckek P, Wheeler NR, Naj AC, Hamilton-Nelson KL, Farrell JJ, Leung YY, Kunkle BW, Vardarajan BN, Schellenberg GD, Mayeux R, Wang LS, Farrer LA, Pericak-Vance M, Martin ER, Haines JL, **Crawford DC**, Bush WS. An association test of the spatial distribution of rare missense variants within protein structures identify Alzheimer's disease-related patterns. *Genome Research* 32(4):778-790 (2022). [PMC8997344](https://pubmed.ncbi.nlm.nih.gov/3997344/)
187. Waksmunski AR, Kinzy TG, Cruz LA, Nealon CL, Halladay CW, Simpson P, Canania RL, Anthony SA, Roncone DP, Sawicki Rogers LR, Leber JN, Dougherty JM, Sullivan JM, Wu W-C, Greenburg PB, Iyengar SK, **Crawford DC**, Peachey NS, Bailey JN. Glaucoma risk scores in the Million Veteran Program. *Ophthalmology* (in press). \*\*\*This article was selected for an oral presentation (Waksmunski) at the Association for Research in Vision and Ophthalmology Conference (ARVO), Denver, Colorado, May 1-4, 2022\*\*\*
188. Liu S, Bush WS, Miskimen K, Gonzalez-Vicente A, Cooke Bailey JN, Konidari I, McCauley JL, Sedor JR, O'Toole JF, **Crawford DC**. T-cell receptor diversity in minimal change disease in the NEPTUNE study. *Pediatric Nephrology* (in press).
189. Waksmunski AR, Kinzy TG, Cruz LA, Nealon CL, Halladay CW, Anthony SA, Greenberg PB, Sullivan JM, Wu W-C, Iyengar SK, **Crawford DC**, Peachey NS, Cooke Bailey JN, VA Million Veteran Program. Glaucoma genetic risk scores in Hispanic Veterans in the Million Veteran Program. *Pacific Symposium on Biocomputing* (in press) \*\*\*This article was selected for an oral presentation (Waksmunski) at the Association for Research in Vision and Ophthalmology Conference (ARVO), Denver, Colorado, May 1-4, 2022\*\*\*
190. Darst BF, Madduri RK, Rodriguez AA, Xiao Y, Sheng X, Saunders EJ, Dadaev T, Brook MN, Hoffmann TJ, Muir K, Wan P, Le Marchand L, Wilkens L, Wang Y, Schleutker J, MacInnis RJ, Cybulski C, Neal DE, Nordestgaard BG, Nielsen SF, Batra J, Clements JA, Australian Prostate Cancer BioResource, Grönberg H, Pashayan N, Travis RC, Park JY, Albanes D, Weinstein S, Mucci LA, Hunter DJ, Penney KL, Tangen CM, Hamilton RJ, Parent M-E, Stanford JL, Koutros S, Wolk A, Sørensen KD, Blot WJ, Yeboah ED, Mensah JE, Lu Y-J, Thibodeau SN, West CM, Maier C, Kibel AS, Cancel-Tassin G, Menegaux F, John EM, Grindedal EM, Khaw K-T, Ingles SA, Vega A, Rosenstein BS, Teixeira MR, NC-LA PCaP Investigators, Kogevinas M, Cannon-Albright L, Huff C, Multigner L,

- Kaneva R, Leach RJ, Brenner H, Hsing AW, Kittles RA, Murphy AB, Logothetis CJ, Neuhausen SL, Isaacs WB, Nemesure B, Hennis AJ, Carpten J, Pandha H, De Ruyck K, Xu J, Razack A, Teo S-H, Canary PASS Investigators, Newcomb LF, Fowke J, Neslund-Dudas C, Rybicki BA, Gamulin M, Usmani N, Claessens F, Gago-Dominguez M, Castela JE, Townsend PA, **Crawford DC**, Petrovics G, Casey G, Roobol MF, Hu JF, Berndt SI, Van Den Eeden SK, Easton DF, Chanock SJ, Cook MB, Wiklund F, Witte JS, Eeles RA, Kote-Jarai Z, Watya S, Gaziano JM, Justice AC, Conti DV, Haiman CA, on behalf of the VA Million Veteran Program. Evaluating approaches for constructing polygenic risk scores for prostate cancer in men of African and European ancestry. (submitted)
191. Drouet DE, Liu S, **Crawford DC**. Assessment of population-appropriate polygenic risk scores for lipid traits in African Americans. (submitted).
192. Tragante V, Sulem P, Thorleifsson G, Frigge ML, Arthur JG, Asselbergs FW, **Crawford DC**, Deaton AM, Eyjolfsson GI, Gretarsdottir S, Halldorsson GH, Helgadóttir A, Jonsdóttir I, Kristjansson RP, Melsted P, Oddson A, Olafsson I, Palsson R, Sigurdardóttir O, Sigurdsson JK, Sveinbjornsson G, Masson G, Arner DO, Torgeirsson G, Thorsteinsdóttir U, Gudbjartsson DF, Holm H, Stefansson K. Genome-wide association analysis of resistant hypertension identifies 24 risk variants and implicates potassium and aldosterone pathways (submitted).  
\*\*\*This article was selected for an oral presentation (Tragante) at the European Society of Human Genetics, Gothenburg, Sweden, June 15-18, 2019\*\*\*

### **PEER-REVIEWED REVIEWS**

2001

1. **Crawford DC**, Acuña JM, and Sherman SL. *FMRI* and the fragile X syndrome: Human genome epidemiology review. *Genetics in Medicine*, 3(5):359-371 (2001). [PMC4493892](#)

2005

2. **Crawford DC** and Nickerson DA. Definition and clinical importance of haplotypes. *Annual Review of Medicine* 56:303-320 (2005). [PMID: 15660514](#)
3. **Crawford DC**, Akey DT, and Nickerson DA. The patterns of natural variation in human genes. *Annual Review of Genomics and Human Genetics* 6:287-312 (2005). [PMID: 16124863](#)

2007

4. **Crawford DC**, Ritchie MD, Rieder MJ. Identifying the genotype behind the phenotype: a role model found in *VKORC1* and its association with warfarin dosing. *Pharmacogenomics* 8(5):487-496 (2007). [PMC3112050](#)

2009

5. Turner SD, **Crawford DC**, Ritchie MD. Methods for optimizing statistical analyses in pharmacogenomics research. *Expert Reviews in Clinical Pharmacology* 2(5):559-570 (2009). [PMC2835152](#)

2014

6. **Crawford DC**, Crosslin DR, Tromp G, Kullo IJ, Kuivaniemi H, Hayes MG, Denny JC, Bush WS, Haines JL, Roden DM, McCarty CA, Jarvik GP, Ritchie MD. eMERGEing progress in genomics---the first seven years. *Frontiers in Genetics* 5:184 (2014). [PMC4060012](#)

2015

7. **Crawford DC**, Goodloe R, Farber-Eger E, Boston J, Pendergrass SA, Haines JL, Ritchie MD, Bush WS. Leveraging epidemiologic and clinical collections for genomic studies of complex traits *Human Heredity* 79(3-4):137-146 (2015). [PMC4528966](#)
8. Pendergrass SA, Verma A, Okula A, Hall M, **Crawford DC**, Ritchie MD. Phenome-wide association studies: embracing complexity for discovery. *Human Heredity* 79(3-4):111-123 (2015). [PMID: 26201697](#)
- 2016
9. Tyler AL, **Crawford DC**, Pendergrass SA. The detection and characterization of pleiotropy: discovery, progress, and promise. *Briefings in Bioinformatics* 17(1):13-22 (2016). [PMID: 26223525](#)
10. Bush WS, **Oetjens MT**, **Crawford DC**. Unravelling the human genome-phenome relationship using phenome-wide association studies. *Nature Reviews Genetics* 17(3):129-145 (2016). [PMID: 26875678](#)
- 2019
11. **Crawford DC\***, Cooke Bailey JN\*, Briggs FBS\*. Mind the gap: Resources required to receive, process, and interpret research-returned whole genome data. *Human Genetics* 138(7):691-701 (2019). [PMC6767905](#)
12. Bush WS, Cooke Bailey JN, Beno MF, **Crawford DC**. Bridging the gaps in personalized medicine value assessment: A review of the need for outcome metrics across stakeholders and scientific disciplines. *Public Health Genomics* 22(1-2):16-24 (2019). [PMC6752968](#)
- 2020
13. Ong E\*, Wang LL\*, O'Toole JF, Schaub J, Steck B, Rosenberg AZ, Dowd F, Barisoni L, Jain S, De Boer I, Valerium MT, Waikar SS, Park C, **Crawford DC**, Alexandrov T, Anderton C, Stoeckert C, Weng C, Diehl AD, Mungall C, Haendel M, Robinson PN, Himmelfarb J, Iyengar R, Kretzler M, Mooney S\*, He Y\*. Modeling Kidney Disease Using Ontology: Perspectives from the KPMP *Nature Reviews Nephrology* 16(11):686-696 (2020). [PMC8012202](#)
- 2022
14. **Liu S**, **Crawford DC**. Maturation and application of phenome-wide association studies. *Trends in Genetics* 38(4):353-363 (2022). [PMC8930498](#)

### **OTHER PUBLICATIONS**

- 2007
1. Williams SM, Canter JA, **Crawford DC**, Moore JH, Ritchie MD, and Haines JL. Problems with genome-wide association studies. *Science* 316(5833):1840-1842 (2007). [PMID: 17605173](#)
- 2010
2. Atkinson EJ, McDonnell SK, Witte JS, **Crawford DC**, Fan Y, Fridley B, Li D, Li L, Rodin A, Sadee W, Speed T, Weiss ST, Yang J, Yerges L, and Schaid DJ. Conference Scene: Lessons learned from the 5th Statistical Analysis Workshop of the Pharmacogenetics Research Network. *Pharmacogenomics* 11(3):297-303 (2010). [PMID: 20235785](#)
- 2011
3. McCarty CA, Chisolm RL, Chute CG, Kullo IJ, Jarvik GP, Larson EB, Masys DR,



- Ritchie MD, Roden DM, Struewing JP, Wolf WA; **eMERGE Team**. The eMERGE Network: a consortium of biorepositories linked to electronic medical records data for conducting genomic studies. *BMC Med Genomics* 4:13 (2011). [PMC3038887](#)
4. Turner S, Armstrong LL, Bradford Y, Carlson CS, **Crawford DC**, Crenshaw AT, de Andrade M, Doheny KF, Haines JL, Hayes GM, Jarvik G, Jiang GL, Ling H, Kullo IJ, Li R, Manolio TA, Matsumoto M, McCarty CA, McDavid AN, Mirel DB, Paschall JE, Pugh E, Rasmussen LV, Wilke RA, Zuvich RL, Ritchie MD. Quality Control Procedures for Genome Wide Association Studies. *Current Protocols in Human Genetics* Chapter 1: Unit 1.19 (2011). [PMC3066182](#)
5. **Crawford DC** and Dilks H. Strategies for Genotyping. *Current Protocols in Human Genetics* Chapter 1: Unit 1.3 (2011). [PMID: 21234876](#)
- 2014
6. Tyler AL, **Crawford DC**, Pendergrass SA. Detecting and characterizing pleiotropy: new methods for uncovering the connection between the complexity of genomic architecture and multiple phenotypes- session introduction. *Pacific Symposium on Biocomputing* 19:183-187 (2014). [PMC4108263](#)
- 2015
7. Pers TH, Karjalainen JM, Chan Y, Westra H-J, Wood AR, Yang J, Lui JC, Vedantam S, Gustafsson S, Esko T, Frayling T, Speliotes EK, **Genetic Investigation of Anthropometric Traits (GIANT) Consortium**, Boehnke M, Raychaudhuri S, Fehrmann RSN, Hirschhorn JN, Franke L. Biological interpretation of genome-wide association studies using predicted gene function. *Nature Communications* 6:5890 (2015). [PMC4420238](#)
- 2016
8. Bush WS, **Crawford DC**. Invited Editorial: Predicting incident coronary heart disease many markers at a time. *Circulation: Cardiovascular Genetics* 9:472-473 (2016).
- 2017
9. Morgan AA, **Crawford DC**, Denny JC, Mooney SD, Aronow, BJ, Brenner SE. Precision medicine: Data and discovery for improved health and therapy. *Pacific Symposium on Biocomputing* 22:348-355 (2017). [PMC6192531](#)
10. Haddad SA, Palmer JR, Lunetta KL, Ng NC, **MEDIA Consortium**, Ruiz-Narvaez EA. A novel *TCF7L2* type 2 diabetes SNP identified from fine mapping in African American women. *PLoS One* 12(3):e0172577 (2017). [PMC5333820](#)
11. Rusu V, Hoch E, Mercader JM, Tenen DE, Gymrek M, Hartigan CR, DeRan M, von Grotthuss M, Fontanillas P, Spooner A, Guzman G, Deik AA, Pierce KA, Dennis C, Clish CB, Carr SA, Wagner BK, Schenone M, Ng MCY, Chen BH, **MEDIA Consortium**, SIGMA T2D Consortium, Centeno-Cruz F, Zerrweck C, Orozco L, Altshuler DM, Schreiber SL, Florez JC, Jacobs SBR, Lander ES. Type 2 diabetes variants disrupt function of *SLC16A11* through two distinct mechanisms. *Cell* 170(1):199-212 (2017). [PMC5562285](#)
- 2018
12. **Crawford DC**, Morgan AA, Denny JC, Aronow BJ, and Brenner SE. Precision medicine: from diplotypes to disparities towards improved health and therapies. *Pacific Symposium on Biocomputing* 23:389-399 (2018). [PMC6182117](#)
13. Bush WS, **Crawford DC**, Briggs F, Freedman D. Integrating community-level data resources for precision medicine research. *Pacific Symposium on Biocomputing* 23:618-

- 622 (2018).
14. Zhan J, **CHARGE ECG Working Group**, Arking DE, Bader JS. Discovering patterns of pleiotropy in genome-wide association studies *bioRxiv* 273540 (2018). [doi.org/10.1101/273540](https://doi.org/10.1101/273540)
- 2019
15. Pendergrass SA, **Crawford DC**. Using Electronic Health Records to Generate Phenotypes for Research. *Current Protocols in Human Genetics* 100(1):e80 (2019). [PMC6318047](https://pubmed.ncbi.nlm.nih.gov/36318047/)
  16. Brenner SE, Bulyk M, **Crawford DC**, Morgan AA, Radivojac P. Precision Medicine: improving health through high-resolution analysis of personal data. *Pacific Symposium on Biocomputing* 24:220-223 (2019). [PMC6526370](https://pubmed.ncbi.nlm.nih.gov/36526370/)
- 2020
17. Brenner SE, Bulyk ML, **Crawford DC**, Morgan AA, Radivojac P, Tatonetti NP. Precision Medicine: addressing the challenges of sharing, analysis, and privacy at scale. *Pacific Symposium on Biocomputing* 25:547-550 (2020).
  18. Cooke Bailey JN, Bush WS, **Crawford DC**. Editorial: The importance of diversity in precision medicine research. *Frontiers in Genetics* 11:875 (2020). [PMC7479241](https://pubmed.ncbi.nlm.nih.gov/37479241/)
- 2021
19. Afanasiev O, Berghout J, Brenner S, Bulyk ML, **Crawford DC**, Chen JH, Daneshjou R, Kidziński L. Computational challenges and artificial intelligence in precision medicine *Pacific Symposium on Biocomputing* 26:166-171 (2021). [PMID: 33691014](https://pubmed.ncbi.nlm.nih.gov/33691014/)
  20. **Crawford DC** and Williams SM. Viewpoint: Global variation in sequencing impedes SARS-CoV-2 surveillance *PLoS Genetics* 17(7):e1009620 (2021). [PMC8282079](https://pubmed.ncbi.nlm.nih.gov/38282079/)
  21. **Crawford DC** and Sedor JR. Editorial: Biobanks linked to electronic health records accelerate genomic discovery *Journal of American Society of Nephrology* 32(8):1828-1829 (2021). [PMC8455265](https://pubmed.ncbi.nlm.nih.gov/38455265/)
  22. Schmidt IM, Colona MR, Kestenbaum BR, Alexopoulos LG, Palsson R, Srivastava A, Liu J, Stillman IE, Rennke HG, Vaidya VS, Wu H, Humphreys BD, Waikar SS; **Kidney Precision Medicine Project (KPMP)**. Cadherin-11, Sparc-related modular calcium binding protein-2, and Pigment epithelium-derived factor are promising non-invasive biomarkers of kidney fibrosis *Kidney International* 100(3):672-683 (2021). [PMC8384690](https://pubmed.ncbi.nlm.nih.gov/38384690/)
- 2022
23. Daneshjou R, Brenner SE, Chen JH, **Crawford DC**, Finlayson SG, Kidziński Ł, Bulyk ML. Precision Medicine: Using Artificial Intelligence to Improve Diagnostics and Healthcare. *Pacific Symposium on Biocomputing* 27:223-230 (2022). [PMID: 34890151](https://pubmed.ncbi.nlm.nih.gov/34890151/)
  24. Butler CR, Appelbaum PS, Ascani H, Aulisio M, Campbell CE, de Boer IH, Dighe AL, Hall DE, Himmelfarb J, Knight R, Mehl K, Murugan R, Rosas SE, Sedor JR, O'Toole JF, Tuttle KR, Waikar SS, Freeman M; **Kidney Precision Medicine Project**. A participant-centered approach to understanding risks and benefits of participation in research informed by the **Kidney Precision Medicine Project**. *American Journal of Kidney Diseases* 80(1):132-138 (2022). [PMC9166631](https://pubmed.ncbi.nlm.nih.gov/39166631/)
  25. Menon R, Bomback AS, Lake BB, Stutzke C, Grewenow SM, Menez S, D'Agati VD, Jain S; **Kidney Precision Medicine Project**. Integrated single-cell sequencing and histopathological analyses reveal diverse injury and repair responses in a participant with acute kidney injury: a clinical-molecular-pathologic correlation. *Kidney International* 101(6):1116-1125 (2022).

## **BOOK CHAPTERS**

1. **Crawford DC** and Sherman SL. Fragile X Syndrome: Application of Gene Identification to Clinical Diagnosis and Population Screening. In Khoury MJ, Little J, and Burke W (eds) Human Genome Epidemiology: A Scientific Foundation for Using Genetic Information to Improve Health and Prevent Disease. New York: Oxford University Press (2003). <https://www.cdc.gov/genomics/resources/books/HuGE/chap23.htm>
2. **Crawford DC** and Howard-Peebles PN. Fragile X: From Cytogenetics to Molecular Genetics. In Gersen S and Keagle M (eds) The Principles of Clinical Cytogenetics. 2<sup>nd</sup> edition. New Jersey: Humana Press Inc (2004).
3. Ritchie MD, **Crawford DC**, Haines JL. A Primer in Statistical Methods in Genetics. In Roden DM (ed) Cardiovascular Genetics and Genomics. 1st edition. Blackwell Publishing (2008).
4. Dumitrescu L, **Crawford DC**. Study Designs in Genetic Epidemiology. In Genetic Analysis of Complex Disease. Available from: VitalSource Bookshelf, (3rd Edition). Wiley Global Research (STMS) (2021).

## **MEDIA**

Big Data in Medical Research. WCPN's *The Sound of Ideas*, Ideastream Public Media, April 26, 2017. <http://www.ideastream.org/programs/sound-of-ideas/nprs-tom-gjeltten-big-data-in-medical-research-q-funding-update>

How has the society benefited your career? American Society of Human Genetics (ASHG) TV, October 19, 2017. <https://www.youtube.com/watch?v=2ylz8oBzuR0>

Chakradhar S. Calculated risk. *Nature Medicine* 25:6-8 (2019). <https://rdcu.be/bfKP8>

Pioneering Geneticist's Podcast Plums Race and Ancestry, LaMont Jones, *Diverse*, May 29, 2019. <https://diverseeducation.com/article/146348/>

In-depth sequencing of SARS-CoV-2 variants crucial in controlling outbreaks. Emily Henderson, Thought Leaders, *News-Medical*, August 2, 2021. <https://www.news-medical.net/news/20210802/In-depth-sequencing-of-SARS-CoV-2-variants-crucial-in-controlling-outbreaks.aspx>

How genomic sequencing makes it possible to track omicron variant spread. Peter O'Dowd, WBUR's *Here and Now*, National Public Radio, Boston, December 1, 2021. <https://www.wbur.org/hereandnow/2021/12/02/genomic-sequencing-omicron>

Why hasn't the U.S. found more Omicron cases? Emily Anthes, the *New York Times*, December 2, 2021. <https://www.nytimes.com/2021/12/02/health/coronavirus-omicron-genetic-surveillance.html?referringSource=articleShare>

Omicron emphasizes the importance of genomic surveillance. Yasmin Tayag, *The Capsule*, Fortune newsletter, December 2, 2021. <https://fortune.com/2021/12/02/covid-variants-omicron-genomic-surveillance/?tpcc=nlcapsule>

### **POSTER PRESENTATIONS FROM SUBMITTED ABSTRACTS**

1996

1. **Crawford D**, Newman J, Meadows K, Ashley A, and Sherman S. Evidence for increased homozygosity in the CGG trinucleotide repeat allele of *FRAXA* and *FRAXE* in a large normal population. American Society of Human Genetics, San Francisco, California, October 29-November 3, 1996.

1997

2. **Crawford DC**, Newman JL, Meadows KL, Taft LF, and Sherman SL. *FRAXA* and haplotype associations: Significant differences between African-American and Caucasian populations. American Society of Human Genetics, Baltimore, Maryland, October 28-November 2, 1997.

1998

3. Gunter C, **Crawford DC**, Iber JC, Sherman SL, and Warren ST. Use of SNP-based haplotypes allows for redefinition of “predisposing factors” for repeat expansion at the *FMR1* locus. American Society of Human Genetics, Denver, Colorado, October 27-31, 1998.

1999

4. **Crawford DC**, Schwartz CE, Warren ST, Sherman SL. Novel repeat structures identified in African-Americans represent a new mechanism leading to fragile X CGG repeat instability. American Society of Human Genetics, San Francisco, California, October 19-23, 1999.
5. **Crawford DC**, Meadows KL, Gunter C, Newman JL, Schwartz CE, Warren ST, Sherman SL. Examination of factors associated with expansion of CGG repeats in an African-American population. 9<sup>th</sup> International Workshop on Fragile X Syndrome and X-linked Mental Retardation, Strasbourg, France, August 23-25, 1999.

2000

6. Sullivan AK, **Crawford DC**, Meadows KL, Wilson B, Sherman SL. Parent-child transmission of intermediate *FMR1* CGG repeat alleles: Examination of factors associated with repeat instability. American Society of Human Genetics, Philadelphia, Pennsylvania, October 3-7, 2000.

2001

7. **Crawford DC**, Caggana M, Temelis C, Harris KH, Lorey F, Nash C, Pass K, and Olney R. Characterization of  $\beta$ -globin haplotypes among an admixed, population-based cohort of newborns with sickle cell disease. American Society of Human Genetics, San Diego, California, October 1-16, 2001.

2003

8. Eberle MA, Carlson CS, **Crawford DC**, Rieder MJ, Nickerson DA. Selecting a minimal set of SNPs for whole-genome association studies. American Society of Human Genetics, Los Angeles, California, November 4-8, 2003.

2004

9. **Crawford DC**, Smith JD, Yi Q, Witrak L, Rieder MJ, Nickerson DA. Genetic and haplotype diversity of the C-reactive protein (*CRP*) gene in 7,000 Americans. American Society of Human Genetics, Toronto, Canada, October 26-30, 2004.
- 2007
10. **Crawford DC**. Candidate gene association studies for the intermediate phenotypes related to coronary heart disease in the Third National Health and Nutrition Examination Survey. Illumina Users Group Meeting, San Diego, California, March 15-17, 2007.
  11. **Crawford DC**, Zimmer SM, Lynfield R, Yi Q, Shephard C, Wong M, Rieder MJ, Livingston MJ, Nickerson DA, Whitney CG, Meisssonier NE, Lingappa J. Common genetic variation in *CD46* may be associated with susceptibility to *Neisseria Meningitidis*. American Society of Human Genetics, San Diego, California, October 23-27, 2007.
- 2008
12. Rieder MJ, Sanders CL, **Crawford DC**. *VKORC1* is associated with bone mineral density and osteoporosis risk in African-Americans from the Third National Health and Nutrition Examination Survey. American Society of Human Genetics, Philadelphia, Pennsylvania, November 11-15, 2008.
  13. Dumitrescu L, **Crawford D**, Zimmer S, Lynfield R, Meisssonier N, Whitney C, McNicholl J, Lingappa J. Genetic susceptibility to invasive pneumococcal disease (IPD). American Society of Human Genetics, Philadelphia, Pennsylvania, November 11-15, 2008.
  14. Brown K, Smith JD, Shephard C, Wong M, Rieder MJ, Nickerson DA, **Crawford DC**. Fasting status and dietary intake influence genetic associations for the *APOA1/C3/A4/A5* gene cluster and triglyceride levels. American Society of Human Genetics, Philadelphia, Pennsylvania, November 11-15, 2008.
  15. **Crawford D**, Ritchie MD, Denny JC, Havens A, Weiner J, Pulley JM, Basford MA, Masys DR, Roden DM, Haines JL. Electronic medical records linked to DNA: A valuable resource for large-scale genetic association studies. American Society of Human Genetics, Philadelphia, Pennsylvania, November 11-15, 2008.
  16. Denny JC, Ritchie MD, **Crawford DC**, Havens A, Weiner J, Watanabe H, Darbar D, Kannankeril PK, Pulley J, Basford M, Haines JL, Masys DR, Roden DM. Using a large electronic medical record to validate 4q25 variants conferring risk for atrial fibrillation. American Heart Association, New Orleans, Louisiana, November 8-12, 2008.
  17. Käab S, Sinner M, George A, Wilde AJJ, Bezzina C, Schulze Bahr E, Guicheney P, Bishopric N, Myerburg R, Schott JJ, Pfeufer A, Hinterseer M, Beckmann BM, Steinbeck G, Perz S, Meitinger S, Wichmann HE, Ingram C, Carter S, Norris K, **Crawford D**, Ritchie M, Roden DM. High density tag SNP candidate gene analysis identifies IKs as a major modulator of genetic susceptibility to drug induced Long QT Syndrome. American Heart Association, New Orleans, Louisiana, November 8-12, 2008.
- 2009
18. **Crawford DC**, Miller EK, Dumitrescu L, Edwards KM, Sparks R, Fawkes D, Dorris SL. The genomics of variable immune response after influenza vaccination in children: a plot study. Genetics and Genomics of Infectious Diseases, Millenia, Singapore, March 21-24, 2009.
  19. Turner SD, Bert RL, **Crawford DC**, Denny JC, Linneman JG, McCarty CA, Peissig PL, Rasmussen LV, Roden DM, Wilke RA, Ritchie MD. Knowledge-drive multi-locus

- analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent biobanks. 11<sup>th</sup> Annual Vanderbilt Human Genetics Symposium, Nashville, Tennessee, October 8, 2009.
20. **Crawford DC**, Dumitrescu L, Brown-Gentry K, Canter JA, Murdock D, Haines JL, Ritchie MD. Epidemiologic Architecture for Genes Linked to Environment (EAGLE): Characterizing genome-wide association study variations associated with inflammation in the National Health and Nutrition Examination Surveys. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  21. Brown-Gentry K, Dumitrescu L, Spencer K, Canter JA, Murdock D, Haines JL, Ritchie MD, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment (EAGLE): Characterizing genome-wide association study variations associated with type 2 diabetes in the National Health and Nutrition Examination Surveys. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  22. Dumitrescu L, Brown-Gentry K, Spencer K, Murdock D, Canter JA, Haines JL, Ritchie MD, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment (EAGLE): Characterizing genome-wide association study variations associated with lipid traits in the National Health and Nutrition Examination Surveys. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  23. Jeff J, Brown-Gentry K, Buxbaum S, Sarpong D, Taylor H, Wilson J, Payne J, Maher J, George A, **Crawford D**, Roden D. *SCN5A* variation is associated with electrocardiogram traits in the Jackson Heart Study. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  24. Ritchie MD, Dumitrescu L, Brown-Gentry K, Pulley J, Basford M, Denny J, Oksenberg JR, Roden DM, Haines JL, **Crawford DC**. Assessing the accuracy of ancestry reported in a biorepository linked to electronic medical records for genetic association studies. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  25. Matisse TC, Ambite JL, Cole SA, **Crawford DC**, Haiman CA, Kooperberg C, Le Marchand L, Manolio TA, North KE, Peters U, Ritchie MD, Hindorff LA, Haines JL, for PAGE. A new PAGE in understanding complex traits: study design for analysis of Population Architecture using Genomics and Epidemiology. American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  26. Rieder MJ, Brown-Gentry K, Canter J, **Crawford DC**. Genetic associations with lactase dehydrogenase, anion gap, and hepatitis in the Third National Health and Nutrition Examination Survey (NHANES III). American Society of Human Genetics, Honolulu, Hawaii, October 20-24, 2009.
  27. Havens A, Schildcrout J, Masys D, Weiner J, Pulley J, Basford M, Ritchie MD, **Crawford DC**, Haines JL, Roden DM, Denny JC. Modulators of normal ECG intervals identified in a large electronic medical record. American Heart Association, Orlando, Florida, November 14-18, 2009.
  28. Bastarache L, Ritchie MD, **Crawford DC**, Basford M, Denny JC. Detecting race and ethnicity using natural language processing. American Medical Informatics Association Annual Symposium, San Francisco, California, November 14-18, 2009.
  29. Käåb S, Ritchie MD, **Crawford DC**, Sinner M, Kannankeril P, Wilde A, Bezzina C, Schulze-Bahr E, Guicheney P, Bishopric N, Nyerburg R, Schott JJ, Pfeufer A, Nakamura Y, Tanaka T, Ingram CR, Crater S, Bradford Y, George AL Jr, Roden DM. Genome-wide association study identifies novel genomic regions association with drug-induced

long QT syndrome. American Heart Association, Orlando, Florida, November 14-18, 2009.

2010

30. Chang M-h, Ned RM, Yang Q, Yesupriya A, Dowling NF, Liu T, Shrader P, Florez J, Kathiresan S, Dupuis J, the MAGIC Investigators, Spencer KL, Pendergrass SA, Khoury MJ, **Crawford DC**, Meigs JB. Race/ethnic variation in type 2 diabetes (T2D)-associated loci and their association in U.S. Adults: the Third National Health and Nutrition Examination Survey (NHANES III). American Diabetes Association 70<sup>th</sup> Scientific Sessions, Orlando, Florida, June 25-29, 2010.
31. Spencer KL, Glenn K, Brown-Gentry K, Murdock D, Canter JA, Haines JL, Ritchie MD, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment (EAGLE): Association of *ARMS2* A69S with Age-related Macular Degeneration in the National Health and Nutrition Examination Surveys. The Association for Research in Vision and Ophthalmology (ARVO), Fort Lauderdale, Florida, May 2-6, 2010.
32. Dumitrescu L, Ritchie MD, Denny J, Pulley J, Basford M, Ramirez A, Masys DR, Haines J, Roden DM, **Crawford DC**. On the utility of biobanks linked to electronic health records in genome-wide association studies. Human Genome Organisation (HUGO), Montpellier, France, May 17-21, 2010.
33. Dumitrescu L, **Crawford DC**, Pendergrass SA, Taylor K, Carty C, Quibrera M, Franceschini N, Cole SA, Schumacher F, Fornage M, Eaton CB, Buyske S, Hindorff L, Manolio TA, MacCluer J, Brown-Gentry K, Buzkova P, Carlson CS, Haessler J, Anderson G, Johnson K, Laston S, Cochran B, Lee ET, Best LG, Devereuz RB, Howard B, Kooperberg C, North KE. Generalizability of GWAS-identified SNPs association with lipids traits in the Population Architecture using Genomics and Epidemiology (PAGE) Study. The Genomics of Common Diseases, Houston, Texas, October 6-9, 2010.
34. Pendergrass SA, Brown-Gentry K, Dudek S, Ambite JL, Avery CL, Buyske S, Cai C, Heiss G, Hindorff L, Kooperberg C, Lin Y, Manolio TA, Matisse T, Wilkens L, Fesinmeyer MD, Hsu C, **Crawford DC**, Ritchie MD. Phenotype-wide association study (PheWAS) within the multi-ethnic studies of the Population Architecture using Genomics and Epidemiology (PAGE) network. The Genomics of Common Diseases, Houston, Texas, October 6-9, 2010.
35. Pendergrass SA, Dudek SM, **Crawford DC**, Ritchie MD. Synthesis-View: visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. International Genetic Epidemiology Society, Boston, Massachusetts, October 10-12, 2010.
36. Turner SD, Berg RL, **Crawford DC**, Denny JC, Linneman JG, McCarty CA, Peissig PL, Rasmussen LV, Roden DM, Wilke RA, Ritchie MD. Knowledge-driven multi-locus analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent biobanks. International Genetic Epidemiology Society, Boston, Massachusetts, October 10-12, 2010.
37. Ritchie M, Armstrong L, Bradford Y, Carlson C, **Crawford DC**, Crenshaw AT, de Andrade M, Doheny K, Haines JL, Hayes G, Jarvik G, Jiang L, Ling H, Kullo I, Li R, Manolio TA, Matsumoto M, McCarty CA, McDavid A, Mirel D, Olson L, Paschall J, Pugh E, Rasmussen LV, Wilke RA, Zuvich RL, Turner SD. Quality control pipeline for genome-wide association studies in the eMERGE Network: Comparing single site QC to

- a merged QC approach. International Genetic Epidemiology Society, Boston, Massachusetts, October 10-12, 2010.
38. **Crawford DC**, Dumitrescu L, Pendergrass SA, Taylor K, Carty C, Quibrera M, Franceschini N, Cole SA, Schumacher F, Fornage M, Eaton CB, Buyske S, Hindorff L, Manolio TA, MacCluer J, Brown-Gentry K, Buzkova P, Carlson CS, Haessler J, Anderson G, Johnson K, Laston S, Cochran B, Lee ET, Best LG, Devereux RB, Howard B, Kooperberg C, North KE. Generalizability of GWAS-identified SNPs association with lipids traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  39. Glenn K, Brown-Gentry K, Allen M, Mayo P, Schnetz-Boutaud N, **Crawford DC**, Thornton-Wells TA. Replication and generalization of genetic risk factors for depression, anxiety and panic attack in European, African, and Mexican Americans from the National Health and Nutrition Examination Surveys. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  40. Spencer KL, Glenn K, Brown-Gentry K, Murdock D, Haines JL, Ritchie MD, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment (EAGLE): Association of *ABCG2* Q141K with Uric Acid Concentration and Gout in the National Health and Nutrition Examination Surveys. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  41. Dudek SM, Pendergrass SA, **Crawford DC**, Ritchie MD. Synthesis-View: Visualization and interpretation of SNP association results for multi-cohort, multi-phenotype data and meta-analysis. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  42. Jeff J, Ramirez A, Denny J, Kho A, Ritchie M, Hayes M, Armstrong L, Basford M, Wolf W, Pacheco J, Chisholm R, Roden D, **Crawford D**. Using electronic health records for genome-wide association studies and admixture mapping to identify SNPs associated with ECG traits in African Americans. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  43. Rampersaud E, Edwards T, Monda K, Norht K, Carlson C, Smoller-Wassertheil S, Neuhaus M, **Crawford D**, Liu S, O'Sullivan M, Edwards DRV, Naj A. Investigation of *FTO* variants and interactions with physical activity among 3,484 Hispanic postmenopausal women in the Women's Health Initiative. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  44. Turner SD, Berg RL, **Crawford DC**, Denny JC, Linneman JG, McCarty CA, Peissig PL, Rasmussen LV, Roden DM, Wilke RA, Ritchie MD. Knowledge-driven multi-locus analysis reveals gene-gene interactions influencing HDL cholesterol level in two independent biobanks. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  45. Ritchie MD, Armstrong L, Bradford Y, Carlson C, **Crawford D**, Crenshaw A, de Andrade M, Doheny K, Haines J, Hayes G, Jarvik G, Jiang L, Ling H, Kullo I, Li R, Manolio T, Matsumoto M, McCarty C, McDavid A, Mirel D, Olson L, Paschall J, Pugh E, Rasmussen L, Wilke R, Zuvich R, Turner S. Quality control pipeline for genome-wide association studies in the eMERGE Network: Comparing single site QC to a merged QC approach. American Society of Human Genetics, Washington, DC, November 2-6, 2010.



46. Dumitrescu L, Glenn K, Brown-Gentry K, Shephard C, Wong M, Rieder MJ, Smith JD, Nickerson DA, **Crawford DC**. *LPA* common variation is associated with Lp(a) levels and myocardial infarction in non-Hispanic blacks in the Third National Health and Nutrition Examination Survey. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  47. Denny JC, Bastarache L, Basford M, Ritchie MD, Pulley J, Bowton E, McCarty C, Peissig P, Rasmussen L, Masys DR, **Crawford DC**, Roden DM. Phenome-wide association study on 40 loci replicates 22 known associations and proposes new disease-SNP associations. American Society of Human Genetics, Washington, DC, November 2-6, 2010.
  48. Denny JC, Bastarache L, **Crawford DC**, Ritchie MD, Basford MA, Pulley JM, Roden DM, Masys DR. Scanning the EMR Phenome for Gene-Disease Associations using Natural Language Processing. American Medical Informatics Association, Washington, DC, November 13-17, 2010.
  49. Clark W, **Crawford D**, Engelhardt B, Brown KD, Kang-Hsien F, Chen H, Savani BN, Schuening F, Greer JP, Kassim AA, Jagasia M. American Society of Hematology, Orlando, Florida, December 4-7, 2010.
- 2011
50. North KE, Buyske S, Boerwinkle E, Ballantyne CM, Jenny NS, Rodriguez CJ, Buzkova P, Schumacher F, Cheng I, Matisse TC, Dumitrescu L, Franceschini N, Cole SA, Kooperberg C, Peters U, Fesinmeyer M, Haessler J, Duggan D, Haiman C, Young A, Lin Y, Assimes TL, Eaton CB, Robinson JG, Le Marchand L, Ambite JL, Hindorff L, Fornage M, Carty C, Manolio TA, MacCluer J, Laston S, Cochran B, Lee ET, Best LG, Howard B, Heiss, **Crawford DC**. The generalization of GWAS based genetic effects for lipid traits in African Americans: the PAGE study. Joint conference – Nutrition, Physical Activity and Metabolism and Cardiovascular Disease Epidemiology and Prevention 2011 Scientific Sessions, Atlanta, Georgia, March 22-25, 2011.
  51. Pendergrass SA, Brown-Gentry KD, Dudek S, Torstenson E, Goodloe R, Ambite J-L, Avery CL, Buyske S, Fesinmeyer MD, Hindorff LA, Kooperberg C, Le Marchand L, Lin Y, Matisse T, Wilken LR, Hsu C-N, **Crawford DC**, Ritchie MD. Phenome-wide association study (PheWAS) for detection of novel SNP-phenotype relationships within the Population Architecture using Genomics and Epidemiology (PAGE) Network. Cold Spring Harbor High Throughput Biology, Suzhou, China, April 19-23, 2011.
  52. Schumacher FR, North KE, Haessler J, Spencer KL, Franceschini N, Monroe KR, Howard BV, Jackson RD, Kao WHL, Kolonel LN, Liu S, Aroda V, Kuller LH, Wilkens LR, Hindorff LA, Ambite J-L, Le Marchand L, **Crawford DC**, Buyske S, Pankow JS, Peters U, Haiman CA. Fine-mapping of type 2 diabetes risk loci in African Americans using the MetaboChip: the PAGE study. American Diabetes Association, San Diego, California, June 24-28, 2011.
  53. Matisse TC, Carlson CS, **Crawford DC**, Haiman CA, Heiss G, Kooperberg C, Le Marchand L, Manolio TA, North KE, Peters U, Ritchie MD, Hindorff LA, Haines JL, for the PAGE Study. Population Architecture using Genomics and Epidemiology: The PAGE Study. Gordon Research Conference, Human Genetics & Genomics, Salve Regina University, Newport, Rhode Island, July 17-24, 2011.
  54. Dumitrescu L, Goodloe R, Brown-Gentry K, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment: Serum vitamins A and E modify HDL-C, LDL-C, and triglyceride GWAS-identified associations in the National Health and Nutrition

- Examination Surveys. The Genomics of Common Diseases, Hinxton, Cambridge, UK, August 30-September 2, 2011.
55. Pendergrass SA, Torstenson ES, Ambite JL, Avery CL, Cai C, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Kooperberg C, Le Marchand L, Lin Y, Matisse TC, Monroe K, North KE, Wilkens LR, Buyske S, **Crawford DC**, Ritchie MD. Phenome-wide association study (PheWAS) for exploration of novel genotype-phenotype associations and pleiotropy using MetaboChip in the PAGE Study. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  56. Kocarnik J, Pendergrass S, Carty C, Pankow J, Schumacher F, Cheng I, Durda P, Junkins, H, Cook N, Liu S, Wactawshi-Wende J, LaCroix A, Jackson B, **Crawford D**, Gross M, Peters U, on behalf of the PAGE Consortium. Exploration of pleiotropic effects of inflammation-related disease GWAS SNPs with C-reactive protein levels in the PAGE Study. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  57. Wu Y, Buyske S, Assimes T, Adair LS, Ballantyne C, Carty C, Cheng I, Duggan D, Dumitrescu L, Eaton CB, Feranil AB, Hindorff LA, Matisse T, Mitchell S, Lin Y, Manolio TA, Peters U, Robinson JG, Schumacher F, Young A, Kooperberg C, **Crawford D**, Mohlke KL, North KE. Fine-mapping of lipid loci in multi-ethnic populations detects known functional variants. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  58. Bush W, North KE, Buyske S, **Crawford D**, and the PAGE Study. A population genetics analysis of MetaboChip data comparing African-American and European-descent populations. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  59. Zhang L, Spencer KL, Voruganti S, Jorgensen N, Fornage M, Best L, Brown-Gentry KD, Cole S, **Crawford DC**, Franceschini N, Gaffo A, Glenn KR, Heiss G, Jenny NS, Kottgen A, Li Q, Liu K, North KE, Umans JG, Kao WHL. Characterization of the associations between rs2231142 (Q141K) in *ABCG2* and serum uric acid and gout in four U.S. Populations: the PAGE Study. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  60. Liu Y, Buyske S, Aragaki A, Peters U, Boerwinkle E, Carlson C, Carty C, **Crawford DC**, Haessler J, Haiman C, Hindorff L, Le Marchand L, Manolio T, Matisse T, Wang W, Kooperberg C, North KE, Li Y. Genotype imputation of MetaboChip SNPs using a study specific reference panel of 3,924 haplotypes in African Americans for the Women's Health Initiative. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  61. Mitchell S, Brown-Gentry KD, Mayo P, Allen M, Schnetz-Boutaud N, Murdock D, **Crawford DC**. Distribution of mitochondrial haplogroups in the National Health and Nutrition Examination Surveys. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  62. Taylor KC, North KE, Carty CL, Dumitrescu L, Hindorff LA, Schumacher FR, Quibrera M, Cole SA, Buyske S, Buzkova P, Brown-Gentry K, Franceschini N, Wilkens LR, Duggan D, Eaton CB, Cochran B, Haiman CA, Le Marchand L, Kooperberg C, the PAGE Study, **Crawford DC**, Fornage M. Replication and discovery of lipid-related loci exhibiting heterogeneity by sex in the Population Architecture using Genomics and

- Epidmeiology (PAGE) Study. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
63. Schumacher FR, North KE, Haessler J, Spencer KL, Franceschini N, Monroe KR, Howard BV, Jackson RD, Kao WHL, Kolonel LN, Liu S, Aroda V, Kuller LH, Wilkens LR, Hindorff LA, Ambite J-L, Le Marchand L, **Crawford DC**, Buyske S, Pankow JS, Peters U, Haiman CA. Fine-mapping of type 2 diabetes risk loci in African Americans using the MetaboChip: the PAGE study. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  64. Bourgeois S, Eriksson N, Jorgensen A, Nilsson C, Burkley B, Wadelius M, Pirmohamed M, Rane A, Lindh J, Rieder MJ, Burmester JK, Caldwell MD, Mushiroda T, Kubo M, Wu A, Roden D, **Crawford D**, Wagner M, Svensson P, Scott S, Desnick R. Klein TE, Nakamura Y, Johnson JA, Deloukas P, International Warfarin Consortium. Meta-analysis of warfarin stable dose in Caucasians. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  65. Ritchie MD, Zuvich RL, Denny JC, **Crawford DC**, Schildcrout JS, Ramirez AH, Pully JM, Basford MA, Chute CG, Kullo IJ, McCarty CA, Chisholm RL, Kho AN, Larson EB, Jarvik GP, Li R, Masys DR, Haines JL, Roden DM, CHARGE, QRS GWAS Consortium. Genome-wide analysis of variability in normal cardiac conduction across multiple electronic medical record systems. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  66. Hayes MG, Kho A, Armstrong LL, Ritchie MD, Pacheco JA, Rasmussen-Torvik L, Just EM, Denny J, **Crawford DC**, Peissig P, Rasmussen LV, Wei W, de Andrade M, Kullo IJ, Crosslin DR, Mirel D, Crenshaw A, Doheny KF, Pugh E, Wolf WA, Lowe WL, Roden DA, Chisholm RL. Use of diverse electronic medical record systems for a genome-wide association study of type 2 diabetes in European- and African-ancestry populations. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  67. Malinowski JR, Denny JC, Bielinski SJ, Basford MA, Bradford Y, Chai HS, Peissig PL, Carrell D, Pathak J, Wilke RA, Rasmussen L, Wang X, Pacheco JA, Kho A, Weston N, Matsumoto M, Newton KM, Li R, Kullo IJ, Chute CG, Chisholm RL, Larson EB, McCarty CA, Masys DR, Roden DM, de Andrade M, Ritchie MD, **Crawford DC** on behalf of the eMERGE Network. Leveraging resources in biobanks from the eMERGE Network: A genome-wide associatoin study of thyroid stimulating hormone levels in European Americans and African Americans. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  68. Jeff J, Armstrong L, Ritchie M, Denny J, Kho A, Basford M, Wolf W, Pacheco J, Doheny K, Mirel D, Pugh E, Crenshaw A, Li R, Manolio T, Chisholm R, Roden D, Hayes G, **Crawford D**. Admixture mapping reveals potential novel loci for type II dibetes in African Americans using electronic medical records as a tool for genome science. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
  69. Denny J, Bastarche L, Ritchie M, Basford M, Pulley J, Zuvich R, Peissig P, Carrell D, Pathak J, Rasmussen L, Pacheco J, Kho A, Weston N, Pendergrass S, Xu H, Li R, Manolio T, Kullo I, Chute C, Chisholm R, Larson E, McCarty C, Masys D, Roden D, **Crawford D**. A phenome-wide analysis of SNPs in the National Human Genome

- Research Institute genome-wide association catalog. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
70. Crosslin D, McDavid A, Weston N, Nelson S, Zheng X, Hart E, de Andrade M, Kullo I, McCarty C, Doheny K, Pugh E, Kho A, Hayes M, Pretel S, Saip A, Ritchie M, **Crawford D**, Crane P, Newton K, Mirel D, Crenshaw A, Larson E, Carlson C, Jarvik G, electronic Medical Records and Genomics (eMERGE) Network. Genetic variation that predicts white blood cell count differential leukocyte types in the eMERGE Network. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
71. Oetjens MT, Denny JC, Baker AR, Dilks HH, Basford MA, Bowton E, Restrepo NA, Youngblood VM, Pulley JM, Roden DM, Masys DDR, Ritchie MD, Crawford DC. Assessment of a pharmacogenomic marker panel in a population taking multiple medications derived from electronic medical records. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.
- 2012
72. Dumitrescu L, Ritchie MD, Denny JC, Bielinski SJ, Peissig P, Pacheco JA, Hayes MG, Jarvik GP, Li R, Kullo IJ, Chute CG, Chisholm RL, Larson EB, McCarty CA, Roden DM, de Andrade M, **Crawford DC**, on behalf of the eMERGE Network. Genome-wide study of resistant hypertension using existing genome data and electronic medical records. Human Genome Meeting, Sydney, Australia, March 11-14, 2012.
73. Jeff JM, Brown-Gentry K, Ritchie MD, Denny J, Kho AN, Armstrong L, Basford M, Pacheco JA, Chisholm RL, Roden DM, Hayes MG, **Crawford DC**. Replication of *SCN5A* associations with ECG traits from electronic medical records and population-based collections in African Americans. Human Genome Meeting, Sydney, Australia, March 11-14, 2012.
74. Pendergrass SA, Frase A, Ambite JL, Avery CL, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Kooperberg C, Le Marchand L, Lin Y, Matisse TC, Mitchell SL, Monroe K, North KE, Wilkens LR, Buyske S, **Crawford DC**, Ritchie MD. A phenome-wide exploration of genotype-phenotype associations and pleiotropy using MetaboChip in the PAGE Study. Human Genome Meeting, Sydney, Australia, March 11-14, 2012.
75. Oetjens MT, Birdwell KA, Denny JC, Roden DM, Bowton E, **Crawford DC**. Use of electronic medical records linked to a biorepository for the discovery of genetic factors associated with risk of developing adverse drug reactions to immunosuppression therapy. Human Genome Meeting, Sydney, Australia, March 11-14, 2012.
76. Fesinmeyer MD, Lin Y, Biggs ML, Bush WS, Butler A, Buyske S, Caberto CP, Carty CL, Cote ML, **Crawford DC**, Dumitrescu L, Fowke JH, Giovino GA, Haiman CA, Heiss G, Hindorff LA, Kooperberg C, Love S-A, Matisse TC, North K, Park SL, Peters U, Wilkens LR, Wise AL, Le Marchand L, Cheng IC. Pleiotropic effects on lung cancer of genetic susceptibility variants identified for other malignancies: The Population Architecture using Genomics and Epidemiology Study. American Association for Cancer Research (AACR) 2012, Chicago, Illinois, March 31-April 4, 2012.
77. Dumitrescu L, Goodloe R, Brown-Gentry K, **Crawford DC**. Epidemiologic Architecture for Genes Linked to Environment: smoking modifies HDL-C, LDL-C, and triglyceride GWAS-identified associations in the National Health and Nutrition Examination Surveys. 4<sup>th</sup> International Conference on Quantitative Genetics, Edinburgh, Scotland, June 17-22, 2012.
78. Jeff JM, Brown-Gentry K, **Crawford DC**. Genetic and environmental modifiers of

- fibrinogen levels in diverse populations from the Third National Health and Nutrition Examination Survey. 4<sup>th</sup> International Conference on Quantitative Genetics, Edinburgh, Scotland, June 17-22, 2012.
79. Mitchell SL, Brown-Gentry K, Hunt L, **Crawford DC**, Murdock DG. Applying a phenome-wide association approach to investigate the effect of mitochondrial DNA levels on diverse phenotypes in the National Health and Nutrition Examination Surveys. 4<sup>th</sup> International Conference on Quantitative Genetics, Edinburgh, Scotland, June 17-22, 2012.
  80. Restrepo NA, Brown-Gentry K, Spencer KL, Mayo P, Allen M, Schnetz-Boutaud N, **Crawford DC**. Investigation of possible quantitative trait modifiers for age-related macular degeneration in the Third National Health and Nutrition Examination Survey as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE). 4<sup>th</sup> International Conference on Quantitative Genetics, Edinburgh, Scotland, June 17-22, 2012.
  81. Oetjens MT, Denny JC, Baker AR, Dilks HH, Basford MA, Bowton E, Restrepo NA, Youngblood VM, Pulley JM, Roden DM, Masys DR, Ritchie MD, **Crawford DC**. Genome-wide association study of heart transplant patients and nephrotoxicity from immunosuppression therapy in a biorepository linked to electronic medical records. 4<sup>th</sup> International Conference on Quantitative Genetics, Edinburgh, Scotland, June 17-22, 2012.
  82. Gong J\*, Haiman CA\*, North KE\*, Buyske S, Bůžková P, Carlson CS, Cheng I, Cooper R, **Crawford D**, Ehret G, Fesinmeyer MD, C-Gu CC, Haessler J, Hindorff LA, Houston D, Irvin MR, Jackson R, Kooperberg C, Kuller CL, Leppert M, Lewis CE, Li R, Lim U, Matise TC, Monda K, Nguyen K-DH, Ritchie M, Schumacher F, Sethupathy P, Wilkens L, Le Marchand L\*\*, Peters U\*\* A systematic mapping survey of GWAS loci for body mass index in more than 20,000 African Americans reduces the number of potential functional variants and identifies independent second signals: MetaboChip results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. Obesity Society, San Antonio, Texas, September 20-24, 2012.
  83. Ritchie MD, Setia SZ, Armstrong GD, Armstrong L, Bradford Y, **Crawford DC**, Crosslin DR, de Andrade M, Doheny KF, Hayes MG, Jarvik GP, Kullo IJ, Li R, McCarty CA, Mirel D, Olson L, Purcell S, Pugh EW, Tromp G, Kuivaniemi H, Lotay V, Gottesman O, Haines JL. Merging genomic data for research in the Electronic Medical Records and GENomics Network: Lessons learned in eMERGE. International Genetic Epidemiology Society, Stevenson, Washington, October 18-20, 2012.
  84. Weeke P, Delaney J, Mosley JD, Kannakeril PJ, Wells Q, Van Driest S, Norris K, Kucera G, Stubblefield T, Tanaka T, Nakamura Y, **Crawford D**, Roden DM. Genetic variants associated with QT prolongation in patients exposed to sotalol: a genome-wide association study. American Heart Association Scientific Session, Los Angeles, California, November 3-7, 2012.
  85. Wu Y, Buyske S, Assimes T, Adair LS, Ballantyne C, Carty CL, Cheng I, Duggan D, Dumitrescu L, Eaton CB, Feranil AB, Hindorff LA, Matise T, Mitchell S, Lin Y, Peters U, Robinson JG, Schumacher F, Young A, Kooperberg C, **Crawford D**, Mohlke KL, North KE. Trans-ethnic MetaboChip genotyping of established lipid loci identifies low frequency susceptibility variants and additional independent signals in known loci.

- American Heart Association Scientific Session, Los Angeles, California, November 3-7, 2012.
86. Wu Y, Waite LL, Jackson AU, Buyske S, Absher D, Carty CL, Cheng I, Duggan D, Dumitrescu L, Guo X, Haiman C, Hindorff LA, Hsiung CA, Hunt SC, Hveem K, Laakso M, Njølstad I, Peters U, Quertermous T, Rauramaa R, Sung Y-J, Tuomileht J, Chen Y-DI, Kooperberg C, Rotter JI, Boehnke M, **Crawford DC**, Assimes TL, North KE, Mohlke KL. Trans-ethnic fine-mapping of lipid loci in African Americans, East Asians, and Europeans identifies population-specific signals and extensive allelic heterogeneity that increases the trait variance explained. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  87. **Crawford DC**, Dumitrescu L, Goodloe R, Brown-Gentry K, Sutcliffe C, Wiseman R, Baker P, Dilks HH, Boston J, McClellan, Jr. B, Mayo P, Allen M, Schnetz-Boutaud N, Haines JL, Pollin TI. Rare variant *APOC3* R19X is associated with cardio-protective profiles in a diverse population-based survey as part of the Population Architecture using Genomics and Epidemiology (PAGE) study. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  88. Restrepo N, Spencer K, Goodloe R, Garrett T, Heiss G, Buzkova P, Jorgensen N, Jensen R, Matisse T, Klein B, Klein R, Tien Yin W, Cornes B, Shyong Tai E, Ritchie M, Haines J, **Crawford D**. Genetic determinants of Age-related Macular Degeneration in Diverse Populations: The Population Architecture using Genomics and Epidemiology (PAGE) Study. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  89. Goodloe R, Brown-Gentry K, Gillani NB, Jin H, Mayo P, Allen M, McClellan B, Boston J, Sutcliffe C, Schnetz-Boutaud N, Dilks HH, **Crawford DC**. Genome-wide association study (GWAS)-identified genetic variants for lipid traits are associated with gallstone disease in the diverse Third National Health and Nutrition Examination Survey. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  90. Brown-Gentry K, Gillani NB, Jin H, McClellan B, Boston J, Sutcliffe C, Dilks HH, **Crawford DC**. Characterization and generalization of *HFE* rs1800562 genotype-phenotype relationships in the diverse National Health and Nutrition Examination Surveys (NHANES) as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE). American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  91. Vega JN, Brown-Gentry K, **Crawford DC**, Thornton-Wells TA. Replication and generalization of genetic risk factors for depression, anxiety and panic attack in a population-based cohort with African, European and Mexican ancestries. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  92. Mitchell S, Brown-Gentry K, Allen M, Hunt L, Mayo P, Schnetz-Boutaud N, **Crawford DC**, Murdock DG. Common cardiovascular disease risk factors are associated with mitochondrial DNA levels. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  93. Wilson S, Brown-Gentry K, Gillani NB, Jin H, McClellan B, Boston J, Sutcliffe C, Dilks HH, **Crawford DC**. Prevalence of *MYH9* common variants associated with non-diabetic end-stage renal disease and chronic kidney disease in the diverse National Health and Nutrition Examination Surveys as part of the Epidemiologic Architecture for Genes

- Linked to Environment (EAGLE). American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
94. Hall MA, Verma A, Brown-Gentry KD, Goodloe R, Boston J, Wilson S, McClellan B, Sutcliffe C, Dilks HH, Gillani NB, Jin H, Mayo P, Allen M, Schnetz-Boutaud N, Pendergrass SA, **Crawford DC**, Ritchie MD. A phenome-wide association study (PheWAS) using multiple National Health and Nutrition Examination Surveys (NHANES) to identify pleiotropy. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  95. Malinowski J, Spencer KL, Carty CL, Franceschini N, Fernández-Rhodes L, Young A, Cheng I, Ritchie MD, Haiman CA, Wilkens L, Wu C, Matisse TC, Carlson CS, Brennan K, Park P, Rajkovic A, Hindorff LA, Buyske S, **Crawford DC**. Genetic variation and age at natural menarche and menopause in African American women from the Population Architecture using Genomics and Epidemiology (PAGE) Study. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  96. Bush WS, Dumitrescu L, **Crawford DC**. Assessment of bias in an EMR-derived cohort. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  97. Oetjens MT, Feng Q, Ramirez AR, Bowton E, Clark T, Roden DM, **Crawford DC**, Wilke RA. Survey of rare variants in pharmacogenes for patients with statin-induced myopathy identified in a biorepository linked to electronic medical records. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  98. Jeff J, Ritchie M, Denny J, Dilks H, Sutcliffe C, Basford M, Roden D, **Crawford D**. Fine mapping the *SCN10A* gene region identifies novel associations with PR interval in African Americans from an electronic medical record population. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  99. Crosslin D, McDavid A, Weston N, Zheng X, Hart E, de Andrade M, Kullo I, McCarty C, Doheny K, Pugh E, Kho A, Hayes M, Ritchie M, Saip A, **Crawford D**, Crane P, Newton K, Li R, Mirel D, Crenshaw, Larson E, Carlson C, Jarvik G. Genetic variation associated with circulating monocyte count in the eMERGE Network. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  100. Dumitrescu L, Ritchie MD, Denny JC, Bielinski SJ, Peissig P, Pacheco JA, Hayes MG, Jarvik GP, Li R, Kullo IJ, Chute CG, Chisholm RL, Larson EB, McCarty CA, Roden DM, de Andrade M, **Crawford DC**, on behalf of the eMERGE Network. Genome-wide study of resistant hypertension using existing genome data and electronic medical records. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
  101. Ritchie MD, Setia S, Armstrong G, Armstrong L, Bradford Y, **Crawford DC**, Crosslin DR, de Andrade M, Doheny K, Hayes MG, Jarvik G, Kullo IJ, Li R, Manolio T, Matsumoto M, McCarty CA, Mirel D, Nelson S, Olson L, Pugh E, Purcell S, Tromp G, Haines JL. Merging genomic data for research in the Electronic MEDical Records and GENomics Network: Lessons learned in eMERGE. American Society of Human Genetics, San Francisco, California, November 6-10, 2012.
- 2013
102. Bush WS\*, Boston J\*, Pendergrass SA, Dumitrescu L, Goodloe R, Brown-Gentry K, Wilson S, McClellan Jr B, Torstenson E, Basford MA, Spencer KL, Ritchie MD, **Crawford DC**. Enabling high-throughput genotype-phenotype associations in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project as part

- of the Population Architecture using Genomics and Epidemiology (PAGE) study. Pacific Symposium on Biocomputing, Hawaii, January 3-7, 2013.
103. Restrepo NA, Garrett T, Buzkova P, Jensen RA, Klein B, Klein R, Wong TY, Tai ES, **Crawford DC** on behalf of the PAGE Study. Genetic determinants of Age-related Macular Degeneration in Diverse Populations: The Population Architecture using Genomics and Epidemiology (PAGE) Study. The Association for Research in Vision and Ophthalmology (ARVO), Seattle, Washington, May 5-9, 2013.
  104. Mitchell S, Pendergrass S, Goodloe R, Brown-Gentry K, McClellan R, Boston J, Allen M, Mayo P, Schnetz-Boutaud N, Murdock DC, **Crawford DC**. Employing a phenome-wide association study approach to investigate the impact of mitochondrial DNA variation on disease. NHLBI Mitochondrial Biology Symposium, Bethesda, Maryland, May 6-7, 2013.
  105. Restrepo N, Garrett T, Buzkova P, Jensen R, Klein B, Klein R, Wong TY, Tai E. S, **Crawford D**. Genetic determinants of Age-related Macular Degeneration in Diverse Populations: the Population Architecture using Genomics and Epidemiology (PAGE) Study. Association for Research in Vision and Ophthalmology (ARVO), Seattle, Washington, May 5-9, 2013.
  106. Verma SS, Armstrong GJ, **Crawford DC**, Bradford Y, de Andrade M, Kullo IJ, Tromp G, Kuivaniemi HS, Armstrong L, Hayes G, Keating B, Crosslin DR, Jarvik GP, Namjou B, Bookman EB, Li R, Ritchie MD. Performance of two imputation methods on large scale data: experiences in the eMERGE network. International Genetic Epidemiology Society, Chicago, Illinois, September 15-17, 2013.
  107. Fernández-Rhodes L, Carty C, Peters U, Matise T, Ambite JL, Demerath E, Dreyfus J, **Crawford D**, Gross M, Pankratz N, Ramos E, Hindorff L, Daviglus M, Kaplan R, Castañeda S, Heiss G, Lim U, Haiman C, Le Marchand L, North K, Franceschini N. Evidence for shared genetic loci between body mass index and menarche timing among 5,357 Hispanic/Latino women in the Population Architecture using Genomics and Epidemiology Consortium. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  108. Hall JB, Bush WS, Pendergrass SA, Goodloe R, Boston J, Farber-Eger E, **Crawford DC**, Mitchell SL. Methodology for mitochondrial phenome-wide association studies. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  109. Farber-Eger E, Boston J, Goodloe R, Wilson SA, Bush WS, **Crawford DC**. Characterization of a Hispanic population from a biorepository linked to de-identified electronic medical records for genetic association and gene-environment studies. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  110. Restrepo N, Goodloe R, Mitchell SL, Murdock DG, Haines JL, **Crawford DC**. The Role of Mitochondrial Variants in the Risk of Age-related Macular Degeneration (AMD) in the National Health and Nutrition Examination Surveys (NHANES). American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  111. Dumitrescu L, Goodloe R, Boston J, Farber-Eger E, Bush WS, **Crawford DC**. Towards a phenome-wide catalog of human clinical traits impacted by genetic ancestry. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  112. **Crawford DC**, Ritchie MD, Dumitrescu L, Pendergrass SA, Goodloe R, Boston J, Farber-Eger E, Dilks HH, Haines JL, Bush WS. A large clinical biorepository linked to de-identified electronic medical records mimics a random sample from the general



- population. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
113. Bush WS, Boston J, Farber-Eger E, Goodloe R, **Crawford DC**. Computational resources required to transform beside data to base-pair research. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  114. Wiley L, Goodloe, Farber-Eger E, Boston J, **Crawford DC**, Bush WS. Association of Metabochip variants to systolic blood pressure in African Americans from a biorepository linked to de-identified electronic medical records. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  115. Villegas R, Goodloe RJ, McClellan B, Boston J, **Crawford DC**. Gene-carbohydrate and gene-fiber interactions and type 2 diabetes in diverse populations from the National Health and Examination Surveys as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  116. Mitchell SL, Pendergrass SA, Goodloe R, Brown-Gentry K, McClellan R, Boston J, Allen M, Mayo P, Schnetz-Boutaud, Murdock DG, **Crawford DC**. Employing a phenome-wide association study approach to investigate the impact of mitochondrial DNA variation on disease. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  117. Malinowski J, Goodloe R, Brown-Gentry K, **Crawford DC**. Cryptic relatedness in epidemiologic collections access for genetic association studies. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  118. Rosse SA, Carlson CS, **Crawford D**, Haessler J, Haiman CA, Matise T, North KE, Pankow J, Pankratz N, Peters U, Young A, Kooperberg C. Population Architecture using Genomics and Epidemiology (PAGE): The association of trans-ethnic genetic variation with glucose and insulin levels in PAGE. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  119. Oetjens MT, Denny JC, Gillani NB, Herrera M, Olson L, Dilks HH, Richardson DM, Bowton E, Roden DM, **Crawford DC**. A phenome-wide association study of ADME core variants in an EMR-linked biobank. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  120. Verma S, Armstrong G, Ritchie M, **Crawford D**, Bradford Y, Andrade M, Kullo I, Tromp G, Kuivaniemi H, Armstrong L, Hayes G, Keating B, Crosslin D, Jarvik G, Namjou B, Bookman E, Li R, eMERGE Network. Performance of two imputation methods on large scale data: experience in the eMERGE network. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  121. Iverson CC, Xu H, Chen Q, Shah A, Dai Q, Waner J, Peterson NB, Olson L, **Crawford DC**, Roden DM, Denny JC, Aldrich MC. Personalized genomics of metformin therapy for improved cancer survival. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  122. Hall MA, Verma SS, Holzinger ER, Berg R, Connolly J, **Crawford DC**, Crosslin DR, de Andrade M, Doheny KF, Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Tromp G, Pendergrass SA, McCarty CA, Ritchie MD. Replication of gene-gene interaction models associated with cataracts in the eMERGE Network. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.

123. Crosslin D, Carrell D, Baldwin E, de Andrade M, Kullo I, Tromp G, Kuivaniemi H, Doheny K, Pugh E, Kho A, Hayes M, Ritchie M, Verma S, Armstrong G, Saip A, Denny J, **Crawford D**, Crane P, Mukherjee S, Bottinger E, Manolio T, Li R, Burt A, Kim D, Keating B, Mirel D, Larson E, Carlson C, Jarvik G, The electronic Medical Records and Genomics (eMERGE) Network. Genetic variation associated with the susceptibility to herpes zoster in the eMERGE Network. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
  124. Gong J, Schumacher F, Hindorff L, Lim U, Haessler J, Carlson C, Rosse S, Buzkova P, Cooper R, Ehret G, Gu C, Irvin M, Graff M, Fernandez-Rhodes L, Boerwinkle E, Matisse T, Marchand L, Kooperberg C, **Crawford D**, Haiman C, North K, Peters U, the Population Architecture using Genomics and Epidemiology Study. Discovery and fine-mapping of BMI loci using Metabochip: a trans-ethnic meta-analysis from the Population Architecture using Genomics and Epidemiology (PAGE) Study. American Society of Human Genetics, Boston, Massachusetts, October 22-26, 2013.
- 2014
125. Mitchell SL\*, Hall JB\*, Goodloe R, Boston J, Farber-Eger E, Pendergrass SA, Bush WS, **Crawford DC**. Methods for investigating the pleiotropic effects of mitochondrial genetic variation on human health and disease. Pacific Symposium on Biocomputing, Hawaii, January 3-7, 2014.
  126. Farber-Eger E, Goodloe R, Boston J, Bush WS, **Crawford DC**. Extracting country-of-origin from electronic medical records for gene-environment studies as part of the Epidemiologic Architecture for Genes Linked to Environment (EAGLE). Pacific Symposium on Biocomputing, Hawaii, January 3-7, 2014.
  127. Dumitrescu L, Goodloe R, Farber-Eger E, Boston J, **Crawford DC**. The effects of electronic medical record phenotyping details on genetic association studies: HDL-C as a case study. Pacific Symposium on Biocomputing, Hawaii, January 3-7, 2014.
  128. Goodloe R, Farber-Eger E, Boston J, **Crawford DC**, Bush WS. Reducing clinical noise for body mass index measures due to unit and transcription errors in the electronic medical record. Pacific Symposium on Biocomputing, Hawaii, January 3-7, 2014.
  129. Wassel C, Wong Q, Goodloe R, Graff M, Tao R, Shao Y, **Crawford D**, Buyske S, Buzkova P, Jenny N, Bielinski S, Pankow J, Rich S, Chen I, Taylor K, Mychaleckyj J, Wise A, Ix J, Rifkin D, Junkins H, Fornage M, Kao L, North K, Franceschini N. Association of genetic variants on the Metabochip with urine albumin-creatinine ratio in African Americans: The Population Architecture using Genomics and Epidemiology (PAGE) Study. American Heart Association Epidemiology and Prevention/Nutrition, Physical Activity and Metabolism 2014 Scientific Sessions, San Francisco, California, March 18-21, 2014.
  130. Seyerle AA, Wassel C, Carty CL, Fornage M, Bielinski SJ, Buyske S, Carnethon MR, **Crawford DC**, Duggan DJ, Gong J, Heckbert SR, Hindorff LA, Jeff JM, Lloyd-Jones, DM, Okin PM, Perez MV, Psaty BM, Rotter JI, Shah SJ, Shohet RV, Soliman EZ, Sotoodehnia N, Wu C, Kooperberg C, Avery CL. Generalization and fine mapping of PR interval loci in Hispanics: The Population Architecture using Genomics and Epidemiology (PAGE) Study. American Heart Association Epidemiology and Prevention/Nutrition, Physical Activity and Metabolism 2014 Scientific Sessions, San Francisco, California, March 18-21, 2014.

131. Iverson CC, Fletcher S, Blume J, Dilks H, Chen H, Deppen SA, Bush WS, **Crawford DC**, Blot WJ, Grogan EL, Aldrich MC. Global African ancestry is not associated with lung cancer survival. American Association for Cancer Research (AACR) Annual Meeting 2014, San Diego, California, April 5-9, 2014.
132. Jeff JM, Brown-Gentry K, Goodloe R, Ritchie MD, Denny JC, Kho AN, Armstrong L, McClellan B, Mayo P, Allen M, Jin H, Gillani NB, Schnetz-Boutaud N, Dilks HH, Basford MA, Pacheco JA, Chisholm RL, Roden DM, Hayes MG, **Crawford DC**. Replication of *SCN5A* associations with electrocardiographic traits in African Americans from clinical and epidemiologic studies. EvoBio, Granada, Spain, April 23-25, 2014.
133. Restrepo N, Goodloe R, Mitchell S, **Crawford D**. The role of mitochondrial variants in the risk of diabetic retinopathy in diverse populations within the National Health and Nutrition Examination Surveys. The Association for Research in Vision and Ophthalmology, Orlando, Florida, May 4-8, 2014.
134. Verma A, Verma SS, Pendergrass SA, **Crawford DC**, Crosslin D, Kuivaniemi H, Bush WS, Bradford Y, Kullo I, Bielinski S. eMERGE phenome-wide association study (PheWAS) identifies clinical associations and pleiotropy for functional variants. International Genetic Epidemiology Society, Vienna, Austria, August 28-30, 2014.
135. Restrepo NA, Goodloe R, Farber-Eger, **Crawford DC**. Generalization and fine-mapping of *CDKN2B-AS1* for primary open-angle glaucoma in African Americans from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
136. Restrepo N, Goodloe R, Farber-Eger E, **Crawford D**. Generalization and fine-mapping of *CDKN2B-AS1* for primary open angle glaucoma in African Americans from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) study. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
137. Iverson CC, Bush WS, **Crawford DC**, Dilks HH, Long J, Blot WJ, Grogan EL, Aldrich MC. Rare and common variants contribute to lung cancer survival in African Americans. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
138. Hayes MG, Armstrong LL, Thompson WK, Pacheco JA, Brilliant M, Peissig PL, de Andrade M, Bielinski SJ, Pathak J, Kullo IJ, **Crawford DC**, Denny JC, Tromp G, Borthwick KM, Shellenberger MJ, Kuivaniemi H, Carrell DS, Jarvik GP, Crosslin DR, Ritchie MD, Smith ME, Chisholm RL, Kho AN. Use of diverse electronic medical record systems for genomewide association study of colonic diverticular disease in European-ancestry populations. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
139. Verma A, Verma S, Pendergrass S, **Crawford D**, Crosslin D, Kuivaniemi H, Bush W, Bradford Y, Kullo I, Bielinski S, Li R, Denny J, Peissig P, Hebring S, Pugh E, Andrade M, Ritchie M, Tromp G. eMERGE phenome-wide association study (PheWAS) identifies clinical associations and pleiotropy for functional variants. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
140. Mitchell SL, Parl A, Turner SD, **Crawford DC**, Murdock DG. RNA-seq analysis reveals potential link between mammalian mitochondrial fatty acid synthesis (mtFAS II), RNA processing, and neurodegeneration. American Society of Human Genetics, San Diego, California, October 18-22, 2014.
141. Malinowski J, Clayton EW, **Crawford DC**. A rapid evidence review for the inclusion of genetic data in clinical care for a common, complex disease. American Society of

Human Genetics, San Diego, California, October 18-22, 2014.

142. Mosley JD, Shaffer CM, Van Driest SL, Weeke PE, Wells QS, Karnes JH, Velez Edwards DR, Wei W, Teixeira PL, Bastarache L, **Crawford DC**, Pacheco JA, Manolio TA, Bottinger EP, McCarty CA, Linneman J, Thompson W, Chisholm RL, Jarvik GP, Crosslin DR, Carrell DS, Larson EB, Jouni H, Kullo IJ, Tromp G, Borthwick KM, Kuivaniemi H, Ritchie MD, Denny JC, Roden DM. A genome-wide association study identified variants in *KCNIP4* associated with ACE inhibitor induced cough. American Society of Human Genetics, San Diego, California, October 18-22, 2014.

2015

143. Restrepo NA, Mitchell SL, Goodloe RJ, Murdock DG, Haines JL, **Crawford DC**. Mitochondrial variation and the risk of age-related macular degeneration across diverse populations. Pacific Symposium on Biocomputing, Hawaii, January 4-8, 2015.
144. Restrepo NA, Goodloe R, Farber-Eger E, **Crawford DC**. G6P missense variant and risk of primary open-angle glaucoma in African Americans from a biorepository linked to de-identified electronic medical records. The Association for Research in Vision and Ophthalmology, Denver, Colorado, May 3-7, 2015.
145. Hollister B, Farber-Eger E, **Crawford DC**, Aldrich MC, Non A. Extracting socioeconomic data from electronic health records for gene-environment studies of blood pressure. Case Western Reserve University Institute for Computational Biology Annual Symposium. Cleveland, Ohio, September 22, 2015.
146. Restrepo NA, Goodloe R, Farber-Eger, E, **Crawford DC**. G6P missense variant (rs1671152) and risk of primary open-angle glaucoma in African Americans from a biorepository linked to de-identified electronic medical records. Case Western Reserve University Institute for Computational Biology Annual Symposium. Cleveland, Ohio, September 22, 2015.
147. **Crawford DC**, Kirsten E Diggins, Restrepo NA, Farber-Eger E, Wells QS. Functional variants in a clinical setting: an example using *APOC3* R19X and extreme triglyceride levels extracted from electronic health records. North Coast Conference on Precision Medicine, Cleveland, Ohio, September 22, 2015.
148. Restrepo NA, Goodloe R, Farber-Eger E, **Crawford D**. Study of the genetic architecture of diabetic retinopathy in African Americans from a de-identified medical records system. American Society of Human Genetics, Baltimore, Maryland, October 6-10, 2015.
149. Hollister B, Farber-Eger E, **Crawford DC**, Aldrich MC, Non A. Extracting socioeconomic data from electronic health records for gene-environment studies of blood pressure. American Society of Human Genetics, Baltimore, Maryland, October 6-10, 2015.
150. **Crawford DC**, Diggins KE, Restrepo NA, Farber-Eger E, Wells QS. Functional variants in a clinical setting: an example using *APOC3* R19X and extreme triglyceride levels extracted from electronic health records. American Society of Human Genetics, Baltimore, Maryland, October 6-10, 2015.
151. Dumitrescu L, Diggins KE, Goodloe R, **Crawford DC**. Testing population-specific quantitative trait associations for clinical outcome relevance in a biorepository linked to electronic health records: *LPA* and myocardial infarction in African Americans. American Society of Human Genetics, Baltimore, Maryland, October 6-10, 2015.

2016

152. Dumitrescu L, Diggins KE, Goodloe R, **Crawford DC**. Testing population-specific quantitative trait associations for clinical outcome relevance in a biorepository linked to electronic health records: *LPA* and myocardial infarction in African Americans. Pacific Symposium on Biocomputing, Big Island, Hawaii, January 4-8, 2016.
  153. **Crawford DC**, Kirsten E Diggins, Restrepo NA, Farber-Eger E, Wells QS. Functional variants in a clinical setting: an example using *APOC3* R19X and extreme triglyceride levels extracted from electronic health records. International Congress of Human Genetics, Kyoto, Japan, April 3-7, 2016.
  154. Hollister BM, Restrepo NA, Farber-Eger E, **Crawford DC**, Aldrich MC, Non AL. Extracting socioeconomic data from electronic health records for gene-environment studies of cancer. Vanderbilt-Ingram Cancer Center (VICC) Annual Scientific Retreat, Nashville, Tennessee, May 6, 2016.
  155. Cooke Bailey JN, Bush WS, Slaven A, Schachere M, **Crawford DC**, Sedor JR, O'Toole JF. Attitudes towards centralized biorepositories among patients in Cleveland, OH: Implications for the Precision Medicine Initiative Cohort Program. North Coast Conference on Precision Medicine, Cleveland, Ohio, September 29, 2016.
  156. Hollister BM, Restrepo N, Farber-Eger E, **Crawford DC**, Non AL, Aldrich MC. Development of a text mining algorithm to extract socioeconomic data from electronic health records for precision medicine research. North Coast Conference on Precision Medicine, Cleveland, Ohio, September 29, 2016.
  157. **Crawford DC**, Cooke Bailey JN, Miskimen K, Slaven A, Schachere M, O'Toole J, Sedor J, Bush WS. Characterizing immune profiles of Clevelanders: The MetroHealth/Institute for Computational Biology Pilot Study (MIPs). North Coast Conference on Precision Medicine, Cleveland, Ohio, September 29, 2016.
  158. Cooke Bailey JN, Bush WS, **Crawford DC**, Sedor JR, O'Toole JF. Attitudes towards centralized biorepositories among patients in Cleveland, OH: Implications for the Precision Medicine Initiative Cohort Program. American Society for Human Genetics, Vancouver, Canada, October 18-22, 2016.
  159. Hollister BM, Restrepo N, Farber-Eger E, **Crawford DC**, Non AL, Aldrich MC. Development of a text mining algorithm to extract socioeconomic data from electronic health records for precision medicine research. American Society for Human Genetics, Vancouver, Canada, October 18-22, 2016.
- 2017
160. El Rouby N, McDonough CW, Gong Y, McClure LA, Mitchell BD, Horenstein RB, Talbert RL, Bradford Y, **Crawford DC**, Ritchie MD, Gitzendanner MA, Takahashi A, Tanaka T, Kubo M, Pepine CJ, Benavente OR, deHoff RM, Johnson JA. A GWAS of resistant hypertension in the International Verapamil SR-Trandolapril Study (INVEST) and secondary prevention of subcortical strokes. American Society of Clinical Pharmacology and Therapeutics, Washington, DC, March 13-18, 2017
  161. Cooke Bailey JN, Bush WS, Slaven A, Schachere M, Goldenberg A, **Crawford DC**, Sedor JR, O'Toole JF. Attitudes towards centralized biorepositories among patients in Cleveland, OH: Implications for the Precision Medicine Initiative Cohort Program. Ethical, Legal, and Social Implications Congress (ELSI CON), Genomics and Society, Farmington, Connecticut, June 5-7, 2017.
  162. Heath KN, Bush WS, Cooke Bailey JN, Miskimen K, Miron P, O'Toole J, Sedor J, **Crawford DC**. Characterization of genetic ancestry among chronic kidney disease

- patients. Intersections: Support of Undergraduate Research and Creative Endeavors (SOURCE), Cleveland, Ohio, August 4, 2017.
163. **Crawford DC**, Bush WS, Cooke Bailey JN, Miskimen K, Miron P, O'Toole J, Sedor JR. Markers of the adaptive immune response are associated with progressively worse chronic kidney disease status. North Coast Conference on Precision Medicine, Cleveland, Ohio, September 28, 2017.
  164. Cooke Bailey JN, **Crawford DC**, Goldenberg A, Slaven A, Pencak J, Schachere M, Bush WS, Sedor JR, O'Toole JF. Survey of attitudes towards biosample collection and genetic testing in a racially diverse CKD population in Cleveland, OH. North Coast Conference on Precision Medicine, Cleveland, Ohio, September 28, 2017.
  165. **Crawford DC**, Bush WS, Cooke Bailey JN, Miskimen K, Miron P, O'Toole J, Sedor JR. Markers of the adaptive immune response are associated with progressively worse chronic kidney disease status. American Society of Human Genetics, Orlando, Florida, October 17-21, 2017.
  166. Iyengar SK, Halladay CW, Hadi T, Igo RP, Greenberg P, **Crawford DC**, Sullivan JM, Fliesler SJ, Wu WC, Konicki PE, Peachey NS. Optimizing accurate classification of electronic health record case control status for age-related macular degeneration in the Million Veteran Project. American Society of Human Genetics, Orlando, Florida, October 17-21, 2017.
  167. Heath KN, **Crawford DC**, Bush WS, Cooke Bailey JN, Miskimen K, Miron P, O'Toole J, Sedor J. Characterization of genetic ancestry among chronic kidney disease patients. Annual Biomedical Research Conference for Minority Students, Phoenix, Arizona, November 1-4, 2017.
  168. **Crawford DC**, Bush WS, Cooke Bailey JN, O'Toole J, Sedor JR. Markers of the adaptive immune response are associated with progressively worse chronic kidney disease status. American Society of Nephrology, New Orleans, Louisiana, October 31-November 5, 2017.
  169. Cooke Bailey JN, **Crawford DC**, Slaven A, Pencak J, Schachere M, Bush WS, Sedor JR, O'Toole JF. Attitudes towards biosample collection and genetic testing in a racially diverse CKD population in Cleveland, OH. American Society of Nephrology, New Orleans, Louisiana, October 31-November 5, 2017.
- 2018
170. Fish AE, **Crawford DC**, Capra JA, Bush WS. Local ancestry transitions modify SNP-trait associations. Pacific Symposium on Biocomputing, Big Island, Hawaii, January 3-7, 2018.
  171. Igo R, Halladay C, **Crawford D**, Hadi T, Greenberg PB, John S, Fliesler S, Damrauer S, Wu W-C, Konicki PE, Peachey N, Iyengar SK. Discovery of three novel risk loci for age-related macular degeneration by trans-ethnic genome-wide association analysis of data from the VA Million Veteran Program. The Association for Research in Vision and Ophthalmology (ARVO), Honolulu, Hawaii, April 29-May 3, 2018.
  172. Iyengar SK, Halladay CW, Hadi T, Anger MD, Nguyen X-M, Igo RP, Greenberg PB, **Crawford D**, Sullivan JM, Damrauer S, Wu W-C, Peachey N. Optimizing case-control classification for age-related macular degeneration in the VA electronic health record using a multi-algorithm data cube approach. The Association for Research in Vision and Ophthalmology (ARVO), Honolulu, Hawaii, April 29-May 3, 2018.
  173. Cooke Bailey JN\*, **Crawford DC\***, Goldenberg A, Slaven A, Pencak J, Schacherer M,

Bush WS, Sedor JR, O'Toole JF. Participating in and return of results from precision medicine research: A survey of diverse participants from a public hospital in the United States. Keystone Symposia's One Million Genomes: From Discovery to Health, Hannover, Germany, June 4-8, 2018.

174. Igo RP, Halladay CW, **Crawford DC**, Hadi T, Greenberg P, Anger MD, Sullivan JM, Fliesler SJ, Damrauer SM, Wu W-C, Konicki PE, Peachey NS, Iyengar SK on behalf of the VA Million Veteran Program. Discovery of three novel risk loci for age-related macular identified by genome-wide association analysis of data form the VA Million Veteran Program. American Society of Human Genetics, San Diego, California, October 16-20, 2018.
175. DeFurio G, Cooke Bailey JN, Kinzy T, Miskimen K, Miron P, Bush WS, O'Toole J, Sedor J, **Crawford DC**. Genetic Variation and Chronic Kidney Disease. Support of Undergraduate Research and Creative Endeavors (SOURCE), Cleveland, Ohio, December 7, 2018.

2019

176. Igo RP, Halladay CW, **Crawford DC**, Hadi T, Greenberg P, Anger MD, Sullivan JM, Fliesler SJ, Wu W-C, Konicki PE, Peachey NS, Iyengar SK, on behalf of the VA Million Veteran Program. Evidence for novel risk loci for age-related macular degeneration on the X chromosome: the VA Million Veteran Program. The Association for Research in Vision and Ophthalmology (ARVO), Vancouver, Canada, April 28 – May 2, 2019.
177. Igo RP, Halladay CW, **Crawford DC**, Hadi T, Greenberg PB, Anger MD, Sullivan JM, Fliesler SJ, Damrauer SM, Wu W-C, Konicki P.E., International Age-related Macular Degeneration Genomics Consortium, Choquet H, Yin J, Patasova K, Jorengson E, Hysi P, Lotery A, Peachey NS, Iyengar SK, VA Million Veteran Program. Large-scale analysis for age-related macular degeneration reveals new risk loci. American Society of Human Genetics, Houston, Texas, October 15-19, 2019.

2020

178. Cooke Bailey JN, Nealon C, Halladay CW, Krymskaya P, Anthony SA, Roncone DP, Canania R, Kinzy TG, Igo R, Greenberg PB, **Crawford DC**, Iyengar SK, Sullivan JM, Wu W-C, Peachey NS. Computable phenotyping for primary open-angle glaucoma using electronic health records in the Million Veteran Program. The Association for Research in Vision and Ophthalmology (ARVO), Baltimore, Maryland, May 1-7, 2020 (cancelled due to SARS-CoV-2/COVID-19).
179. Igo R, Kinzy TG, Halladay CW, **Crawford DC**, Greenberg PB, Sullivan JM, Fliesler SJ, Wu W-C, Choquet H, Patasova K, Jorgenson E, Hysi PG, Lotery AJ, Cooke Bailey J, Peachey NS, Iyengar SK. Phenome-wide association analysis on risk variants for age-related macular degeneration reveals shared genetic influences with a wide range of disorders: The Million Veteran Program. The Association for Research in Vision and Ophthalmology (ARVO), Baltimore, Maryland, May 1-7, 2020 (cancelled due to SARS-CoV-2/COVID-19).
180. Darst BF, Bensen JT, Ingles SA, Rybicki BA, Nemesure B, John EM, Fowke JH, Stevens VL, Berndt SI, Huff CD, Park JY, Zheng W, Ostrander EA, Srivastava S, Carpten J, Sellers TA, Sanderson M, **Crawford DC**, Cussenot O, Cullen J, Kittles RA, Xu J, Kote-Jarai Z, Multigner L, Parent M-E, Menegaux F, Cancel-Tassin G, Kibel AS, Klein EA, Goodman PJ, Hu JJ, Casey G, Hennis AJ, Thompson IM, Leach R, Mohler JL, Fontham ET, Smith GJ, Taylor JA, Eeles RA, Brureau L, Chanock SJ, Watya S, Stanford JL,

- Mandal D, Isaacs WB, Cooney KA, Blot WJ, Conti DV, Haiman CA. A germline variant at 8q24 contributes to familial clustering of prostate cancer in men of African ancestry. American Association for Cancer Research (AACR) Annual Meeting, virtual due to SARS-CoV-2/COVID-19, June 22-24, 2020.
181. Nealon CL, Halladay CW, Kinzy TG, Simpson P, Canania RL, Anthony SA, Roncone DP, Sawicki Rogers LR, Leber JN, Dougherty JM, Sullivan JM, Igo Jr. RP, Greenberg PB, **Crawford DC**, Iyengar SK, Wu W-C, Peachey NS, Cooke Bailey JN. Computable phenotyping for primary open-angle glaucoma in the Million Veteran Program. Million Veteran Program Science Meeting, virtual due to SARS-CoV-2/COVID-19, September 24-25, 2020.
182. Nealon CL, Halladay CW, Kinzy TG, Simpson P, Canania RL, Anthony SA, Roncone DP, Igo RP Jr, Greenberg PB, **Crawford DC**, Iyengar SK, Sullivan JM, Wu W-C, Peachey NS, Cooke Bailey JN on behalf of the Million Veteran Program. Identifying primary open angle glaucoma utilizing computable phenotyping in electronic health records within the Million Veteran Program. American Academy of Optometry, virtual due to SARS-CoV-2/COVID-19, October 2-5, 2020.
183. Liu S, Miskimen K, Cooke Bailey JN, Konidari I, McCauley JL, Bush WS, Sedor JR, O'Toole JF, **Crawford DC**. Longitudinal changes in T-cell receptor sequence diversity in minimal change disease. American Society of Human Genetics, virtual due to SARS-CoV-2/COVID-19, October 27-31, 2020.
- 2021
184. Drouet D, Liu S, **Crawford DC**. Assessment of population-appropriate polygenic risk scores for lipid traits in African Americans. Martha L. Lepow, MD & Irwin H. Lepow, MD PhD, Medical Student Research Day (Lepow Day), virtual due to SARS-CoV-2/COVID-19, Case Western Reserve University, February 4, 2021.
185. Cooke Baily J, Kinzy TG, Nealon C, Halladay C, Simpson P, Canania R, Anthony S, Roncone D, Sawicki-Rogers L, Leber J, Dougherty J, Greenberg PG, Wu W-C, Sullivan JM, **Crawford D**, Iyengar S. POAG genetic risk score performs worse in African-descent than European-descent samples, highlighting need for expanded genetic studies in diverse populations. The Association for Research in Vision and Ophthalmology (ARVO), virtual due to SARS-CoV-2/COVID-19, May 1-7, 2021.
186. Cruz LA, Nealon CL, Kinzy TG, Halladay CW, Simpson P, Canania RL, Anthony SA, Roncone DP, Sawicki-Rogers L, Leber J, Dougherty J, Greenberg P, Sullivan J, Wu W-C, Iyengar SK, **Crawford DC**, Peachey NS, Cooke Bailey JN. Today's genetic risk scores for primary open-angle glaucoma underperform in African-descent participants from the Veteran Administration's Million Veteran Program (MVP). American Society of Human Genetics, virtual due to SARS-CoV-2/COVID-19, October 18-22, 2021.
187. Waksmunski AR, Nealon CL, Kinzy TG, Halladay CW, Simpson P, Canania RL, Anthony SA, Roncone DP, Sawicki-Rogers L, Leber J, Dougherty J, Greenberg PB, **Crawford DC**, Iyengar SK, Sullivan JM, Wu W-C, Peachey NS, Cooke Bailey JN. Evaluation of genetic risk scores for incisional surgeries in primary open-angle glaucoma patients. American Society of Human Genetics, virtual due to SARS-CoV-2/COVID-19, October 18-22, 2021.
188. Drouet D, Liu S, **Crawford DC**. Assessment of population-appropriate polygenic risk scores for lipid traits in African Americans. American Society of Human Genetics, virtual due to SARS-CoV-2/COVID-19, October 18-22, 2021.



2022

189. Jin B, Capra JA, Benchek P, Wheeler N, Naj AC, Hamilton-Nelson KL, Farrell JJ, Leung YY, Kunkle B, Vadarajan B, Schellenberg GD, Mayeux R, Wang L, Farrer LA, Pericak-Vance MA, Martin ER, Haines JL, **Crawford DC**, Bush WS. Spatial Distribution of Rare Missense Variants Within Protein Structures is Associated with AD Risk. Alzheimer's Association International Conference, San Diego, California, July 31 – August 4, 2022.
190. Liu S, Gunzler DD, Gunzler SA, **Crawford DC**, Briggs FBS. Data-driven genome-wide association study of longitudinal pain and mobility trajectories among cases of Parkinson's disease from the Fox Insight Data Exploration Network. American Society of Human Genetics, Los Angeles, California, October 25-29, 2022.
- 191.