

Curriculum Vitae

PERSONAL INFORMATION

Dana C. Crawford

EDUCATION

Institution and Location	Degree	Years	Scientific Field
Vanderbilt University, Nashville, TN	B.S. Cum Laude	1991-1995	Molecular Biology
Emory University, Atlanta, GA	Ph.D.	1995-2000	Genetics and Molecular Biology

POST-DOCTORAL FELLOWSHIPS

Dr. Deborah Nickerson, Department of Genome Sciences, University of Washington, Seattle, WA (July 2002- January 2006).

Epidemic Intelligence Service Officer, Centers for Disease Control and Prevention, National Center on Birth Defects and Developmental Disabilities, Atlanta, GA (July 2000-July 2002).

PH.D. THESIS

Title: Factors involved in fragile X CGG repeat instability and their ultimate impact on world populations

Ph.D. Thesis Committee (list): 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

PROFESSIONAL/ACADEMIC APPOINTMENTS

Associate Professor with tenure, Department of Population and Quantitative Health Sciences (formerly Epidemiology and Biostatistics); Assistant Director for Population and Diversity Research, Institute for Computational Biology, Case Western Reserve University (January 13, 2015 - present)

Associate Professor (secondary appointment), Department of Genetics and Genome Sciences, Case Western Reserve University (June 2016- present)

Visiting Associate Professor, Department of Epidemiology and Biostatistics, Institute for Computational Biology, Case Western Reserve University (July 8, 2014 – January 12, 2015)

Associate Professor with tenure, Department of Molecular Physiology and Biophysics, Vanderbilt University (July 2012-July 2014)

Assistant Director and Investigator, Center for Human Genetics Research, Vanderbilt University (July 2013-March 2014)

Assistant Professor, Division of Human Genomics, Department of Molecular Physiology and Biophysics; Investigator, Center for Human Genetics Research, Vanderbilt University (September 18, 2006 – 2012)

Acting Assistant Professor, Department of Genome Sciences, University of Washington (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
C.W. Cotterman Award (best post-doctoral paper, American Journal of Human Genetics)	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	2014

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

American Society of Human Genetics (ASHG) Co-moderator for Session 31: Neurogenetics, San Diego, CA	2007
American Society of Human Genetics (ASHG) Co-moderator for Session 29: Genomics II, Philadelphia, PA	2008
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

Curriculum Vitae: DANA C. CRAWFORD

Pharmacogenomics Research Network (PGRN) Statistical Analysis Resource (P-STAR) expert consultant	2010-2015
American Society of Human Genetics (ASHG) Abstract reviewer for topic 5: Complex Traits and Polygenic Disorders	June 2012
American Society of Human Genetics (ASHG) Co-moderator for Session 61: Missing Heritability, Interactions, & Sequencing, San Francisco, CA	2012
Indonesian-American Kavli Frontiers of Science Symposium Organizer	2013-2014
Southern Community Cohort Study (SCCS) Publications Committee	2013-2014
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 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
American Society of Human Genetics (ASHG) 10th Annual DNA Day Essay Contest Judge, Round One	March 2015
11 th Annual DNA Day Essay Contest Judge, Round Two	March 2016
12 th Annual DNA Day Essay Contest Judge, Round One	March 2017
Annual Biomedical Research Conference for Minority Students (ABRCMS) poster judge, Seattle, WA	2015-present
Keystone Symposia Health Disparities Workshops Working Group	2016-present
Million Veterans Program (MVP) Statistical Genetics Work Group	2016-present

Translational Bioinformatics (TBI) Summit Scientific Program Committee	2016-2017
External Advisory Committee member, Orofacial Pain: Prospective Evaluation and Risk Assessment (OPPERA) project funded by NIH/NIDCR	2016-present
Informatics Domain Task Force (iDTF) member, Clinical & Translational Science Awards (CTSA)	2017-present
<u>NIH STUDY SECTIONS/GRANT REVIEW COMMITTEES</u>	
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 Sep 13, 2013 Dec 4, 2014 Mar 17, 2015 June 19, 2015 Sept 14, 2015 Dec. 2, 2015

Curriculum Vitae: DANA C. CRAWFORD

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 Mar 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

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

EDITORIAL DUTIES

Academic Editor, *PLoS One*

2012-present

Editor (Genetics section), *Pediatric Research*

2012-2016

AD HOC JOURNAL REVIEWER

Acta Cardiologica

American Heart Journal

American Journal of Epidemiology

American Journal of Human Genetics

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

Circulation Cardiovascular Research

Circulation Research

Clinical and Experimental Medicine

Computers in Biology and Medicine

Coronary Artery Disease

Diabetes

Epidemiology and Infection

European Journal of Human Genetics

European Journal of Medical Genetics

Expert Review of Precision Medicine and Drug Development

Gene

Genetic Epidemiology

Genetics

Genetics in Medicine

Genome Research

Hepatology

Human Biology

Human Molecular Genetics

Human Mutation

Influenza and Other Respiratory Viruses

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 Cellular and Molecular Medicine
Journal of Human Genetics
Journal of Pediatric Endocrinology and Metabolism
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 (also guest editor)
PLoS One
Physiological Genomics
Science
Scientific Reports
Tropical Medicine
The Pharmacogenomics Journal

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

Curriculum Vitae: DANA C. CRAWFORD

Vanderbilt University BioVU Review Committee (Member)
(Vice-chair) Jun 2011-2014
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 Epidemiology and Biostatistics
committee member 2015-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, Institute for Computational Biology
Annual Symposium, Cleveland, OH
“Present-Day Problems and Potentials for Precision Medicine”
Speakers: Drs. Jonathan Haines (Case Western Reserve University),
Marylyn Ritchie (The Pennsylvania State University), Casey Overby
(University of Maryland), Blanca Himes (University of Pennsylvania),
Vence Bonham, (NHGRI), and William Stewart (The Ohio State University)
Organizing Committee Chair 2015

Case Western Reserve University, Institute for Computational Biology
Annual Symposium Workshop, Cleveland, OH
“Mining Electronic Health Records for Precision Medicine Research”
Instructors: Drs. Sarah Pendergrass (The Pennsylvania State University)
and Janina Jeff (Mount Sinai)
Organizing Committee Chair 2015

Case Western Reserve University, Department of Epidemiology and
Biostatistics, Health Disparities Search Committee, member 2015-2016

Case Western Reserve University, School of Medicine, Committee on Appointments, Promotion, & Tenure, member 2016-2019

Case Western Reserve University, Institute for Computational Biology Annual Symposium, Cleveland, OH
“Precision Medicine for All: Ensuring Diversity in Participants and in Practice”
Speakers: Esteban Burchard (University of California San Francisco), Darcy Freedman (Case Western Reserve University), Aaron Goldenberg (Case Western Reserve University), David Kaelber (the MetroHealth System), the (Henrietta) Lacks family, Jacob McCauley (University of Miami), Minoli Perera (Northwestern University), Tim Thornton (University of Washington)
Organizing Committee Chair 2016

Departmental Search Committee Officer for Inclusion, Diversity and Equal Opportunity
Biomedical Data Science Search Committee
Cancer Epidemiology Search Committee
Director of the MPH Program Search Committee 2016-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. 11th 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, 11th 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.

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. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, April 27, 2009.
5. EAGLE Update. PAGE Steering Committee Meeting, Seattle, WA, September 24, 2009.
6. Inflammation Workgroup Update. PAGE Steering Committee Meeting, Seattle, WA, September 24, 2009.
7. Preliminary Lipids Analysis in EAGLE. PAGE Steering Committee Meeting and External Scientific Panel, Seattle, WA, September 24-25, 2009.
8. Preliminary Data from Vanderbilt Genome-Electronic Records (VGER) QRS Study. eMERGE Steering Committee Meeting, Bethesda, MD, November 19, 2009.
9. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, January 14, 2010.
10. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, January 14, 2010.
11. Vanderbilt Genome-Electronic Records (VGER) QRS Study. eMERGE Steering Committee Meeting, Bethesda, MD, April 12, 2010.
12. Genomics Workgroup: Next Steps in Genomics. eMERGE Steering Committee Meeting, Bethesda, MD, April 12, 2010.
13. EAGLE Update. PAGE Steering Committee Meeting, Nashville, TN, June 8, 2010.
14. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Nashville, TN, June 8, 2010.
15. Fine mapping in African American samples for QRS and T2D. eMERGE Steering Committee Meeting, Bethesda, MD, August 30, 2010.
16. Hypothyroidism. eMERGE Steering Committee Meeting and External Scientific Panel, Bethesda, MD, August 31, 2010.
17. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, October 19, 2010.
18. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting and External

- Scientific Panel, Bethesda, MD, October 19-20, 2010.
19. EAGLE Update. PAGE Steering Committee Meeting, Marina del Rey, CA, February 14, 2011.
 20. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Marina del Rey, CA, February 14, 2011.
 21. Network-wide Phenotype Update: Hypothyroidism. eMERGE Steering Committee Meeting, Bethesda, MD, April 25, 2011.
 22. 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.
 23. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, June 8, 2011.
 24. Phase 1 Genomics Workgroup Highlights. eMERGE Steering Committee Meeting, Bethesda, MD, July 25, 2011.
 25. Hypothyroidism/TSH: eMERGE Network-wide Projects eMERGE Steering Committee Meeting, Bethesda, MD, July 26, 2011.
 26. Resistant Hypertension Update: eMERGE Network-wide Project. eMERGE Steering Committee Meeting, Bethesda, MD, July 26, 2011.
 27. Genomics Workgroup eMERGE II Goals. eMERGE Steering Committee Meeting and External Scientific Panel, Rockville, MD, October 18, 2011.
 28. Genetic risk scores and eMERGE. eMERGE Steering Committee Meeting, Bethesda, MD, February 9, 2012.
 29. EAGLE Update. PAGE Steering Committee Meeting, Chapel Hill, NC, March 5, 2012.
 30. PAGE-wide lipids analysis. PAGE Steering Committee Meeting, Chapel Hill, NC, March 6, 2012.
 31. Genomics Workgroup Update. eMERGE Steering Committee Meeting, Minneapolis, MN, June 5, 2012.
 32. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, June 19, 2012.
 33. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, June 20, 2012.
 34. PAGE Reproduction Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, June 20, 2012.

35. EAGLE Update. PAGE Steering Committee Meeting, Bethesda, MD, October 18, 2012.
36. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Bethesda, MD, October 19, 2012.
37. PAGE Lipids Project Group Update. PAGE Steering Committee Meeting, Seattle, WA, March 14, 2013.
38. EAGLE Summary. PAGE Steering Committee Meeting, Seattle, WA, March 15, 2013.
39. Resistant Hypertension Update. eMERGE Steering Committee Meeting, Philadelphia, PA, June 3, 2013.
40. Null Variants. eMERGE Steering Committee Meeting, Bethesda, MD, October 7, 2013.

INVITED PRESENTATIONS (NATIONAL AND INTERNATIONAL)

1. 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.
2. 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.
3. 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.
4. 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.
5. 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.
6. Applying from the PGA Resource - Haplotypes. BayGenomics Program for Genomic Applications, San Francisco, CA, April 27, 2004.
7. SeattleSNPs and Applications in Pharmacogenetics. Rosetta, Seattle, WA, July 22, 2005.
8. 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.

9. 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.
10. 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.
11. 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
12. 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.
13. 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.
14. Genomics and Vaccine Safety. Understanding the Genomic Basis of Vaccine Safety. Centers for Disease Control and Prevention, Atlanta, GA, January 30-31, 2008.
15. 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.
16. Genetic determinants of lipids among nonfasting children. Department of Medical Genetics (Chair: Dr. Philip Giampietro), Marshfield, WI, August 13, 2008.
17. 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.
18. 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.
19. 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.
20. Using NHANES to determine the Epidemiologic Architecture for Genes Linked to Environment (EAGLE). HudsonAlpha Spring Symposium, Huntsville, AL, March 30, 2010.

21. Using Biobanks Linked to Electronic Health Records to Move from Base Pairs to Bedside. Illumina Discovery Symposium, Montreal, Canada, October 11, 2011.
22. 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.
23. 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.
24. Trans-ethnic comparisons for the role of genetics in diabetes: the PAGE Study. American Diabetes Association, Philadelphia, PA, June 9, 2012.
25. 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.
26. Big Genetic Epidemiology. American College of Epidemiology. Louisville, KY, September 24, 2013.
27. Genetic Association Studies in Diverse Populations. Division of Human Genetics (Director: Ray Hershberger), The Ohio State University, Columbus, OH, October 28, 2013.
28. 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.
29. Approaches to Gene-Nutrient Studies Based on Experiences from the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) Study. 3rd International Vitamin Conference, Washington, DC, May 12-15, 2014.
30. 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.
31. 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.
32. All In! Cleveland and Precision Medicine. Center for Systems Genomics, The Pennsylvania State University, August 26, 2015.
33. All In! Cleveland and Precision Medicine. Program in Personalized and Genomic Medicine, University of Maryland, November 18, 2015

34. Phenome-wide Association Studies. Understanding the Function of Human Genome Variation, Keystone Symposia, Uppsala, Sweden, June 1, 2016.
35. All In! Cleveland and Precision Medicine. Single Nucleotide Polymorphisms and Human Disease, Gordon Research Conference, Mount Holyoke, South Hampton, MA, June 16, 2016.
36. All In! Cleveland and Precision Medicine. Computational Challenges for Precision Medicine, MidAtlantic Bioinformatics Conference, Philadelphia, PA, October 26, 2016.

MEDIA

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

TRAINEES/MENTEES

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

Dapo Akingbade (2007) Rotation student
Chelsea Cupp (2009) Rotation student
Kirsten Diggins (2012) Rotation student
Haley Eidem (2013) Rotation student
Rachel Hoffman (2013) Rotation student
Lindsay Gordon (2010) Rotation student
Gunnar Kwakye (2006) Rotation student
Carrie Shaffer (2007) Rotation student
Corinne Simonti (2013) Rotation student
Clare Spielman (2013) Rotation student
Krystal Tsosie (2012) Rotation student
Olivia Veatch (2009) Rotation student
Amy Wotawa (2008) Rotation student
Victoria Youngblood (2011) Rotation student

Carrie Buchanan (2011-2013) Masters committee member
Anna (Davis) Cummings, PhD, MS (2006-2012) Rotation student; Chair of thesis committee
Laura D'Aoust (2010-2014) Rotation student; Chair of thesis committee
Todd Edwards, PhD, MS (2006-2008) Thesis committee

Jake Hall (2010-2014) Rotation student; Masters committee member
Emily Holzinger (2008-2013) Rotation student; Masters committee member
Nuri Kodaman (2009-2014) Masters committee member
Mary Ellen Koran (2012-2014) Thesis committee
Jude McElroy, PhD (2010-2012) Chair of thesis committee
Sabrina Mitchell, PhD (2007-2010) Thesis committee
Kelli Ryckman, PhD, MS (2007-2008) Thesis committee
Rafal Sabota (2012-2015) Masters committee member; Chair of thesis committee
Stephen Turner, PhD, MS (2007-2011) Chair of thesis committee; Masters committee member
Marquitta White (2009-2014) Rotation student; Thesis committee
Laura Wiley (2013-2014) Chair of thesis committee
Rebecca Zuvich, 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

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

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

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

Nicole 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

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

Past Postdoctoral Students

Sarah Pendergrass, PhD, MS (2009-2011)

Assistant Professor, Geisinger Biomedical and Translational Informatics Program (2015-present)

Research Associate, Penn State University (2011-2015)

Named one of Genome Technology's PIs of Tomorrow 2014

Janina Jeff, PhD, MS (2012-2013)

Global Bioinformatics Specialist, Illumina (2015-present)

Post-doctoral fellow, Mount Sinai (2013-2015)

Logan Dumitrescu, PhD, MS (2011-2013)

Neuroimaging Analyst, Vanderbilt Memory & Alzheimer's Center, Vanderbilt University Medical Center (2016-present)

Regulatory writing expert, Synchrogenix (2013-2016)

Sabrina Mitchell, PhD (2010-2015)

Staff Scientist, Division of Genetic Medicine, Vanderbilt University Medical Center (2017-present)

Post-doctoral fellow, Vanderbilt University Medical Center (2015-2017)

Past Other Students/Mentees

Roberto Reyes, 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.

Sarah Laper, Eastern Virginia medical school student (2015) Summer volunteer research

(Poster presentation and travel scholarship; declined due to conflict in schedule). 9th Annual

National Conference on Health Disparities and 2016 National Environmental Justice Conference and Training Program, Washington, DC, March 9, 2016.

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

Current Graduate Students

Andrea Waksmunski (2017-present) Genetics and Genomic Sciences PhD thesis committee chair

Abby Statler (2017-present) Population and Quantitative Health Sciences (formerly Epidemiology and Biostatistics) PhD thesis committee chair

Current Postdoctoral Students

Current Other Students/Mentees

Jessica Cooke Bailey, PhD (2016- present) Research Mentor for Case Western Reserve University Instructor and KL2 scholar

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

TEACHING ACTIVITIES

Previous Classes and Lectures

- Spring 1997 Human and Molecular Genetics (MEDI 545/IBS 505). Small-group seminar facilitator teaching assistant. (Teaching requirement for Ph.D. program)
- Spring 1999 Human and Molecular Genetics (MEDI 545/IBS505). Small-group seminar facilitator substitute teaching assistant.
- October 25, 2006 American Society of Human Genetics Outreach to Teach. Honors Biology...Only the Beginning. Vanderbilt University, Nashville, TN. Lecturer.
- September 19, 2007 Epidemiology 1: Research Design. Genome-wide association studies--why all the excitement? Vanderbilt University, Nashville, TN. Lecturer.
- February 27, 2008 Capstone Course. Genome-wide association studies. Rheumatoid arthritis. Vanderbilt University, Nashville, TN. Lecturer.
- 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.
- Spring 2008-2009 Tutorials in Statistical and Population Genetics. Vanderbilt University graduate course MPB/HGEN 371. One-hour journal-club style presentations 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.
- 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.
- December 2, 2010 Personalize This! Direct-to-Consumer Genetic Products. Biological Sciences 105, Vanderbilt University, Nashville, TN. Lecturer.

Curriculum Vitae: DANA C. CRAWFORD

- 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.
- November 29, 2011 Personalize This! Direct-to-Consumer Genetic Products. Biological Sciences 105, Vanderbilt University, Nashville, TN. Lecturer.
- November 27, 2012 Personalize This! Direct-to-Consumer Genetic Products. Biological Sciences 105, Vanderbilt University, Nashville, TN. Lecturer.
- November 19, 2013 Personalize This! Direct-to-Consumer Genetic Products. Biological Sciences 105, Vanderbilt University, Nashville, TN. Lecturer.
- 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.
- October 22, 2015 Genetics and Population Health. Introduction to Population Health EPBI 440, Case Western Reserve University, Cleveland, OH. Lecturer.
- November 16, 2015 Personalize This! Direct-to-Consumer Genetic Testing. EPBI 501, Case Western Reserve University, Cleveland OH. Lecturer.

Current Classes and Lectures

- Spring 2015-present Communicating in Population Health Science Research, course director.

Case Western Reserve University graduate course. EPBI444. A two-hour graduate-level class covering various forms of scientific communication including writing and oral presentations. This course is required of all Masters and PhD students in Epidemiology and Biostatistics.

Spring 2015, 2017 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.

Fall 2015-present 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. 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 the Department of Epidemiology and Biostatistics and is an elective for other Masters and PhD students.

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)₂ 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.

Workshops

Curriculum Vitae: DANA C. CRAWFORD

- 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.
- May 4-8, 2008 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.
- April 20-24, 2009 Genetic Analysis of Complex Human Diseases. Gene-Gene and Gene-Environment Interactions. Miami Institute for Human Genomics, University of Miami, FL. Lecturer.
- May 15-19, 2010 Genetic Analysis of Complex Human Diseases. Genome and Variation Databases; Gene-Gene and Gene-Environment Interactions. Miami Institute for Human Genomics, University of Miami, FL. 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 29, 2011 Personalized Medicine. Vanderbilt Medical School II (VMS II), Vanderbilt University School of Medicine, Nashville, TN. Lecturer.
- May 22-26, 2011 Genetic Analysis of Complex Human Diseases. Genome and Variation Databases; Gene-Gene and Gene-Environment Interactions. Miami Institute for Human Genomics, University of Miami, FL. Lecturer.
- April 26, 2012 Personalized Medicine. Vanderbilt Medical School II (VMS II), Vanderbilt University School of Medicine, Nashville, TN. Lecturer.
- May 21-24, 2012 Genetic Analysis of Complex Human Diseases. Genome and Variation Databases; Gene-Gene and Gene-Environment Interactions. Miami Institute for Human Genomics, University of Miami, FL. Lecturer.
- May 20-23, 2013 Genetic Analysis of Complex Human Diseases. Genome and Variation Databases; Gene-Gene and Gene-Environment Interactions. Miami Institute for Human Genomics, University of Miami, FL. Lecturer.
- October 29-31, 2015 Genomic Discovery, Collaboration, and Translation Using Electronic Health Records. Speakers: Drs. Dana Crawford (CWRU), Sarah Pendergrass (Geisinger), and Janina Jeff (Mount Sinai). Society for the Advancement of Chicanos and Native Americans in Science (SACNAS) National Conference, Gaylord National Resort and Convention Center, Washington, DC. Scientific Symposia Organizer and Speaker.
- October 13-15, 2016 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). Society for the Advancement of Chicanos and

Native Americans in Science (SACNAS) National Conference, Long Beach Convention Center, Long Beach, CA. Scientific Symposia Organizer.

RESEARCH SUPPORT

ACTIVE

1R13 HG009481-01 (Crawford) 09/20/2016-07/31/2018

NIH/NHGRI

North Coast Conference on Precision Medicine

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

I01 BX003364A1 (Konicki/Peachey) 10/01/2016-09/31/2017

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

PENDING

1UG3 DK114908-01 (Poggio) 07/01/2017-06/30/2022

NIH/NIDDK

Cleveland KPMP Recruitment Network Site

The Cleveland KPMP Recruitment Network Site proposes to recruit patients with chronic kidney disease for the larger Kidney Precision Medicine Project (KPMP). *Score: 18*

Role: Co-investigator

1U54 TR001960-01A1 (Konstan) 04/01/2018-03/31/2023

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)

1R21 AG059330-01 (Crawford) 04/01/2018-03/31/2020

NIH/NIA

T-cell receptor repertoire in chronic kidney disease

This proposal describes the next-generation sequencing of somatic T-cell receptors in chronic kidney disease patients ascertained from MetroHealth System in Cleveland, OH. T-cell receptor diversity will be examined in context of CKD-related biomarkers and CKD status to better understand if T-cell receptor sequences contribute to risk prediction or the generation of hypothesis for biological mechanisms that explain the disease process and its associated sequelae.

Role: PI

COMPLETED

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

SUL1 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 HG006385-03S1 (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

5U01 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

5R01CA092447-12 (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 (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 HG004798-04S2 (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.

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

3U01 HG004798-02S2 (Crawford) 05/21/2010-04/30/2011

NIH/NHGRI

Epidemiologic Architecture for Genes Linked to Environment

The goal of this supplement is 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

3U01 HG004798-01S1 (Crawford) 10/01/09-09/30/2010

NIH/NHGRI

Epidemiologic Architecture for Genes Linked to Environment

This ARRA supplement provided funds for genotyping ancestry informative markers in NHANES III and NHANES 1999-2002.

Role: PI

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) awards 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

Underlined authors represent Crawford lab trainees.

PEER REVIEWED ARTICLES

1. Qu S, Perlaky SE, Organ EL, **Crawford D**, and Cavener DR. Mutations at the Ser50 residue of translation factor eIF-2 α 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](#)
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](#)
4. **Crawford DC**, Meadows KL, Newman JL, Taft LF, Pettay DL, Gold LB, Hersey SJ, Hinkle EF, Stanfield ML, Holmgreen 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](#)
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, Rohlf 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](#)
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](#)
 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. *MMWR Morb Mortal Wkly Rep*, 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 β -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](#)
 13. **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 at the 2003 American Society of Human Genetics meeting and was selected as winner of the 2004 American Society of Human Genetics C.W. Cotterman Award***
 14. **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](#)
 15. 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](#)
 16. **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](#)
 17. **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](#) ***Featured in the 2007 Genome Technology's "Tomorrow's PIs" issue***
18. **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 at the 2006 American Society of Human Genetics meeting in the session titled "Cardiovascular Genetics."***
 19. **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](#)
 20. **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](#)
 21. 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](#)
 22. **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](#)
 23. 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](#)
 24. 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](#)
 25. Ritchie MD*, Denny JC*, **Crawford DC***, Havens AK, Weiner JB, Pulley JM, Basford MA, Balsler 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](#) *** Featured in the *J Am Med Inform Assoc*'s "2010 Translational bioinformatics year in review" (issue 18 in 2011).***
 26. 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](#) *** featured in *Nature Biotechnology* (issue 29 in 2011), in the *J Am Med Inform Assoc*'s "2010 Translational bioinformatics year in review" (issue 18 in 2011), and as a "trailblazing idea" in the Nashville Scene (8/12/2010).***
 27. 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](#)
28. 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](#)
 29. Denny JC, Ritchie MD, **Crawford DC**, Schildcrout J, Havens A, Pulley J, Basford M, Masys DR, Haines J, Roden DM. Identification of genomic predictors of atrioventricular conduction *Circulation* 122(20):2016-21 (2010). [PMC2991609](#)
 30. **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](#)
 31. 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](#)
 32. 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](#)
 33. 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](#)
 34. 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](#)
 35. 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](#)
 36. 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](#)
 37. 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](#)
 38. 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](#)
 39. 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 *J AM Med Inform Assoc* 18(4):387-391 (2011). [PMC3128409](#)
40. **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](#) ***Voted “Top 10 Paper” in the Vanderbilt Epidemiology Center for 2011***
41. 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](#)
42. **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 manuscript is featured on the cover of the journal’s issue****
43. 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](#)
44. Matisse 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](#)
45. 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 at the 2011 International Congress of Human Genetics meeting in the session titled “Statistical Genetics II: Expanding Genome-Wide Association Studies” and was featured by Medscape Medical News (10/17/2011).***
46. 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](#)
47. 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](#)
 48. 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](#)
 49. Kääb 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](#)
 50. 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 JJ, 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](#)
 51. 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](#)
 52. 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](#).
53. 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](#)
 54. 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, Ranter 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](#)
 55. 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](#)
 56. 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](#)
 57. 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](#)
 58. Mitchell S, Welch-Burke T, Dumitrescu L, Lomenick JP, Murdock D, **Crawford DC**, The Urea Cycle Disorders Consortium, Summar M. Peptide tyrosine tyrosine levels are increased in patients with urea cycle disorders *Molecular Genetics and Metabolism* 106(1):39-42 (2012). [PMC3336020](#)
 59. 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](#)
60. [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](#)
 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. 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](#)
 63. 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](#)
 64. 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](#)
 65. [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 at the 2011 International Congress of Human Genetics meeting in the session titled "Statistical Genetics II: Expanding Genome-Wide Association Studies"***
 66. 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](#)
 67. 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](#)
 68. **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 at the 2013 Pacific Symposium on Biocomputing***
69. 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](#)
 70. 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](#)
 71. 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](#)
 72. 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](#)
 73. Fesinmeyer M, KE North, 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, Le Marchand 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](#)
 74. 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, Le Marchand 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](#)
75. 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 Rongling, 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](#)
76. 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](#)
77. 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](#)
78. 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](#)
79. 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](#)
80. 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](#)

81. 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)**
82. 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](#)
83. Ding K, de Andrade M, Manolio T, **Crawford DC**, Rasmussen-Torvik LJ, Ritchie MD, Denny JC, Masys DR, Jouni H, Pachecho 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](#)
84. 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, Langaee 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](#)
85. 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](#) ***Selected as one of the 10 best articles for 2013 published in the *American Journal of Epidemiology****
86. 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](#)
87. Carlson CS, Matisse 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](#)
88. 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***
89. 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](#)
90. 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](#)
91. 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, Bshopric 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](#)
92. 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](#)
93. 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](#)
94. 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 *Nat 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)***
 95. 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](#)
 96. [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 at the 2014 Pacific Symposium on Biocomputing***
 97. [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 at the 2014 Pacific Symposium on Biocomputing***
 98. 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 at the 2014 Pacific Symposium on Biocomputing***
 99. [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](#)
 100. [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 reveals novel loci for type 2 diabetes in African Americans *PLoS One* 9(3):e86931 (2014). [PMC3940426](#)
 101. 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](#)
102. 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](#)
 103. [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](#)
 104. 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](#)
 105. 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](#)
 106. [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](#)
 107. 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](#)
 108. 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](#) ***This article is considered “highly accessed” by the journal (defined in *BMC* as “those articles that have been especially highly accessed, relative to their age, and the journal in which they are published.”)***
 109. 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 RJJ, 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](#)
110. 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](#)
111. 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, Yasmeen 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](#)
112. Restrepo NA*, Spencer KL*, Goodloe R, Garrett T, Heiss G, Bůžková P, Jorgensen N, Jensen RA, Matisse 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](#)
113. 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](#)
114. 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](#)***This article is considered “highly accessed” by the journal (defined in *BMC* as “those articles that have been especially highly accessed, relative to their age, and the journal in which they are published.”)***
115. 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, Hyppönen 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, Kivimaki 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](#)
116. 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](#)
117. 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](#)
118. 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](#)
119. 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](#)
120. **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](#)
121. **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](#)
 122. 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](#)
 123. 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](#)
 124. **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 at the 2015 Pacific Symposium on Biocomputing***
 125. **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](#)
 126. **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](#)
 127. 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, Ittermann 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-Kiukaanniemi 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. *Nature* 518 (7538):187-196 (2015). [PMC4338562](#)
128. 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, Morken 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, Witteman 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](#)
129. 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, Matise 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](#)
130. 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,

- Böttinger 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](#)
131. 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](#)***This article is considered “highly accessed” by the journal (defined in *BMC* as “those articles that have been especially highly accessed, relative to their age, and the journal in which they are published.”)***
132. 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](#)
133. 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](#)
134. 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](#)
135. 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](#)
136. 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](#)

137. 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](#)
138. 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](#)
139. 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 at the 2016 Pacific Symposium on Biocomputing***
140. 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 at the 2016 Pacific Symposium on Biocomputing***
141. 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](#)
142. 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 at the 2014 American Society of Human Genetics meeting in the session titled "Pharmacogenetics: From Association to Action."***
143. 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, Porreala 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](#)
144. 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](#)
145. 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](#)
146. 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](#)
147. 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 Jt Summits Transl Sci Proc* 2016:221-230 (2016). [PMC5001772](#)***This article was selected for an oral presentation at the AMIA 2016 Joint Summits on Translational Science***
148. 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 Jt Summits Transl Sci Proc* 2016:33-40 (2016). [PMC5001747](#)***This article was selected for an oral presentation at the AMIA 2016 Joint Summits on Translational Science***
149. 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](#)
150. 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).
151. 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 article was selected for an oral presentation at the 2017 Pacific Symposium on Biocomputing***
152. 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).***
153. 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](#)
154. Haddad SA, Plamer 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](#)

155. Avery CL, Wassel CL, Richard MA, Highland HM, Bien S, Zubair N, Soliman EZ, Fornage M, Bielenski 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 regions in global populations identifies signals unique to African and Hispanic descent populations *Heart Rhythm* 14(4):572-580 (2017).
156. 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 *Cell* 170(1):199-212 (2017).
157. 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
158. 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 Jt Summits Transl Sci Proc* (in press). ***This article was selected for an oral presentation at the AMIA 2017 Joint Summits on Translational Science***
159. 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 Jt Summits Transl Sci Proc* (in press). ***This article was selected for an oral presentation at the AMIA 2017 Joint Summits on Translational Science***
160. 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 DC**, 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 Molecular Genetics* (in press).
161. 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, 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* (in press).
162. Gong J, Nishimura KK, Haessler J, Bien S, Graff M, Lim U, Fernandez-Rhodes L, Lu Y, Gross M, Fornage M, Yoneyama S, Isasi C, Aviles-Santa L, Buzkova P, Daviglus M, Lind D, Tao R, Goodloe R, Bush WS, Farber-Eger E, Boston J, Dilks HH, Ehret G, Gu CC,

- Lewis CE, Ngyuen K-D H, Cooper R, Leppert M, Irvin MR, Bottinger EP, Wilkens LR, Haiman CA, Sheu WH-H, Guo X, Hung Y-J, Jia Y, Lee I-T, Absher D, Wu I-C, Taylor KD, Lee W-J, Liu Y, Juang J-MJ, Quertermous T, Wang T-D, Rotter JI, Assimes TL, Hsiung CA, Chen Y-D 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 identified four new loci associated with BMI (submitted).
163. El Rouby N, McDonough CW, Gong Y, McClure LA, Mitchell BD, Orenstein 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 (submitted).
164. 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 (submitted). ***This article was selected for an oral presentation at the 2017 Translational Bioinformatics in Precision Medicine and 7th Annual Translational Bioinformatics Conference***
165. **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 (submitted).***This article was selected for an oral presentation at the 2017 Translational Bioinformatics in Precision Medicine and 7th Annual Translational Bioinformatics Conference***
166. **Crawford DC**, Cooke Bailey JN, Miskimen K, Miron P, McCauley JL, Sedor JR, O'Toole JF, Bush WS. Adding another 'omics to precision medicine research: somatic T-cell receptor diversity in a chronic kidney disease patient population (submitted).
167. Fish AE, **Crawford DC**, Capra JA, Bush WS. Local ancestry transitions modify SNP-trait associations (submitted).
168. Mitchell SL, Farber-Eger E, Veatch OJ, Goodloe RJ, Wells QS, Murdock DG, **Crawford DC**. Hi-MC: A novel method for high-throughput mitochondrial haplogroup classification (in preparation).
169. Justice AE, Jorgensen NW, Carty CL, North KE, Avery C, Allen M, Bien SA, Cole S, Dilks HH, Duggan DJ, Gillani NB, Goodloe R, Graff M, Kooperberg C, Liu K, Mayo P, Psaty B, Richard MA, Schnetz-Boutard N, Wu C, Franceschini N, Fornage M, **Crawford DC**, Buzkova P. Evaluating association of blood pressure genetic variants with pulse pressure in multi-ethnic populations: The PAGE Study (in preparation).
170. Fernández-Rhodes* L, Malinowski J*, Wang Y*, Tao R*, Pankratz N*, Jeff JM*, Yoneyama S*, Yao J*, Corbett S, Carty C, Demerath E, Heiss G, Peters U, Ryckman K, Kooperberg C, Hindorff L, Ramos E, Setiawan W, Le Marchand L, Haiman C, Ambite JL, Buzkova P, **Crawford D**, Spencer K, Gross M, Daviglus M, Kaplan R, Castañeda SF, Talavera GA, Hunt SC, Rao DC, Schwander K, Chakravarti A, Raffel LJ, Guo X, Bielinski S, Rotter JI, Chen Y-DI, Vaidya D, Gottesman O, Abul-Husn NS, Bottinger EP, Loos RJF, Matisse T, Franceschini N, North KE. Three novel loci and eight previously-described loci are associated with female reproductive milestones in more than 45,000 United States women of African, Hispanic/Latina, Asian and American Indian/Alaskan Native descent in the Population Architecture using Genomics and Epidemiology (PAGE) study (in preparation).

171. Malinowski J, Naylor H, Clayton EW, **Crawford DC**. A rapid evidence review for the inclusion of genetic data in clinical care for a common, complex disease (in preparation).
172. Iverson CC, Fletcher S, Blume J, Wenzlaff AS, Schwartz AG, Chen H, Depeen SA, Bush WS, **Crawford DC**, Chanock SJ, Blot WJ, Gorgan EL, Aldrich MC. Global African ancestry is not associated with lung cancer survival (in preparation).
173. Pendergrass SA, Buyske S, Frase A, Dudek S, Wallace J, Ambite J-L, Bookman E, Avery CL, Bůžková P, Deelman E, Fesinmeyer MD, Haiman C, Heiss G, Hindorff LA, Hsu C-N, Jackson RD, Kooperberg C, Lin Y, Le Marchand L, Matisse TC, Monroe KR, Moreland L, North KE, Park L, Reiner A, Wallace R, White K, Wilkens LR, **Crawford DC**, Ritchie MD. The Population Architecture using Genomics and Epidemiology (PAGE) network and an investigation of pleiotropy in African Americans using Metabochip (in preparation).
174. **Crawford DC**, Spencer KL, Pendergrass SA, Dumitrescu L, Thornton-Wells T, Jeff JM, Bush WS, Brown-Gentry K, Glenn K, McClellan R, Canter J, Murdock D, Fowke JH, Haines JL, Ritchie MD. Using the National Health and Nutrition Examination Surveys (NHANES) to determine the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) (in preparation).

PEER-REVIEWED REVIEWS

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](#)
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](#)
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](#)
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](#)
6. 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](#)
7. **Crawford DC** and Dilks H. Strategies for Genotyping *Current Protocols in Human Genetics* Chapter 1: Unit 1.3 (2011). [PMID: 21234876](#)
8. **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](#)
9. **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](#)
10. 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](#)
 11. 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](#)
 12. 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](#)

OTHER PUBLICATIONS

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](#)
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
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. 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](#)
5. Bush WS, **Crawford DC**. Invited Editorial: Predicting incident coronary heart disease many markers at a time *Circulation Cardiovascular Genetics* 9:472-473 (2016).
6. 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).

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).
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*. 2nd

- 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 Scott WK and Ritchie MD (ed) Genetic Analysis of Complex Diseases. 2nd edition (submitted).

PRESENTATIONS FROM SUBMITTED ABSTRACTS

1. **Crawford DC**, Sun F, Meadows KL, Newman JL, Taft LF, Ashley-Koch AE, Sherman SL. Approaches to investigating the mutational processes of the FMR1 gene: coalescent modeling and haplotype associations in two populations. European Molecular Biology Organization Workshop, London, England, April 1-3, 1998.
2. **Crawford DC**, Meadows KL, Newman JL, Gunter C, Schwartz C, Nolin S, Sherman SL. FRAXA and haplotype associations using flanking STR markers and a biallelic marker in Caucasians and African-Americans. 6th International Fragile X Syndrome Conference, Asheville, NC, July 26-29, 1998.
3. **Crawford DC**, Meadows KL, Newman JL, Gold LB, Taft LF, Pettay D, Sherman SL. Examining the prevalence and phenotype consequence of FRAXA alleles in a special needs population from metropolitan Atlanta. 6th International Fragile X Syndrome Conference, Asheville, NC, July 26-29, 1998.
4. **Crawford D**, Meadows K, Newman J, Taft L, Gunter C, Warren S, Sherman S. Examining the mutational history of the fragile X syndrome using flanking STRs and SNPs. American Society of Human Genetics, Denver, CO, Oct. 27-31, 1998.
5. **Crawford DC**, Wilson B, Sherman SL. Factors involved in the initial mutation of the fragile X CGG repeat as determined by sperm small-pool PCR. American Society of Human Genetics, Philadelphia, PA, Oct. 3-7, 2000.
6. **Crawford DC**, Brown J, Bashor B, Olney R, Moore C, Erickson D. 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. Altman, MD, in NY Times.com on May 1, 2001. ***
7. **Crawford DC**, Carlson CS, Rieder MJ, Eberle MA, Kruglyak L, Nickerson DA. Haplotype diversity across 100 candidate genes for inflammation and lipid metabolism. American Society of Human Genetics, Los Angeles, CA, Nov. 4-8, 2003.
8. **Crawford DC**, Smith JD, Shephard C, Wong M, Witrak L, Rieder MJ, Nickerson DA. Genotype-phenotype correlations in 7,000 Americans: *CRP* haplotypes are significantly associated with high plasma C-reactive protein levels in African- and Mexican-

- Americans. American Society of Human Genetics, Salt Lake City, UT, Oct. 25-29, 2005.
9. **Crawford DC**, Smith JD, Shephard, C, Wong M, Witrak L, Rieder MJ, Nickerson DA. Genetic variation is associated with C-reactive protein levels in a survey of 7,000 Americans. Keystone Symposia on Genome Sequence Variation and the Inherited Basis of Common Disease and Complex Traits, Big Sky, MN, January 8-13, 2006.
 10. **Crawford DC**, Nord AS, Badzioch MD, Ranchalis J, Ahearn M, Bertucci C, Wijsman EM, Rieder MJ, Nickerson DA, Jarvik GP. *VLDLR* common genetic variation is associated with very low-density lipoprotein (VLDL), high-density lipoprotein (HDL), and low-density lipoprotein (LDL) particle density. American Society of Human Genetics, New Orleans, LA, October 9-13, 2006.
 11. Brown K, Smith JD, Shephard C, Wong M, Rieder MJ, Nickerson DA, **Crawford DC**. *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.
 12. Kaab S, Sinner M, Kannankeril P, Wilde A, Bezzina C, Schulze-Bahr E, Guicheney P, Bishopric N, Myerburg R, Schott J-J, Pfeufer A, Hinterseer M, Beckmann B-M, Steinbeck G, Perz S, Meitinger T, Wichmann H-E, Ingram CR, Carter S, Norris K, Bradford Y, **Crawford DC**, Ritchie MD, George Jr AL, Roden DM. Genome-wide association study identifies novel genomic regions associated with drug-induced long QT-syndrome, Pharmacogenetics Research Network (PGRN) Statistical Analysis Workshop V, Rochester, MN, April 15, 2009.
 13. **Crawford DC**, Heiss G, Kooperberg C, Le Marchand L, Matisse TC, Ambite JL, Buyske S, Cole SA, Haiman CA, Manolio TA, North KE, Peters U, Ritchie MD, Hindorff LA, Haines JL, for the PAGE Study. Population Architecture using Genomics and Epidemiology (PAGE) – from SNPs to GWAS and beyond. American Public Health Association, Denver, CO, November 6-10, 2010.
 14. **Crawford DC**, Denny JC, Ritchie MD, Basford MA, Bradford Y, Chai HS, Zuvich RL, Bastarache L, Peissig P, 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 C, Chisholm RL, Larson EB, McCarty CA, Masys DR, Roden DM, Bielinski SJ, de Andrade M. Genome-wide study of autoimmune hypothyroidism using existing genomic data and electronic medical records. International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011.