Curriculum Vitae

Professional Name Megan LaVoy Grove
Legal Name Megan LaVoy Grove-Gaona

Business Address The University of Texas Health Science Center at Houston
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Human Genetics Center
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Research Interests

Molecular genetics laboratory techniques, genotyping, biobanking, epigenetics, metabolomics, multi-omics, genetic epidemiology, cardiovascular disease epidemiology, gene-environment interaction

Education

Master of Science in Human and Molecular Genetics December 2006
Thesis: "Gene-environment interaction in the Atherosclerosis Risk in Communities (ARIC) study"
Advisor: Eric Boerwinkle, PhD
The University of Texas Health Science Center at Houston Graduate School of Biomedical Sciences, Houston, TX

Bachelor of Science in Biology/Magna Cum Laude May 1997
Stephen F. Austin State University, Nacogdoches, TX

High School Honors Graduate/Salutatorian May 1993
Santa Fe High School, Santa Fe, TX

Professional Positions

Sept 2018 to present *Faculty Associate*, *Associate Director – Human Genetics Center Laboratory;* Human Genetics Center, Department of Epidemiology, Human Genetics and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

Dec 2016 to Aug 2018 *Principal Laboratory Specialist*, *Associate Director – Human Genetics Center Laboratory;* Human Genetics Center, Department of Epidemiology, Human Genetics and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

Aug 2014 to Nov 2016 *Program Manager - Research*, Human Genetics Center, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

June 2010 to July 2014 *Research Coordinator II*, Human Genetics Center, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

May 2002 to May 2010 *Research Associate*, Human Genetics Center, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

Oct 2000 to April 2002 *Senior Research Assistant*, Human Genetics Center, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX

Sept 1997 to Sept 2000 *Research Assistant I*, The Center for Human Genetics, Institute of Molecular Medicine, The University of Texas Health Science Center at Houston, Houston, TX

June 1997 to Aug 1997 *Grant Hire*, Office of Education Access and Equity, Summer Research Program, The University of Texas Health Science Center at Houston, Houston, TX

Awards and Honors

- Best Poster Award for "Interaction of immune-related genetic polymorphisms and breastfeeding duration with *Helicobacter pylori* prevalence: the Pasitos Cohort Study," Presented by DNA Genotek at the American Society of Human Genetics – October 2014
- Golden Tiger Award for CHARGE Consortium Exome Chip Contribution – December 2012
- Alpha Chi National Honor Society – August 1995 to May 1997
- Beta Beta Beta National Honor Society – Secretary, August 1995 to May 1997
- Frances Hazel Ross Pre-Med Scholarship, Stephen F. Austin State University – August 1995 to May 1996
- Who's Who Among Students in American Colleges and Universities – August 1995 to May 1996
- Ralph W. Steen Scholarship – August 1996 to May 1997
- Welch Foundation Grant for "Complex Binding of Metals with Thiadiazoles" – August 1994 to May 1995
- American Business Women's Association Scholarship – August 1993 to 1996

Committees and Activities

NIH Collaborative Studies and Consortia

2022-present NHLBI Trans-Omics for Precision Medicine (TOPMed) Program Epigenetics Working Group
2022-present DSHS Sample Workflow Committee
2018-present Member, University of Texas System Health Biobank Governing Committee
2018-present Member, ARIC Operations Committee
2017-present Member, ARIC Laboratory Committee
2015-present NHGRI Center for Disease Genomics (CCDG) Program
2015-present NHLBI Trans-Omics for Precision Medicine (TOPMed) Program
2012-present Member, CHARGE Epigenetics Working Group
2011-present Member, ARIC Epigenetics Working Group
2009-2012 NHLBI Exome Sequencing Project (ESP)
2009-present Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium
2009-2021 NIH Fogarty International Center Epidemiological Research in Jamaica (ERAJ) Study
2007-2010 NHGRI Gene, Environment Association Studies (GENEVA) Consortium
2006-2011 NHLBI Candidate Gene Association Resource (CARe)

2006-2009	NHLBI SNP Typing for Association with Multiple Phenotypes from Existing Epidemiologic Data (STAMPEED)
2005-2016	Pharmacogenomic Evaluation of Antihypertensive Responses (PEAR) Study
2001-present	Texas Medical Center (TexGen) Study
2000-2014	NHLBI Genetics of Hypertension Associated Treatments (GenHAT) Study
2000-2013	Genetic Epidemiology of Responses to Antihypertensives (GERA) Study
1997-present	NHLBI Rochester Family Heart Study (RFHS)
1997-present	NHLBI Family Blood Pressure Program (FBPP); Genetic Epidemiology Network of Arteriopathy (GENOA)
1997-present	NHLBI Atherosclerosis Risk in Communities (ARIC) Study

Professional Memberships

2013-present	Member, American Society of Human Genetics

University and School Activities

2020-2023	COVID-19 vaccination security, storage and temperature monitoring subgroup
2020-2021	UT Supply Chain Alliance CORE RFP Committee
2017-2020	University of Texas System Health Biobank standard policies, processes, and procedures (SO3P) workgroup member
2016	School of Public Health 100% Exhaust vs Recirculation Subcommittee
2012	School of Public Health Flood Mitigation Project Committee
2012-present	Tours and demonstrations in cooperation with various UTHealth offices for philanthropic purposes
2011	UT System Supply Chain Alliance, Strategic Sourcing Team
2009	Environmental, Health and Safety Laboratory Risk Assessment and Loss Prevention Project
2002-present	Lead Manager and Coordinator, School of Public Health Rees Scientific Freezer Monitoring System

Media

News Releases. Johns Hopkins Medicine. December 16, 2014. "Amount of Mitochondrial DNA Predicts Frailty and Mortality." http://www.hopkinsmedicine.org/news/media/releases/amount_of_mitochondrial_dna_predicts_frailty_and_mortality

Pioneers magazine. UTHealth School of Public Health. Spring 2015. "Searching for answers about Alzheimer's." Available online at https://sph.uth.edu/about-us/Pioneers-magazine/

Science Daily. September 21, 2016. "Smoking has a very broad, long-lasting impact on the human genome." Available online at https://www.sciencedaily.com/releases/2016/09/160921215106.htm

UTSystem News. Friday, February 3, 2017. "New UT System Health Biobank to advance scientific discovery." Available online at http://www.utsystem.edu/news/2017/02/03/new-ut-system-health-biobank-advance-scientific-discovery

The Insider. UTHealth. February 10, 2017. "UTHealth awarded $3.5 million to develop UT System Health Biobank initiative." Available online at https://inside.uth.edu/inside/story.htm?id=4897113b-2b6e-48dc-97d4-a1496f3f75dd&utm_source=UTHealth+Insider%3A+Feb.+22%2C+2017&utm_campaign=Feb.+22&utm_medium=email

UTHealth Cizik School of Nursing. School of Nursing Newsroom. "New biobank network based at School of Nursing will expedite discoveries." Available online at https://nursing.uth.edu/news/detail.htm?id=f5919077-0d25-422a-b398-f07132b0bbd8

Peer Review

2014 Reviewer, Nature Protocols

Teaching and Training Experience

May 2023-present Mentor, Graduate Research Assistant, Fernique Pinder, The University of Texas Health Science Center at Houston, School of Public Health

Dec 2022-present Mentor, Graduate Research Assistant, Abena Agyei, The University of Texas Health Science Center at Houston, School of Public Health

Jun-Aug 2022 Co-Mentor, Visiting Scholar, Benjamin Black, The University of Tulsa

Dec-Jan 2018 Mentor, Visiting Student, Nathan Zheng, Cornell University

July-Dec 2017 Mentor, Visiting Student, Edward Ni, Rice University

Summer 2017 Co-Mentor, Pablo Arenaz III, BUILDing SCHOLARS Peer Mentoring Program, The University of Texas at El Paso

April 2011 Trainer, ARIC Visit 5 Examination Laboratory Methods

Summer 2006 Guest Lecturer, PH2780, Applied Genetic Methods in Public Health

Presentations

Dec 2017 Houston Baptist University-Under the Microscope Seminar Series, Houston, TX, "Applied Laboratory Methods in Multi-Omic Studies"

July 2017 NHLBI Trans-Omics for Precision Medicine (TOPMed) Site Visit, Houston, TX, "TOPMed Centralized Omics Resource (CORE) Task 3 – Genome-wide DNA Methylation"

Sept 2016 NHLBI Trans-Omics for Precision Medicine (TOPMed) Site Visit, Houston, TX, "TOPMed Centralized Omics Resource (CORE) Task 3 – Genome-wide DNA Methylation"

Sept 2013 CHARGE Consortium/GIANT Collaborative Meeting, "CHARGE Exome Chip Annotation"

Dec 2012 CHARGE Consortium Meeting, Houston, TX, "CHARGE Exome Chip Data Distribution"

Oct 2012 ARIC Steering Committee Meeting, Houston, TX, "ARIC DNA Lab Update"

Sept 2012 CHARGE Consortium Analysis Workshop, Boston, MA, "CHARGE Exome Chip Overview, Joint Calling and QC"

Sept 2012 MESA Steering Committee Meeting, Silver Spring, MD, "CHARGE Exome Chip Genotyping Project"

May 2012 CHARGE Consortium Meeting, "CHARGE Exome Chip Update"

Sept 2011 ARIC Steering Committee Meeting, Houston, TX, "ARIC DNA Lab Update"

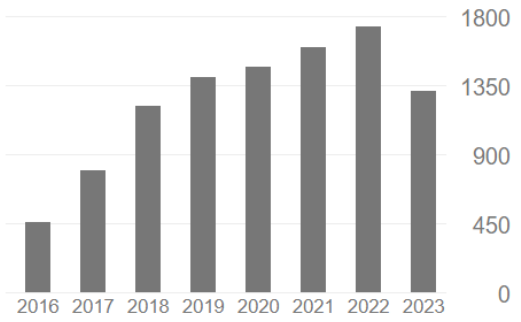
Oct 2010 Sequenom User Group Meeting, Foster City, CA, "Gene x Physical Activity Interaction: Is it in your jeans?"

July 2004 ARIC Steering Committee Meeting, Houston, TX, "Whole Genome Amplification: Easy as Phi"

Publications (N=133)

Google Scholar Citation Indices*	All	Since 2017
Citations	10976	8774
h-index	48	41
i10-index	104	96

*Last updated 10/16/2023



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My bibliography: https://www.ncbi.nlm.nih.gov/myncbi/megan.grove.1/bibliography/public/

2023

1. Liu X, Sun X, Zhang Y, Jiang W, Lai M, Wiggins KL, Raffield LM, Bielak LF, Zhao W, Pitsillides A, Haessler J, Zheng Y, Blackwell TW, Yao J, Guo X, Qian Y, Thyagarajan B, Pankratz N, Rich SS, Taylor KD, Peyser PA, Heckbert SR, Seshadri S, Boerwinkle E, **Grove ML**, Larson NB, Smith JA, Vasan RS, Fitzpatrick AL, Fornage M, Ding J, Carson AP, Abecasis G, Dupuis J, Reiner A, Kooperberg C, Hou L, Psaty BM, Wilson JG, Levy D, Rotter JI, Bis JC; TOPMed mtDNA Working Group in NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium; Satizabal CL, Arking DE, Liu C. Association Between Whole Blood-Derived Mitochondrial DNA Copy Number, Low-Density Lipoprotein Cholesterol, and Cardiovascular Disease Risk. J Am Heart Assoc. 2023 Oct 7:e029090. doi: 10.1161/JAHA.122.029090. Online ahead of print. PMID: 37804200

2. Hong YS, Battle SL, Shi W, Puiu D, Pillalamarri V, Xie J, Pankratz N, Lake NJ, Lek M, Rotter JI, Rich SS, Kooperberg C, Reiner AP, Auer PL, Heard-Costa N, Liu C, Lai M, Murabito JM, Levy D, **Grove ML**, Alonso A, Gibbs R, Dugan-Perez S, Gondek LP, Guallar E, Arking DE. Deleterious heteroplasmic mitochondrial mutations are associated with an increased risk of overall and cancer-specific mortality. Nat Commun. 2023 Sep 30;14(1):6113. doi: 10.1038/s41467-023-41785-7. PMID: 37777527

3. Cornelissen A, Gadhoke NV, Ryan K, Hodonsky CJ, Mitchell R, Bihlmeyer N, Duong T, Chen Z, Dikongue A, Sakamoto A, Sato Y, Kawakami R, Mori M, Kawai K, Fernandez R, Ghosh SKB, Braumann R, Abebe B, Kutys R, Kutyna M, Romero ME, Kolodgie FD, Miller CL, Hong CC, **Grove ML**, Brody JA, Sotoodehnia N, Arking DE, Schunkert H, Mitchell BD, Guo L, Virmani R, Finn AV. Polygenic Risk Score Associates with Atherosclerotic Plaque Characteristics at Autopsy. bioRxiv. 2023 Jul 7:2023.07.05.547891. doi: 10.1101/2023.07.05.547891. Preprint. PMID: 37461703

4. Moon JY, Chai JC, Yu B, Song RJ, Chen GC, Graff M, Daviglus ML, Chan Q, Thyagarajan B, Castaneda SF, **Grove ML**, Cai J, Xue X, Mossavar-Rahmani Y, Vasan RS, Boerwinkle E, Kaplan RC, Qi Q. Metabolomic Signatures of Sedentary Behavior and Cardiometabolic Traits in US Hispanics/Latinos: Results from HCHS/SOL. Med Sci Sports Exerc. 2023 Oct 1;55(10):1781-1791. doi: 10.1249/MSS.0000000000003205. Epub 2023 May 12. PMID: 37170952

2022

5. Saroukhani S, Samms-Vaughan M, Bressler J, Lee M, Byrd-Williams C, Hessabi M, **Grove ML**, Shakespeare-Pellington S, Loveland KA, Rahbar MH. Additive or Interactive Associations of Food Allergies with Glutathione S-Transferase Genes in Relation to ASD and ASD Severity in Jamaican Children. J Autism Dev Disord. 2022 Nov 27. doi: 10.1007/s10803-022-05813-7. Online ahead of print. PMID: 36436147

6. Rahbar MH, Samms-Vaughan M, Zhao Y, Saroukhani S, Bressler J, Hessabi M, **Grove ML**, Shakespeare-Pellington S, Loveland KA. Interactions between Environmental Factors and Glutathione S-Transferase (GST) Genes with Respect to Detectable Blood Aluminum Concentrations in Jamaican Children. Genes (Basel). 2022 Oct 20;13(10):1907. doi: 10.3390/genes13101907. PMID: 36292793

7. Keshawarz A, Joehanes R, Guan W, Huan T, DeMeo DL, **Grove ML**, Fornage M, Levy D, O'Connor G. Longitudinal change in blood DNA epigenetic signature after smoking cessation. 2022 Oct;17(10):1098-1109. doi: 10.1080/15592294.2021.1985301. Epub 2021 Oct 6. PMID: 34570667

8. Qi Q, Li J, Yu B, Moon JY, Chai JC, Merino J, Hu J, Ruiz-Canela M, Rebholz C, Wang Z, Usyk M, Chen GC, Porneala BC, Wang W, Nguyen NQ, Feofanova EV, **Grove ML**, Wang TJ, Gerszten RE, Dupuis J, Salas-Salvadó J, Bao W, Perkins DL, Daviglus ML, Thyagarajan B, Cai J, Wang T, Manson JE, Martínez-González MA, Selvin E, Rexrode KM, Clish CB, Hu FB, Meigs JB, Knight R, Burk RD, Boerwinkle E, Kaplan RC. Host and gut microbial tryptophan metabolism and type 2 diabetes: an integrative analysis of host genetics, diet, gut microbiome and circulating metabolites in cohort studies. Gut. 2022 Jun;71(6):1095-1105. doi: 10.1136/gutjnl-2021-324053. Epub 2021 Jun 14. PMID: 34127525

9. Rahbar MH, Samms-Vaughan M, Kim S, Saroukhani S, Bressler J, Hessabi M, **Grove ML**, Shakspeare-Pellington S, Loveland KA. Genes (Basel). Detoxification role of metabolic Glutathione S-Transferase (GST) genes in blood lead concentrations of Jamaican children with and without Autism Spectrum Disorder. 2022 May 29;13(6):975. doi: 10.3390/genes13060975. PMID: 35741737

10. Battle SL, Puiu D; TOPMed mtDNA Working Group, Verlouw J, Broer L, Boerwinkle E, Taylor KD, Rotter JI, Rich SS, **Grove ML**, Pankratz N, Fetterman JL, Liu C, Arking DE. A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. 2022 May 17;4(2):lqac034. doi: 10.1093/nargab/lqac034. eCollection 2022 Jun. PMID: 35591888

11. Rahbar MH, Samms-Vaughan M, Zhao Y, Saroukhani S, Zaman SF, Bressler J, Hessabi M, **Grove ML**, Shakspeare-Pellington S, Loveland KA. Additive and Interactive Associations of Environmental and Sociodemographic Factors with the Genotypes of Three Glutathione S-Transferase Genes in Relation to the Blood Arsenic Concentrations of Children in Jamaica. Int J Environ Res Public Health. 2022 Jan 1;19(1):466. doi: 10.3390/ijerph19010466. PMID: 35010728

12. Longchamps RJ, Yang SY, Castellani CA, Shi W, Lane J, **Grove ML**, Bartz TM, Sarnowski C, Liu C, Burrows K, Guyatt AL, Gaunt TR, Kacprowski T, Yang J, De Jager PL, Yu L, Bergman A, Xia R, Fornage M, Feitosa MF, Wojczynski MK, Kraja AT, Province MA, Amin N, Rivadeneira F, Tiemeier H, Uitterlinden AG, Broer L, Van Meurs JBJ, Van Duijn CM, Raffield LM, Lange L, Rich SS, Lemaitre RN, Goodarzi MO, Sitlani CM, Mak ACY, Bennett DA, Rodriguez S, Murabito JM, Lunetta KL, Sotoodehnia N, Atzmon G, Ye K, Barzilai N, Brody JA, Psaty BM, Taylor KD, Rotter JI, Boerwinkle E, Pankratz N, Arking DE. Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. Hum Genet. 2022 Jan;141(1):127-146. doi: 10.1007/s00439-021-02394-w. Epub 2021 Dec 2. PMID: 34859289

2021

13. Wang P, Castellani CA, Yao J, Huan T, Bielak LF, Zhao W, Haessler J, Roby J, Sun X, Guo X, Longchamps RJ, Manson JE, **Grove ML**, Bressler J, Taylor KD, Lappalainen T, Kasela S, Van Den Berg DJ, Hou L, Reiner A, Liu Y, Boerwinkle E, Smith JA, Peyser PA, Fornage M, Rich SS, Rotter JI, Kooperberg C, Arking DE, Levy D, Liu C; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. Epigenome-wide association study of mitochondrial genome copy number. Hum Mol Genet. 2021 Dec 27;31(2):309-319. doi: 10.1093/hmg/ddab240. PMID: 34415308

14. Bressler J, Davies G, Smith AV, Saba Y, Bis JC, Jian X, Hayward C, Yanek L, Smith JA, Mirza SS, Wang R, Adams HHH, Becker D, Boerwinkle E, Campbell A, Cox SR, Eiriksdottir G, Fawns-Ritchie C, Gottesman RF, **Grove ML**, Guo X, Hofer E, Kardia SLR, Knol MJ, Koini M, Lopez OL, Marioni RE, Nyquist P, Pattie A, Polasek O, Porteous DJ, Rudan I, Satizabal CL, Schmidt H, Schmidt R, Sidney S, Simino J, Smith BH, Turner ST, van der Lee SJ, Ware EB, Whitmer RA, Yaffe K, Yang Q, Zhao W, Gudnason V, Launer LJ, Fitzpatrick AL, Psaty BM, Fornage M, Arfan Ikram M, van Duijn CM, Seshadri S, Mosley TH, Deary IJ. Association of low-frequency and rare coding variants with information processing speed. Transl Psychiatry. 2021 Dec 4;11(1):613. doi: 10.1038/s41398-021-01736-6. PMID: 34864818. Correction: Transl Psychiatry. 2022 Mar 1;12(1):88. doi: 10.1038/s41398-022-01852-x. PMID: 35232957***

15. Schlosser P, Tin A, Matias-Garcia PR, Thio CHL, Joehanes R, Liu H, Weihs A, Yu Z, Hoppmann A, Grundner-Culemann F, Min JL, Adeyemo AA, Agyemang C, Ärnlöv J, Aziz NA, Baccarelli A, Bochud M, Brenner H, Breteler MMB, Carmeli C, Chaker L, Chambers JC, Cole SA, Coresh J, Corre T, Correa A, Cox SR, de Klein N, Delgado GE, Domingo-Relloso A, Eckardt KU, Ekici AB, Endlich K, Evans KL, Floyd JS, Fornage M, Franke L, Fraszczyk E, Gao X, Gào X, Ghanbari M, Ghasemi S, Gieger C, Greenland P, **Grove ML**, Harris SE, Hemani G, Henneman P, Herder C, Horvath S, Hou L, Hurme MA, Hwang SJ, Jarvelin MR, Kardia SLR, Kasela S, Kleber ME, Koenig W, Kooner JS, Kramer H, Kronenberg F, Kühnel B, Lehtimäki T, Lind L, Liu D, Liu Y, Lloyd-Jones DM, Lohman K, Lorkowski S, Lu AT, Marioni RE, März W, McCartney DL, Meeks KAC, Milani L, Mishra PP, Nauck M, Navas-Acien A, Nowak C, Peters A, Prokisch H, Psaty BM, Raitakari OT, Ratliff SM, Reiner AP, Rosas SE, Schöttker B, Schwartz J, Sedaghat S, Smith JA, Sotoodehnia N, Stocker HR, Stringhini S, Sundström J, Swenson BR, Tellez-Plaza M, van Meurs JBJ, van Vliet-Ostaptchouk JV, Venema A, Verweij N, Walker RM, Wielscher M, Winkelmann J, Wolffenbuttel BHR, Zhao W, Zheng Y; Estonian Biobank Research Team; Genetics of DNA Methylation Consortium, Loh M, Snieder H, Levy D, Waldenberger M, Susztak K, Köttgen A, Teumer A. Meta-analyses identify DNA methylation associated with kidney function and damage. Nat Commun. 2021 Dec 9;12(1):7174. doi: 10.1038/s41467-021-27234-3. PMID: 34887417

16. Tin A, Schlosser P, Matias-Garcia PR, Thio CHL, Joehanes R, Liu H, Yu Z, Weihs A, Hoppmann A, Grundner-Culemann F, Min JL, Kuhns VLH, Adeyemo AA, Agyemang C, Ärnlöv J, Aziz NA, Baccarelli A, Bochud M, Brenner H, Bressler J, Breteler MMB, Carmeli C, Chaker L, Coresh J, Corre T, Correa A, Cox SR, Delgado GE, Eckardt KU, Ekici AB, Endlich K, Floyd JS, Fraszczyk E, Gao X, Gào X, Gelber AC, Ghanbari M, Ghasemi S, Gieger C, Greenland P, **Grove ML**, Harris SE, Hemani G, Henneman P, Herder C, Horvath S, Hou L, Hurme MA, Hwang SJ, Kardia SLR, Kasela S, Kleber ME, Koenig W, Kooner JS, Kronenberg F, Kühnel B, Ladd-Acosta C, Lehtimäki T, Lind L, Liu D, Lloyd-Jones DM, Lorkowski S, Lu AT, Marioni RE, März W, McCartney DL, Meeks KAC, Milani L, Mishra PP, Nauck M, Nowak C, Peters A, Prokisch H, Psaty BM, Raitakari OT, Ratliff SM, Reiner AP, Schöttker B, Schwartz J, Sedaghat S, Smith JA, Sotoodehnia N, Stocker HR, Stringhini S, Sundström J, Swenson BR, van Meurs JBJ, van Vliet-Ostaptchouk JV, Venema A, Völker U, Winkelmann J, Wolffenbuttel BHR, Zhao W, Zheng Y; Estonian Biobank Research Team;

Genetics of DNA Methylation Consortium, Loh M, Snieder H, Waldenberger M, Levy D, Akilesh S, Woodward OM, Susztak K, Teumer A, Köttgen A. Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nat Commun. 2021 Dec 9;12(1):7173. doi: 10.1038/s41467-021-27198-4. PMID: 34887389

17. Stilp AM, Emery LS, Broome JG, Buth EJ, Khan AT, Laurie CA, Wang FF, Wong Q, Chen D, D'Augustine CM, Heard-Costa NL, Hohensee CR, Johnson WC, Juarez LD, Liu J, Mutalik KM, Raffield LM, Wiggins KL, de Vries PS, Kelly TN, Kooperberg C, Natarajan P, Peloso GM, Peyser PA, Reiner AP, Arnett DK, Aslibekyan S, Barnes KC, Bielak LF, Bis JC, Cade BE, Chen MH, Correa A, Cupples LA, de Andrade M, Ellinor PT, Fornage M, Franceschini N, Gan W, Ganesh SK, Graffelman J, **Grove ML**, Guo X, Hawley NL, Hsu WL, Jackson RD, Jaquish CE, Johnson AD, Kardia SLR, Kelly S, Lee J, Mathias RA, McGarvey ST, Mitchell BD, Montasser ME, Morrison AC, North KE, Nouraie SM, Oelsner EC, Pankratz N, Rich SS, Rotter JI, Smith JA, Taylor KD, Vasan RS, Weeks DE, Weiss ST, Wilson CG, Yanek LR, Psaty BM, Heckbert SR, Laurie CC. A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. Am J Epidemiol. 2021 Oct 1;190(10):1977-1992. doi: 10.1093/aje/kwab115. PMID: 33861317. Preprint: bioRxiv, 2020.06. 18.146423

18. Liu X, Longchamps RJ, Wiggins KL, Raffield LM, Bielak LF, Zhao W, Pitsillides A, Blackwell TW, Yao J, Guo X, Kurniansyah N, Thyagarajan B, Pankratz N, Rich SS, Taylor KD, Peyser PA, Heckbert SR, Seshadri S, Cupples LA, Boerwinkle E, Grove ML, Larson NB, Smith JA, Vasan RS, Sofer T, Fitzpatrick AL, Fornage M, Ding J, Correa A, Abecasis G, Psaty BM, Wilson JG, Levy D, Rotter JI, Bis JC; TOPMed mtDNA Working Group in NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Satizabal CL, Arking DE, Liu C. Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genom. 2021 Oct 13;1(1):100006. doi: 10.1016/j.xgen.2021.100006. PMID: 35036986

19. Damotte V, van der Lee SJ, Chouraki V, Grenier-Boley B, Simino J, Adams H, Tosto G, White C, Terzikhan N, Cruchaga C, Knol MJ, Li S, Schraen S, **Grove ML**, Satizabal C, Amin N, Berr C, Younkin S; Alzheimer's Disease Neuroimaging Initiative, Gottesman RF, Buée L, Beiser A, Knopman DS, Uitterlinden A, DeCarli C, Bressler J, DeStefano A, Dartigues JF, Yang Q, Boerwinkle E, Tzourio C, Fornage M, Ikram MA, Amouyel P, de Jager P, Reitz C, Mosley TH, Lambert JC, Seshadri S, van Duijn CM. Plasma amyloid β levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genome-wide association study in over 12,000 non-demented participants. Alzheimers Dement. 2021 Oct;17(10):1663-1674. doi: 10.1002/alz.12333. Epub 2021 May 18. PMID: 34002480

20. Rahbar MH, Samms-Vaughan M, Hessabi M, Bressler J, Gillani S, **Grove ML**, Shakspeare-Pellington S, Loveland KA. Correlation between concentrations of four heavy metals in cord blood and childhood blood of Jamaican children. J Environ Sci Health A Tox Hazard Subst Environ Eng. 2021 Sep 20:1-10. doi: 10.1080/10934529.2021.1973821. Epub 2021 Sep 20. PMID: 34542373

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    *Roger R. Williams Award for Genetic Epidemiology and the Prevention and Treatment of Atherosclerosis
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22. **Grove ML***, Volcik K, Brown E. Interaction of immune-related genetic polymorphisms and breastfeeding duration with *Helicobacter pylori* prevalence: the Pasitos Cohort Study. American Society of Human Genetics, poster, 2014. San Diego, CA, USA.
*Best Poster Award, DNA Genotek

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25. Demerath EW, Guan W, Pankow JS, **Grove ML**, North KE, Fornage M, Bressler J, Mosley TH, Boerwinkle E. Genome-wide methylation study of body mass index (BMI) in African American adults: preliminary data from the ARIC study. Circulation 127 (S12), A052. American Heart Association, 2013. Dallas, TX, USA.

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29. Rahbar MH, Samms-Vaughan M, Loveland KA, Ardjomand-Hessabi M, Bressler J, Pearson DA, Chen Z, **Grove ML**, Shakespeare-Pellington S, Bloom K, Boerwinkle E. Metabolic Genes and Blood Lead Concentrations in Jamaican Children with and without Autism Spectrum Disorders. Am J Epidemiol 175, S126. Society for Epidemiologic Research, poster, 2012. Minneapolis, MN, USA.

30. Rahbar MH, Samms-Vaughan M, Loveland KA, Ardjomand-Hessabi M, Chen Z, Bressler J, Pellington S, **Grove ML**, Bloom KM, Pearson DA, Lalor GC, Boerwinkle E. Seafood Consumption and Blood Mercury Concentrations in Jamaican Children with and without Autism Spectrum Disorders. The International Meeting for Autism Research, poster, 2012. Toronto, Ontario, Canada.

31. Rahbar MH, Samms-Vaughan M, Ardjomand-Hessabi M, Loveland KA, Dickerson A, Chen Z, Bressler J, Shakespeare-Pellington S, **Grove ML**, Wirth J, Bloom K, Pearson DA, Boerwinkle E. Blood arsenic concentrations of Jamaican children with and without Autism Spectrum Disorders. Translational Science, poster, 2012. Washington, DC, USA.

32. Rahbar MH, Samms-Vaughan M, Loveland KA, Boerwinkle E, Bressler J, Pearson DA, Assassi P, Pellington S, Beecher C, **Grove ML**, Ardjomand-Hessabi M, Bloom K. Paternal and maternal age are jointly related to autism spectrum disorders in Jamaican children. The International Meeting for Autism Research, poster, 2011. San Diego, CA, USA.

33. Rahbar MH, Loveland KA, Samms-Vaughan M, Boerwinkle E, Bressler J, del Junco D, Pearson DA, Assassi P, Pellington S, **Grove ML**, Bloom K, Beecher C, Brooks K, Ardjomand-Hessabi M. Gene-environment related epidemiological research on autism in Jamaica. The International Meeting for Autism Research, poster, 2010. Philadelphia, PA, USA.

34. Bell RJ, Herring S, **Grove ML**, Boerwinkle E, Braun MC, Doris PA. Genetic architecture of hypertensive renal injury in the spontaneously hypertensive rat (SHR-SP). American Society of Nephrology Renal Week, poster, 2009. San Diego, CA, USA.

35. Bell R, Dmitrieva R, Herring S, **Grove ML**, Boerwinkle E, Doris PA. Renal injury and blood pressure in SHR-A3 are controlled by genomic loci affecting Tcf2 splicing. Hypertension 54 (4), e45. High Blood Pressure Research Conference, oral presentation, 2009. Chicago, IL, USA.

36. Canos D, Avery C, Franceschini N, Maeda N, Muallem H, Heiss G, **Grove M**, Boerwinkle E, North K. The consistent effect of low density lipoprotein-receptor mutations on incident coronary heart disease across strata of APOE alleles: The ARIC study. Am J Epidemiol 167 (11), S70. Society for Epidemiologic Research, poster, 2008. Chicago, IL, USA.

37. Knowles JW, Assimes TL , Priest JR, Tabor H, Southwick A, Volcik KA, Boerwinkle E, **Grove ML**, Sidney S, Risch N, Irbibarren C, Go A, Myers R, Fortmann S, Hlatky M, Quertermous T. Failure to replicate an association of a single nucleotide polymorphism in the oxidized LDL receptor gene (ORL1) with CAD. American Heart Association Young Investigators Forum, poster, 2006. San Francisco, CA, USA.

38. Dmitrieva RI, Hinojos CA, Boerwinkle E, **Grove M**, Fornage M, Doris P. Identical by descent mapping of hypertension genes in SHR. Hypertension 48 (4), e62. Council for High Blood Pressure Research, poster, 2006. Chicago, IL, USA.

Internet Resources

UTHealth Core Facilities, Human Genetics Center Laboratory
https://uthealth.corefacilities.org//service_center/show_external/3992?name=human-genetics-center-laboratory

UTHealth Rees Scientific (Freezer Monitoring)
https://utsph.bloomfire.com/posts/538642-rees-scientifc-freezer-monitoring

Active Research Support

75N92022D00001 (PI: Couper) 11/15/2022 – 11/14/2023 1.20 CM
NHLBI / University of North Carolina at Chapel Hill
Atherosclerosis Risk in Communities (ARIC) Study - Coordinating Center
A supplement to the parent contract will allow for extraction of RNA to be provided to the TOPMed program for RNA sequencing.
Role: Co-Investigator

5R01HL143885 (PI: Gordon-Larson) 11/01/2022 – 3/31/2024 0.48 CM
NHLBI / University of North Carolina at Chapel Hill
Leveraging multi-omics approaches to examine metabolic challenges of obesity in relation to cardiovascular diseases
This project will provide untargeted metabolome profiles on Coronary Artery Risk Development in Young Adults (CARDIA) Study samples.
Role: Consortium Principal Investigator

5R01AG072592 (PI: Hyacinth) 09/15/2021 – 05/31/2023 1.20 CM
NIA / University of Cincinnati
Cerebral small vessel disease burden and racial disparity in vascular cognitive impairment and Alzheimers disease and its related dementias
The University of Texas Health Science at Houston, School of Public Health will be responsible for genotyping of ~1,900 samples for five selected variants in the Apolipoprotein E and Triggering Receptor Expressed on Myeloid Cells 1 genes and a quality control array to ascertain ethnicity and gender.
Role: Consortium Principal Investigator

HHSN268201800002I/75N92022F00001 (PI: Abecasis) 04/01/2022 – 03/31/2023 1.02 CM
NHLBI / University of Michigan
Tran-Omics for Precision Medicine (TOPMed) Informatics Research Center (IRC)
Deliverables for this contact include quality control and preliminary analysis of structural variants from whole genome sequencing data, metabolomics and methylation data provided by TOPMed.
Role: Co-Investigator

HHSN268201600033I (PI: Gibbs) 09/25/2020 –09/24/2024 2.40 CM
NHLBI / Baylor College of Medicine
TOPMed Centralized Omics Resource (CORE)
Task 5 will provide targeted and non-targeted metabolite profiling for plasma or serum samples from individuals included in designated NHLBI Trans-Omics for Precision Medicine (TOPMed) program Project Studies.
Role: Co-Investigator

1R01AR073178-01 (PI: Tin) 09/01/2018 – 11/30/2023 1.20 CM
NIH / University of Mississippi Medical Center
Identifying Novel Biological Pathways for Gout by Integrating DNA Methylation and Genetics
The Human Genetics Center Laboratory will run the MethylationEPIC array on 1,300 samples in order to characterize methylation and evaluate epigenetic patterns associated with gout.
Role: Consortium Principal Investigator

1R01AG061022-01 (mPI: Gonzales/Fornage) 03/15/2019 – 01/31/2024 0.60 CM
NIH / University of California-San Diego
Neurocognitive Aging, MCI and Alzheimer's Disease DNA Methylation Among Diverse Latinos
In this project we will ascertain genome-wide methylation measurements in a subset of Hispanic Community Health Study / Study of Latinos (HCHS/SOL) participants in order to determine epigenetic profiles of neurocognitive traits.
Role: Co-Investigator

1R01HL141824-01 (PI: Yu) 04/01/2018 - 03/31/2023 0.60 CM
NIH / NHLBI
Metabolic Signatures Underlying Cardiac Function for Heart Failure in Multi-Ethnic Populations
The goal of this project is to use multi-omics technologies to identify novel genetic determinants and metabolic signatures associated with cardiac dysfunction and heart failure risk.
Role: Co-Investigator

1R01DK116028-01 (PI: Sotres-Alvarez) 07/01/2020 – 06/30/2023 0.60 CM
NIH / University of North Carolina at Chapel Hill
Preconceptional Health of Latinas and its Association with Child Adiposity
The Human Genetics Center (HGC) Laboratory at the University of Texas Health Science at Houston, School of Public Health will be responsible for DNA isolation and genotyping of 444 Hispanic Community Health Study / Study of Latinos (HCHS/SOL) children.
Role: Consortium Principal Investigator

1R01HL148050 (PI: Ballantyne) 07/01/2019 – 06/30/2023 0.60 CM
NIH / Baylor College of Medicine
Clonal Hematopoiesis in Humans: Determinants of Development and Progression
This project will assess the association of hematopoeitc cell mutations with cardiovascular disease in an ethnically diverse cohort.
Role: Co-investigator

U01 HL096812 (mPI: (Coresh/ Gottesman) 09/26/2019 – 12/30/2023 0.60 CM
NIH / Johns Hopkins University
ARIC Neurocognitive Study (ARIC-NCS) Renewal
This renewal, including ARIC visits 8-11 (2020-2023) will build upon our prior studies, which demonstrated the importance of midlife vascular risk factors in the development of cognitive decline and dementia, by also considering factors associated with maintenance of both cognitive and physical function. Finally, this study will identify potential targets for prevention by evaluating a concept called cognitive reserve, which refers to maintenance of cognitive function despite abnormalities seen on brain imaging; this set of studies could contribute to prevention and reduction in the worldwide burden of Alzheimer's and other dementias.
Role: Co-investigator

R01DK124399 (PI: Grams) 03/01/2022 – 2/28/2023 0.90 CM
NIH / New York University
Integrative Omics, Chronic Kidney Disease, and Adverse Outcomes in Older Adults
The objective of the proposed research is to apply an integrated approach combining genetics, epigenetics, proteomics, and metabolomics in a deeply phenotyped cohort to yield novel insights into the pathogenesis and prognosis of chronic kidney disease, and potentially uncover novel targets.
Role: Co-investigator

Completed Research Support

Gift account (PI: Boerwinkle) 09/01/2016 - 08/31/2023 0.36 CM
John L. Hern (JLH) Foundation
Stay Off the List!
For this project, we propose to develop novel predictive methods and a mechanistic understanding of the development of end-stage heart and kidney failure to prevent the need for transplants in many patients.
Role: Co-Investigator

1R01HL154385 (PI: Andrade) 08/15/2020 – 06/30/2022 0.60 CM
NHLBI / University of Washington
Structural and Nucleotide Variation as Genomic Risks for Venous Thrombosis: TOPMed and INVENT Collaboration
In this project we will validate structural variants associated with venous thrombosis that will be discovered from TOPMed studies using the analysis commons.
Role: Co-investigator

R01MD013349 (MPI: Aiello & Harris) 07/01/2018 – 07/31/2022 0.60 CM
NIH / University of North Carolina at Chapel Hill
The Add Health Epigenome Resource: Life Course Stressors and Epigenomic Modifications in Adulthood
This research will assess epigenome-wide DNA methylation patterns by life exposure to psychosocial stressors in adulthood.
Role: Co-Investigator

RP180166 (PI: Hildebrandt) 03/01/2018 - 02/28/2022 0.60 CM
CPRIT
Molecular Mechanisms of Anthracycline Response in Cardiomyocytes and Link to Genetic Susceptibility to Cardiotoxicity in Long-term Childhood Cancer Survivors
This proposal will test the hypothesis that functional changes occur in the human cardiomyocyte following exposure to anthracyclines and that identification of the key mediators of these molecular mechanisms can provide a biological link to genetic susceptibility to cardiotoxicity in long-term childhood cancer survivors previously treated with anthracyclines.
Role: Co-Investigator

R01HL131136-S1 (Boerwinkle) 9/5/2018 - 11/30/2020 0.60 CM
NIH / NHLBI
Epigenetics of Successful Aging - Administrative Supplement
This supplement will make available and analyze TOPMed and related data in an “Analysis Commons” where harmonized phenotype, genome sequence and other-omics data from multiple studies are brought together,

analyzed and interpreted to promote novel gene and variant discovery.
Role: Co-Investigator

4R00HL130580-03 (PI: Justice) 04/01/2016 – 08/31/2020 0.60 CM
NIH / NHLBI / Geisinger Health System
Sex- and Smoking- Specific DNA Methylation Signatures of Central Adiposity Change
This project will examine differential epigenetic effects on central adiposity by age and time, and to examine the causal relationships between central adiposity change, methylation, and environmental exposures.
Role: Consortium Principal Investigator

R01DK101505 (PI: Kelly) 08/21/2015 – 05/31/2020 0.96 CM
NIH / Tulane University
Whole-exome Sequencing Study of Diabetic Nephropathy
The overall objective of the proposed study is to identify novel genes and functional variants associated with diabetic nephropathy (DN) by conducting whole-exome sequencing, follow-up targeted sequencing, and replication studies among DN cases and controls of African and European ancestry.
Role: Co-Investigator

2P01CA138338-06 (PI: Hecht) 09/21/2016 – 08/30/2021 0.60 CM
NIH / U of Minnesota
Mechanisms of Ethnic/Racial Differences in Lung Cancer Due to Cigarette Smoking
The Human Genetics Center Laboratory will process ~400 samples using the MethylationEPIC array s in order to characterize methylation differences in lung cancer cases that may be due to cigarette smoking.
Role: Consortium Principal Investigator

5R01ES022165 (PI: Rabhar) 09/12/2013 - 04/30/2019 0.60 CM
NIH / NIEHS / NICHD / FIC
Epidemiological Research on Autism in Jamaica - Phase II
This case/control study assesses the role of heavy metals and genetic variation in Jamaican children with Autism Spectrum Disorders.
Role: Program Manager – Research

Gift account (mPI:Northrup/Sing Au/Hixson/Morrison) 12/01/2016 - 11/30/2018 0.36 CM
UTHealth President's Collaborative Research Award
Unlocking the Mysteries of Neural Tube Defects
This project aims to investigate folate deficiency in relation to neural tube defects using multi-omics approaches in human cell models.
Role: Co-Investigator

5R21DK112087-02 (PI: Tin) 09/01/2017 – 08/31/2018 0.96 CM
NIH / Johns Hopkins University
Risk of Chronic Kidney Disease Associated with GSTM1 Deletions
The Human Genetics Center Laboratory will be responsible for genotyping of 200 samples using a quantitative PCR assay to identify significantly associated metabolites with *GSTM1* copy number or *APOL1* G1 and G2 risk variants.
Role: Consortium Principal Investigator

5U01HL120393-04 (PI: Rice) 03/01/2018 – 08/31/2018 0.60 CM

NIH / U of Washington

Annotation of dbGaP Variables for TOPMed

In this project we will annotate Atherosclerosis Risk in Communities (ARIC) phenotype variables that reside in the database of Genotypes and Phenotypes (dbGaP) for categorization within the NIH Commons.

Role: Consortium Principal Investigator

5U01AG049506-03 (PI: Boerwinkle) 06/15/2014 - 05/31/2018 0.60 CM

NIH / NIA

Sequence-based Discovery of AD Risk & Protective Alleles

This project seeks to identify genes from whole genome sequence data associated with increased risk of or protection from Alzheimer's Disease.

Role: Program Manager - Research

5UL1TR000371-09 (PI: McPherson) 06/27/2012 - 05/31/2018 0.60 CM

NIH / NCATS

Center for Clinical and Translational Sciences

The goal of the Center for Clinical and Translational Sciences (CCTS) is to facilitate clinical and translational research at The University of Texas Health Science Center at Houston, The University of Texas M.D. Anderson Cancer Center, and the Memorial Hermann Hospital System.

Role: Program Manager – Research

1R21DK112087-01 (PI: Grams) 04/01/2017 - 03/31/2018 0.60 CM

NIH / Johns Hopkins University

Metabolomics and Genomics in African Americans with CKD

The Human Genetics Center Laboratory will be responsible for genotyping 800 samples with the Multi-Ethnic Global (MEG) genotyping array further understand the relationship between genomics and chronic kidney disease progression in African Americans.

Role: Consortium Principal Investigator