Curriculum Vitae – 10/17/2025

Name	Paul S. de Vries	Address	1200 Pressler Street, Suite E-429, Houston, TX
Nationality	Dutch (US permanent resident)		
Telephone	+1 (713) 500 9809	E-mail	paul.s.devries@uth.tmc.edu

---

Research Interests

I work on large scale genomic studies within a variety of international consortia to unravel the genetic determinants of cardiovascular disease and its risk factors, with a special emphasis on hemostatic factors. I believe that, as genetic epidemiologists, we have the responsibility to not only discover new associations, but to also translate them into meaningful biological and clinical insights. As such I am particularly interested in approaches such as Mendelian randomization, which has the potential to transform our understanding of disease etiology, and genetic risk prediction, which may give us new tools to prevent disease.

Experience

09/2023 – Present	*Associate Professor with Tenure* Human Genetics Center, Department of Epidemiology, School of Public Health, University of Texas Health Science Center at Houston (UTHealth-SPH), Houston, TX, USA
11/2018 – 09/2023	*Tenure Track Assistant Professor* Human Genetics Center, Department of Epidemiology, School of Public Health, UTHealth-SPH, Houston, TX, USA
08/2017 – 11/2018	*Non-Tenure Track Assistant Professor* Human Genetics Center, Department of Epidemiology, UTHealth-SPH, Houston, TX, USA
04/2016 – 07/2017	*Postdoctoral Research Fellow* Human Genetics Center, Department of Epidemiology, UTHealth-SPH, Houston, TX, USA
05/2014 – 06/2014	*Visiting Researcher* Faculty of Medicine, School of Public Health, Imperial College, London, United Kingdom
08/2012 – 01/2016	*Doctoral Research Fellow* Cardiovascular Group, Department of Epidemiology, Erasmus Medical Center, Rotterdam, the Netherlands

02/2012 – 08/2012	*Research Intern* School of Nutrition and Translational Research in Metabolism, Maastricht University, Maastricht, the Netherlands

---

Education

08/2012 – 01/2016	*Molecular Epidemiology* PhD Erasmus University Rotterdam, Rotterdam, the Netherlands
08/2011 – 08/2012	*Public Health: Specialization in Epidemiology* MSc Maastricht University, Maastricht, the Netherlands
02/2008 – 06/2011	*Life Sciences* BSc – Honours Program University College Maastricht, Maastricht, the Netherlands

---

Published Manuscripts

*Contributed equally as first or last authors.

Mentored trainees from UTHealth are underlined.

Manuscripts with > 20 authors are shown with condensed author lists.

H-index: 46 (Google Scholar, 10/17/2025)

Citations: 10,690 (Google Scholar, 10/17/2025)

First and last author manuscripts

1. Friedman RK, Heath AS, Huffman JE, Baker JT, Hasbani NR, Gagliano Taliun SA, Chen MH, Howard TE, Lewis JP, Pantratz N, Patil S, Reiner AP, Thibord F, Yanek LR, Yao J, Chen HH, Curran JE, Faraday N, Guo X, Wheeler MM, […], **de Vries PS.** (2025) Genetic study of von Willebrand factor antigen levels ≤ 50 IU/dL identifies variants associated with increased risk of VWD and bleeding. *Journal of Thrombosis and Haemostasis*. 23(8):2410-2421.
2. Hahn J, Temprano-Sagrera G, Hasbani NR, Ligthart S, Dehghan A, Wolberg AS, Smith NL, Sabater-Lleal M, Morrison AC, **de Vries PS.** (2024) Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein levels. *Journal of Thrombosis and Haemostasis*. 22(12):3448-3459.
3. Huffman JE, Nicholas J, Hahn J, Heath AS, Raffield LM, Yanek LR, Brody JA, Thibord F, Almasy L, Bartz TM, Bielak LF, Bowler RP, Carrasquilla GD, Chasman DI, Chen MH, Emmert DB, Ghanbari M, Haessler J, Hottenga JJ, Kleber ME, [...] **de Vries PS***, Sabater-Lleal M*, Morrison AC*, Smith NL*. (2024) Whole-genome analysis of plasma fibrinogen reveals population-differentiated genetic regulators with putative liver roles. *Blood*. 144(21):2248-2265.
4. **de Vries PS**, Reventun P, Brown MR, Heath AS, Huffman JE, Le NQ, Bebo A, Brody JA, Temprano-Sagrera G, Raffield LM, Ozel AB, Thibord F, Jain D, Lewis JP, Rodriguez BAT, Pankratz N, Taylor KD,

Polasek O, Chen MH, Yanek LR, et al. (2024) A genetic association study of circulating coagulation Factor VIII and von Willebrand Factor levels. *Blood.* 143(18):1845-1855.

5. **de Vries PS**, Conomos MP, Singh K, Nicholson CJ, Jain D, Hasbani NR, Jiang W, Lee S, Cardenas CLL, Lutz SM, Wong D, Guo X, Yao J, Young EP, Tcheandjieu C, Hilliard AT, Bis LC, Bielak LF, Brown MR, Musharoff S, et al. (2023) Whole-genome sequencing uncovers two loci for coronary artery calcification and identifies ARSE as a regulator of vascular calcification. *Nature Cardiovascular Research*. 2:1159-1172.
6. Hasbani NR, Westerman KE, Kwak SH, Chen H, Li X, Di Corpo D, Wessel J, Bis JC, Sarnowski C, Wu P, Bielak LF, Guo X, Heard-Costa N, Kinney GL, Mahaney MC, Montasser ME, Palmer ND, Raffield LM, Terry JG, […], **de Vries PS**. (2023) Type 2 Diabetes Modifies the Association of CAD Genomic Risk Variants With Subclinical Atherosclerosis. *Circulation Genomics and Precision Medicine*. 16(6):e004176.
7. Bebo A, Jarmul JA, Pletcher MJ, Hasbani NR, Couper D, Nambi V, Ballantyne CM, Fornage M, Morrison AC, Avery CL, **de Vries PS**. (2023) Coronary heart disease and ischemic stroke polygenic risk scores and atherosclerotic cardiovascular disease in a diverse, population-based cohort study. *PLoS One*. 8(6):e0285259.
8. Hahn J, Bressler J, Domingo-Relloso A, Chen MH, McCartney DL, Teumer A, van Dongen J, Kleber ME, Aïssi D, Swenson BR, Yao J, Zhao W, Huang J, Xia Y, Brown MR, Costeira R, de Geus EJC, Delgado GE, Dobson DA, Elliott P, [...], **de Vries PS.** (2023) DNA methylation analysis identifies novel genetic loci associated with circulating fibrinogen levels in blood. *Journal of Thrombosis and Haemostasis*. 21(5):1135-1147.
9. Hasbani NR, Ligthart S, Brown MR, Heath AS, Bebo A, Ashley KE, Boerwinkle E, Morrison AC, Folsom AR, Aguilar D, **de Vries PS**. (2022) American Heart Association's Life's Simple 7: Lifestyle recommendations, polygenic risk, and lifetime risk of coronary heart disease. *Circulation*. 23(1):148.
10. Liu J*, **de Vries PS***, Del Greco M F, Johansson Å, Schraut KE, Hayward C, van Dijk KW, Franco OH, Hicks AA, Vitart V, Rudan I, Campbell H, Polašek O, Pramstaller PP, Wilson JF, Gyllensten U, van Duijn CM, Dehghan A, Demirkan A. (2022) A multi-omics study of circulating phospholipid markers of blood pressure. *Scientific Reports*. 12(1):574.
11. Castaneda AB, Petty LE, Scholz M, Jansen R, Weiss S, Zhang X, Schramm K, Beutner F, Kirsten H, Schminke U, Hwang SJ, Marzi C, Dhana K, Seldenrijk A, Krohn K, Homuth G, Wolf P, Peters MJ, Dörr M, Peters A, […], Dehghan A*, **de Vries PS*** (2021). Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. *Human Molecular Genetics*. 31(7):1171-1182.
12. Ligthart S*, Hasbani NR*, Ahmadizar F, van Herpt TTW, Leening MJG, Uitterlinden AG, Sijbrands EJG, Morrison AC, Boerwinkle E, Pankow JS, Selvin E, Ikram MA, Kavousi M, **de Vries PS***, Dehghan A*. (2021) Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. *Diabetes Medicine*. 38(10):e14639.
13. **de Vries PS***, Sabater-Lleal M*, Huffman JE*, Marten J*, Song C, Pankratz N, Bartz TM, de Haan HG, Delgado GE, Eicher JD, Martinez-Perez A, Ward-Caviness CK, Brody JA, Chen MH, de Maat MPM, Frånberg M, Gill D, Kleber ME, Rivadeneira F, Soria JM, et al. (2019) A genome-wide association study identifies new loci for Factor VII and implicates Factor VII in ischemic stroke etiology. *Blood*. 135(5):620-635.
14. Maners J*, Gill D*, Pankratz N, Laffan MA, Wolberg AS, de Maat MPM, Ligthart S, Tang W, Ward-Caviness CK, Fornage M, Debette S, Dichgans M, McKnight B, Boerwinkle E, CHARGE Inflammation Working Group, INVENT Consortium, MEGASTROKE consortium of the International Stroke Genetics Consortium (ISGC), Smith NL, Morrison AC, Dehghan A*, **de Vries PS***. (2020). A Mendelian randomization of γ' fibrinogen and total fibrinogen levels on venous thromboembolism and ischemic stroke. *Blood*. 136(26):3062-3069.

15. Hahn J*, Fu YP*, Brown MR*, Bis JC*, **de Vries PS***, Feitosa MF, Yanek LR, Weiss S, Giulianini F, Smith AV, Guo X, Bartz TM, Becker DM, Becker LC, Boerwinkle E, Brody JA, Chen YI, Franco OH, Grove M, Harris TB, et al. (2020) Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. *PLoS One*. 15(11):e0230035.
16. Small AM, Huffman JE, Klarin D, Sabater-Lleal M, Lynch JA, Assimes TL, Sun YV, Miller D, Freiberg MS, Morrison AC, Rader DJ, Wilson PWF, Cho K, Tsao PS, Chang KM, Smith NL, O'Donnell CJ, **de Vries PS***, Damrauer SM*. (2020). Mendelian Randomization Analysis of Hemostatic Factors and their Contribution to Peripheral Artery Disease. *ATVB*. 41(1):380-386.
17. **de Vries PS***, Brown MR*, Bentley AR*, Sung YJ, Winkler TW, Ntalla I, Schwander K, Kraja AT, Guo X, Franceschini N, Cheng CY, Sim X, Vojinovic D, Huffman JE, Musani SK, Li C, Feitosa MF, Richard MA, Noordam R, Aschard H, et al. (2019) Multi-Ancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*. 188(6):1033-1054.
18. Sabater-Lleal M*, Huffman JE*, **de Vries PS***, Marten J*, Mastrangelo MA, Song C, Pankratz N, Ward-Caviness CK, Yanek LR, Trompet S, Delgado GE, Guo X, Bartz TM, Martinez-Perez A, Germain M, de Haan HG, Ozel AB, Polasek O, Smith AV, Eicher JD, Reiner AP, et al. (2019) Genome-wide association trans-ethnic meta-analyses identifies novel associations regulating coagulation Factor VIII and von Willebrand Factor plasma levels. *Circulation*. 139(5):620-635.
19. **de Vries PS***, Yu B*, Feofanova EV, Metcalf GA, Brown MR, Zeighami AL, Liu X, Muzny DM, Gibbs RA, Boerwinkle E, Morrison AC. et al. (2017) Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. *Human Molecular Genetics*. 26(17):3442-3450.
20. **de Vries PS**, Sabater-Lleal M, Chasman DI, Trompet S, Ahluwalia TS, Teumer A, Kleber ME, Chen MH, Wang JJ, Attia JR, Marioni RE, Steri M, Weng LC, Pool R, Grossmann V, Brody JA, Venturini C, Tanaka T, Rose LM, Oldmeadow C, et al. (2017) Comparison of HapMap and 1000 Genomes reference panels in a large-scale genome-wide association study. *PLOS O*ne. 12(1):e0167742.
21. **de Vries PS***, van Herpt TT*, Ligthart S, Hofman A, Ikram MA, van Hoek M, Sijbrands EJ, Franco OH, de Maat MP, Leebeek FW, Dehghan A. (2017) ADAMTS13 activity as a novel risk factor for incident type 2 diabetes mellitus: a population-based cohort study. *Diabetologia*. 60(2):280-286.
22. Yu B*, **de Vries PS***, Metcalf GA, Wang Z, Feofanova EV, Liu X, Muzny DM, Wagenknecht LE, Gibbs RA, Morrison AC, Boerwinkle E. (2016) Whole genome sequence analysis of serum amino acid levels. Geno*me Biology*. 17(1):237.
23. Sedaghat S*, **de Vries PS***, Boender J, Sonneveld MA, Hoorn EJ, Hofman A, de Maat MP, Franco OH, Ikram MA, Leebeek FW, Dehghan A. (2016). Von Willebrand factor, ADAMTS13 activity and decline in kidney function: a cohort study. *American Journal of Kidney Diseases.* 68(5):726-732.
24. **de Vries PS**, Chasman DI, Sabater-Lleal M, Chen MH, Huffman JE, Steri M, Tang W, Teumer A, Marioni RE, Grossmann V, Hottenga JJ, Trompet S, Müller-Nurasyid M, Zhao JH, Brody JA, Kleber ME, Guo X, Wang JJ, Auer PL, Attia JR, et al. (2016). A meta-analysis of 120246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics.* 25(2):358-70.
25. **de Vries PS**, Kavousi M, Ligthart S, Uitterlinden AG, Hofman A, Franco OH, Dehghan A. (2015) Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. *International Journal of Epidemiology.* 44(2):682-8.
26. **de Vries PS**, Boender J, Sonneveld MA, Rivadeneira F, Ikram MA, Rottensteiner H, Hofman A, Uitterlinden AG, Leebeek FW, Franco OH, Dehghan A, de Maat MP. (2015) Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. *Blood.* 125(25):3949-55.
27. **de Vries PS**, Gielen M, Rizopoulos D, Rump P, Godschalk R, Hornstra G, Zeegers MP. (2014) Association between polyunsaturated fatty acid concentrations in maternal plasma phospholipids during

pregnancy and offspring adiposity at age 7: the MEFAB cohort. *Prostaglandins, Leukotrienes & Essential Fatty Acids.* 91(3):81-5.

Other manuscripts

1. Selvaraj MS, Li X, Li Z, Van Buren E, Haidermota S, Postupaka D, Hornsby W, Bis JC, Brody JA, Cade BE, Chung RH, Curran JE, Damrauer SM, de Las Fuentes L, de Vries PS, Duggirala R, Freedman BI, Graff M, Guo X, Hidalgo BA, et al. (2025) Whole genome sequence analysis of low-density lipoprotein cholesterol across 246 K individuals. *Genome Biology*. In press.
2. Nagarajan P, Winkler TW, Bentley AR, Miller CL, Kraja AT, Schwander K, Lee S, Wang W, Brown MR, Morrison JL, Giri A, O'Connell JR, Bartz TM, de Las Fuentes L, Gudmundsdottir V, Guo X, Harris SE, Huang Z, Kals M, Kho M, Lefevre C, et al. (2025) A large-scale genome-wide study of gene-sleep duration interactions for blood pressure in 811,405 individuals from diverse populations. *Molecular Psychiatry*. Epub ahead of print.
3. Bentley AR, Brown MR, Musani SK, Schwander KL, Winkler TW, Sims M, Kilpeläinen TO, Aschard H, Bartz TM, Bielak LF, Chai JF, Chitrala KN, Franceschini N, Graff M, Guo X, Hartwig FP, Horimoto ARVR, Lim E, Liu Y, Manning AK, et al. (2025) Multi-ancestry genome-wide association analyses incorporating SNP-by-psychosocial interactions identify novel loci for serum lipids. *Translational Psychiatry*. 15(1):207.
4. Georgakis MK, Malik R, Bounkari OE, Hasbani NR, Li J, Huffman JE, Shakt G, Tack RWP, Kimball TN, Asare Y, Morrison AC, Tsao NL, Judy R, Mitchell BD, Xu H, Montasser ME, Do R, Kenny EE, Loos RJF, Terry JG, […], **de Vries PS**, Dichgans M. (2025) Rare damaging CCR2 variants are associated with lower lifetime cardiovascular risk. *Genome Medicine*. 17(1):27.
5. Iyer KR, Clarke SL, Guarischi-Sousa R, Gjoni K, Heath AS, Young EP, Stitziel NO, Laurie C, Broome JG, Khan AT, Lewis JP, Xu H, Montasser ME, Ashley KE, Hasbani NR, Boerwinkle E, Morrison AC, Chami N, Do R, Rocheleau G, […], **de Vries PS**, Assimes TL. (2025) Unveiling the Genetic Landscape of Coronary Artery Disease Through Common and Rare Structural Variants. *Journal of the American Heart Association*. 14(4):e036499.
6. Li X, Chen H, Selvaraj MS, Van Buren E, Zhou H, Wang Y, Sun R, McCaw ZR, Yu Z, Jiang MZ, DiCorpo D, Gaynor SM, Dey R, Arnett DK, Benjamin EJ, Bis JC, Blangero J, Boerwinkle E, Bowden DW, Brody JA, et al. (2025) A statistical framework for multi-trait rare variant analysis in large-scale whole-genome sequencing studies. *Nature Computational Science*. Epub ahead of print.
7. Jakubek YA, Ma X, Stilp AM, Yu F, Bacon J, Wong JW, Aguet F, Ardlie K, Arnett DK, Barnes K, Bis JC, Blackwell T, Becker LC, Boerwinkle E, Bowler RP, Budoff MJ, Carson AP, Chen J, Cho MH, Coresh J, et al. (2025) Genomic and phenotypic correlates of mosaic loss of chromosome Y in blood. *American Journal of Human Genetics*. 112(2):276-290.
8. Dzaye O, Razavi AC, Dardari ZA, Wang FM, Honda Y, Nasir K, Coresh J, Howard-Claudio CM, Jin J, Yu B, **de Vries PS**, Wagenknecht L, Folsom AR, Blankstein R, Kelly TN, Whelton SP, Mortensen MB, Wang Z, Chatterjee N, Matsushita K, Blaha MJ. (2024) Polygenic Risk Scores and Extreme Coronary Artery Calcium Phenotypes (CAC=0 and CAC≥1000) in Adults ≥75 Years Old: The ARIC Study. *Circulation Cardiovascular Imaging*. 17(11):e016377.
9. Rocheleau G, Clarke SL, Auguste G, Hasbani NR, Morrison AC, Heath AS, Bielak LF, Iyer KR, Young EP, Stitziel NO, Jun G, Laurie C, Broome JG, Khan AT, Arnett DK, Becker LC, Bis JC, Boerwinkle E, Bowden DW, Carson AP, […], **de Vries PS**, Do R. (2024) Rare variant contribution to the heritability of coronary artery disease. *Nature Communications*. 15(1):8741.
10. Dobson DA, Fish RJ, **de Vries PS**, Morrison AC, Neerman-Arbez M, Wolberg AS. (2024) Regulation of fibrinogen synthesis. *Thrombosis Research*. 242:109134.
11. Kwak SH, Hernandez-Cancela RB, DiCorpo DA, Condon DE, Merino J, Wu P, Brody JA, Yao J, Guo X, Ahmadizar F, Meyer M, Sincan M, Mercader JM, Lee S, Haessler J, Vy HMT, Lin Z, Armstrong ND, Gu S,

Tsao NL, et al. (2024) Time-to-Event Genome-Wide Association Study for Incident Cardiovascular Disease in People With Type 2 Diabetes. *Diabetes Care*. Online ahead of print.

12. Zhu X, Yang Y, Lorincz-Comi N, Li G, Bentley AR, **de Vries PS**, Brown M, Morrison AC, Rotimi CN, Gauderman WJ, Rao DC, Aschard H; CHARGE Gene-lifestyle Interactions Working Group. (2024) An approach to identify gene-environment interactions and reveal new biological insight in complex traits. Nature Communications. 15(1):3385.
13. Guirette M, Lan J, McKeown NM, Brown MR, Chen H, **de Vries PS**, Kim H, Rebholz CM, Morrison AC, Bartz TM, Fretts AM, Guo X, Lemaitre RN, Liu CT, Noordam R, de Mutsert R, Rosendaal FR, Wang CA, Beilin LJ, Mori TA, et al. (2024) Genome-Wide Interaction Analysis With DASH Diet Score Identified Novel Loci for Systolic Blood Pressure. *Hypertension*. 81(3):552-560.
14. Armstrong ND, Srinivasasainagendra V, Ammous F, Assimes TL, Beitelshees AL, Brody J, Cade BE, Ida Chen YD, Chen H, **de Vries PS**, Floyd JS, Franceschini N, Guo X, Hellwege JN, House JS, Hwu CM, Kardia SLR, Lange EM, Lange LA, McDonough CW, et al. (2023) Whole genome sequence analysis of apparent treatment resistant hypertension status in participants from the Trans-Omics for Precision Medicine program. *Frontiers in Genetics*. 14:1278215.
15. Reventun P, Toledano-Sanz P, Alcharani N, Viskadourou M, Morrison AC, Sabater-Lleal M, Wolberg AS, **de Vries PS**, Smith NL, Osburn WO, Arvanitis M, Lowenstein CJ. (2024) CD36 regulates factor VIII secretion from liver endothelial cells. Blood Advances. 8(1):143-149.
16. Gallego-Fabrega C, Temprano-Sagrera G, Cárcel-Márquez J, Muiño E, Cullell N, Lledós M, Llucià-Carol L, Martin-Campos JM, Sobrino T, Castillo J, Millán M, Muñoz-Narbona L, López-Cancio E, Ribó M, Alvarez-Sabin J, Jiménez-Conde J, Roquer J, Tur S, Obach V, Arenillas JF, et al. (2023) A multi-trait genetic Study of Hemostatic factors and Hemorrhagic transformation after stroke treatment. *Journal of Thrombosis and Haemostasis.* S1538-7836(23)00870-X
17. de Las Fuentes L, Schwander KL, Brown MR, Bentley AR, Winkler TW, Sung YJ, Munroe PB, Miller CL, Aschard H, Aslibekyan S, Bartz TM, Bielak LF, Chai JF, Cheng CY, Dorajoo R, Feitosa MF, Guo X, Hartwig FP, Horimoto A, Kolčić I, et al. (2023) Gene-educational attainment interactions in a multi-population genome-wide meta-analysis identify novel lipid loci. *Frontiers in Genetics*. 14:1235337.
18. Wang Y, Selvaraj MS, Li X, Li Z, Holdcraft JA, Arnett DK, Bis JC, Blangero J, Boerwinkle E, Bowden DW, Cade BE, Carlson JC, Carson AP, Chen YI, Curran JE, **de Vries PS**, Dutcher SK, Ellinor PT, Floyd JS, Fornage M, et al. (2023) Rare variants in long non-coding RNAs are associated with blood lipid levels in the TOPMed whole-genome sequencing study. *American Journal of Human Genetics*. 110(10):1704-1717.
19. Kavousi M, Bos MM, Barnes HJ, Lino Cardenas CL, Wong D, Lu H, Hodonsky CJ, Landsmeer LPL, Turner AW, Kho M, Hasbani NR, **de Vries PS**, Bowden DW, Chopade S, Deelen J, Benavente ED, Guo X, Hofer E, Hwang SJ, Lutz SM, et al. (2023) Multi-ancestry genome-wide study identifies effector genes and druggable pathways for coronary artery calcification. *Nature Genetics*. 55(10):1651-1664.
20. Lee MP, Dimos SF, Raffield LM, Wang Z, Ballou AF, Downie CG, Arehart CH, Correa A, **de Vries PS**, Du Z, Gignoux CR, Gordon-Larsen P, Guo X, Haessler J, Howard AG, Hu Y, Kassahun H, Kent ST, Lopez JAG, et al. (2023) Ancestral diversity in lipoprotein(a) studies helps address evidence gaps. *Open Heart*. 10(2):e002382.
21. van de Vegte YJ, Eppinga RN, van der Ende MY, Hagemeijer YP, Mahendran Y, Salfati E, Smith AV, Tan VY, Arking DE, Ntalla I, Appel EV, Schurmann C, Brody JA, Rueedi R, Polasek O, Sveinbjornsson G, Lecoeur C, Ladenvall C, Zhao JH, Isaacs A,et al. (2023) Genetic insights into resting heart rate and its role in cardiovascular disease. *Nature Communications*. 1(1):4646.
22. Ji Y, Temprano-Sagrera G, Holle LA, Bebo A, Brody JA, Le NQ, Kangro K, Brown MR, Martinez-Perez A, Sitlani CM, Suchon P, Kleber ME, Emmert DB, Bilge Ozel A, Dobson DA, Tang W, Llobet D, Tracy RP, Deleuze JF, Delgado GE, et al. (2023) Antithrombin, protein C and protein S: Genome and

transcriptome wide association studies identify 7 novel loci regulation plasma levels. *ATVB*. 43(7):e254-e269.

23. Zheng J, Wheeler E, Pietzner M, Andlauer TFM, Yau MS, Hartley AE, Brumpton BM, Rasheed H, Kemp JP, Frysz M, Robinson J, Reppe S, Prijatelj V, Gautvik KM, Falk L, Maerz W, Gergei I, Peyser PA, Kavousi M, **de Vries PS**, et al. (2023) Lowering of circulating sclerostin may increase risk of atherosclerosis and its risk factors: evidence from a genome-wide association meta-analysis followed by Mendelian randomization. *Arthritis & Rheumatology*. Online ahead of print.
24. Westerman KE, Walker ME, Gaynor SM, Wessel J, DiCorpo D, Ma J, Alonso A, Aslibekyan S, Baldridge AS, Bertoni AG, Biggs ML, Brody JA, Chen YI, Dupuis J, Goodarzi MO, Guo X, Hasbani NR, Heath A, Hidalgo B, Irvin MR, et al (2023) Investigating gene-diet interactions impacting the association between macronutrient intake and glycemic traits. *Diabetes*. 72(5):653-665.
25. Dron JS, Patel AP, Zhang Y, Jurgens SJ, Maamari DJ, Wang M, Boerwinkle E, Morrison AC, **de Vries PS**, Fornage M, Hou L, Lloyd-Jones DM, Psaty BM, Tracy RP, Bis JC, Vasan RS, Levy D, Heart-Costa N, Rich SS, Guo X, et al. (2023) Rare protein-truncating DNA variants in APOB or PCSK9, low-density lipoprotein cholesterol, and risk of coronary artery disease. *JAMA Cardiology*. 8(3):258-267.
26. Dobson DV, Holle LA, Lin FC, Huffman JE, Luyendyk JP, Flick MJ, Smith NL, **de Vries, PS**, Morrison AC, Wolberg AS. (2023) Novel genetic regulators of fibrinogen synthesis identified by an in vitro experimental platform. *Journal of Thrombosis and Haemostasis*. 21(3):522-533.
27. Kanoni S, Graham SE, Wang Y, Surakka I, Ramdas S, Zhu X, Clarke SL, Bhatti KF, Vedantam S, Winkler TW, Locke AE, Marouli E, Zajac GJM, Wu KHH, Ntalla I, Hui Q, Klarin D, Hilliard AT, Wang Z, Xue C, et al. (2022) Implicating genes, pleiotropy and sexual dimorphism at blood lipid loci through trans-ancestry meta-analysis. *Genome Biology*. 23(1):268.
28. Li X, Quick C, Zhou H, Gaynor SM, Liu Y, Chen H, Selvaraj MS, Sun R, Dey R, Arnett DK, Bielak LF, Bis JC, Blangero J, Boerwinkle E, Bowden DW, Brody JA, Cade BE, Correa A, Cupples LA, Curran JE, et al. (2022) Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole-genome sequencing studies. *Nature Genetics.* 55(1):154-164.
29. Majarian TD, Bentley AR, Laville V, Brown MR, Chasman DI, **de Vries PS**, Feitosa MF, Franceschini N, Gauderman WJ, Marchek C, Levy D, Morrison AC, Province M, Rao DC, Schwander K, Sung YJ, Rotimi CN, Aschard H, Gu CC, Manning AK. (2022) Multi-omics insights into the biological mechanisms underlying gene-by-lifestyle interactions with smoking and alcohol consumption detected by genome-wide trans-ancestry meta-analysis. *Frontiers in genetics*. 13:954713.
30. Elgart M, Goodman MO, Isasi C, Chen H, **de Vries PS**, Xu H, Manichaikul AW, Franceschini N, Psaty BM, Rich SS, Rotter JI, Lloyd-Jones DM, Fornage M, Correa A, Heard-Costa NL, Vasan RS, Hernandez R, Kaplan RC, Redline S, Sofer T. (2022) Correlations between complex human phenotypes vary by genetic background, gender, and environment. *Cell Reports Medicine*. 3(12):100844.
31. Wheeler MM, Stilpt AM, Rao S, Halldórsson BV, Beyter D, Wen J, Mikhaylova AV, McHugh CP, Lane J, Jiang MZ, Raffield LM, Jun G, Sedlazeck FJ, Metcalf G, Yao Y, Bis JB, Chami N, **de Vries PS**, Pinkal Desai, James S. Floyd, et al. (2022) Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program. *Nature Communications*. 13(1):7592.
32. Aragam KG, Jiang T, Goel A, Kanoni S, Wolford BN, Atri DS, Weeks EM, Wang M, Hindy G, Zhou W, Grace C, Roselli C, Marston NA, Kamanu FK, Surakka I, Muñoz Venegas L, Sherliker P, Koyama S, Ishigaki K, Åsvold BO, et al. (2022) Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants. *Nature Genetics*. Online ahead of print.
33. Li Z, Li X, Zhou H, Gaynor SM, Selvaraj MS, Arapoglou T, Quick C, Liu Y, Chen H, Sun R, Dey R, Arnett DK, Auer PL, Bielak LF, Bis JC, Blackwell TW, Blangero J, Boerwinkle E, Bowden DW, Brody JA, et al. (2022) A framework for detecting noncoding rare variant associations of large-scale whole-genome sequencing studies. *Nature Methods*. 19(12):1599-1611.

34. Selvaraj MS, Li X, Li Z, Pampana A, Zhang DY, Park J, Aslibekyan S, Bis JC, Brody JA, Cade BE, Chuang LM, Chung RH, Curran JE, de Las Fuentes L, **de Vries PS**, Duggirala R, Freedman BI, Graff M, Guo X, Heard-Costa N, et al. (2022) Whole genome sequence analysis of blood lipid levels in >66,000 individuals. *Nature Communications*. 13(1):5995.
35. Thibord F, Klarin D, Brody JA, Chen MH, Levin MG, Chasman DI, Goode EL, Hveem K, Teder-Laving M, Martinez-Perez A, Aïssi D, Daian-Bacq D, Ito K, Natarajan P, Lutsey PL, Nadkarni GN, **de Vries PS**, Cuellar-Partida G, Wolford BN, Pattee JW, et al. (2022) Cross-Ancestry Investigation of Venous Thromboembolism Genomic Predictors. *Circulation*. 146(16):1225-1242.
36. Elgart M, Lyons G, Romero-Brufao S, Kurniansyah N, Brody JA, Guo X, Lin HJ, Raffield LM, Gao Y, Chen H, **de Vries PS**, Lloyd-Jones DM, Lange LA, Peloso GM, Fornage M, Rotter JI, Rich SS, Morrison AC, Psaty BM, Levy D, et al. (2022) Non-linear machine learning models incorporating SNPs and PRS improve polygenic prediction in diverse human populations. *Communications Biology.* 5(1):856.
37. Ramdas S, Judd J, Graham SE, Kanoni S, Wang Y, Surakka I, Wenz B, Clarke SL, Chesi A, Wells A, Bhatti KF, Vedantam S, Winkler TW, Locke AE, Marouli E, Zajac GJM, Wu KH, Ntalla I, Hui Q, Klarin D, et al. (2022) A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids. *American Journal of Human Genetics*. 109(8):1366-1387.
38. DiCorpo D, Gaynor SM, Russell EM, Westerman KE, Raffield LM, Majarian TD, Wu P, Sarnowski C, Highland HM, Jackson A, Hasbani NR, **de Vries PS**, Brody JA, Jain D, Wang H, D'Oliveira Albanus R, Varshney A, Yanek LR, Lange L, Palmer ND, et al. (2022) Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program. *Communications Biology*. 5(1):756.
39. Temprano-Sagrera G, Sitlani CM, Bone WP, Martin-Bornez M, Voight BF, Morrison AC, Damrauer SM, **de Vries PS**, Smith NL, Sabater-Lleal M. (2022) Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. *Journal of Thrombosis and Haemostasis*. 20(6):1331-1349.
40. Pankratz N, Wei P, Brody JA, Chen MH, **de Vries PS**, Huffman JE, Stimson MR, Auer PL, Boerwinkle E, Cushman M, de Maat MPM, Folsom AR, Franco OH, Gibbs RA, Haagenson KK, Hofman A, Johnsen JM, Kovar CL, Kraaij R, McKnight B, et al. (2022) Whole exome sequencing of 14,389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. *Human Molecular Genetics*. 31(18):3120-3132.
41. Kelly TN, Sun X, He KY, Brown MR, Taliun SAG, Hellwege JN, Irvin MR, Mi X, Brody JA, Franceschini N, Guo X, Hwang SJ, **de Vries PS**, Gao Y, Moscati A, Nadkarni GN, Yanek LR, Elfassy T, Smith JA, Chung RH, et al. (2022) Insights from a large-scale whole-genome sequencing study of systolic blood pressure, diastolic blood pressure, and hypertension. *Hypertension*. 79(8):1656-1667.
42. Nakao T, Bick AG, Taub MA, Zekavat SM, Uddin MM, Niroula A, Carty CL, Lane J, Honigberg MC, Weinstock JS, Pampana A, Gibson CJ, Griffin GK, Clarke SL, Bhattacharya R, Assimes TL, Emery LS, Stilp AM, Wong Q, Broome J, et al. (2022) Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. *Science Advances*. 8(14):eabl6579.
43. Laville V, Majarian T, Sung YJ, Schwander K, Feitosa MF, Chasman DI, Bentley AR, Rotimi CN, Cupples LA, **de Vries PS**, Brown MR, Morrison AC, Kraja AT, Province M, Gu CC, Gauderman WJ; CHARGE Gene-Lifestyle Interactions Working Group, Rao DC, Manning AK, Aschard H. (2022) Gene-lifestyle interactions in the genomics of human complex traits. *European Journal of Human Genetics*. 30(6):730-739.
44. Stacey D, Chen L, Stanczyk PJ, Howson JMM, Mason AM, Burgess S, MacDonald S, Langdown J, McKinney H, Downes K, Farahi N, Peters JE, Basu S, Pankow JS, Tang W, Pankratz N, Sabater-Lleal M, **de Vries PS**, Smith NL; CHARGE Hemostasis Working Group, et al. (2022) Elucidating mechanisms of

genetic cross-disease associations at the PROCR vascular disease locus. *Nature Communications*. 13(1):1222.

45. He KY, Kelly TN, Wang H, Liang J, Zhu L, Cade BE, Assimes TL, Becker LC, Beitelshees AL, Bielak LF, Bress AP, Brody JA, Chang YC, Chang YC, **de Vries PS**, Duggirala R, Fox ER, Franceschini N, Furniss AL, Gao Y, et al. (2022) Rare coding variants in RCN3 are associated with blood pressure. *BMC Genomics*. 23(1):148.
46. DiCorpo D, LeClair J, Cole JB, Sarnowski C, Ahmadizar F, Bielak LF, Blokstra A, Bottinger EP, Chaker L, Chen YI, Chen Y, **de Vries PS**, Faquih T, Ghanbari M, Gudmundsdottir V, Guo X, Hasbani NR, Ibi D, Ikram MA, Kavousi M, et al. (2022) Partitioned polygenic scores associate with disease outcomes in 454,193 individuals across 13 cohorts. *Diabetes Care*. 45(3):674-683.
47. Hindy G, Dornbos P, Chaffin MD, Liu DJ, Wang M, Selvaraj MS, Zhang D, Park J, Aguilar-Salinas CA, Antonacci-Fulton L, Ardissino D, Arnett DK, Aslibekyan S, Atzmon G, Ballantyne CM, Barajas-Olmos F, Barzilai N, Becker LC, Bielak LF, Bis JC, et al. (2022) Rare coding variants in 35 genes associate with circulating lipid levels-A multi-ancestry analysis of 170,000 exomes. *American Journal of Human Genetics*. 109(1):81-96.
48. Graham SE, Clarke SL, Wu KH, Kanoni S, Zajac GJM, Ramdas S, Surakka I, Ntalla I, Vedantam S, Winkler TW, Locke AE, Marouli E, Hwang MY, Han S, Narita A, Choudhury A, Bentley AR, Ekoru K, Verma A, Trivedi B, et al. (2021) The power of genetic diversity in genome-wide association studies of lipids. *Nature*. 600(7890):675-679.
49. Sun D, Richard M, Musani SK, Sung YJ, Winkler TW, Schwander K, Chai JF, Guo X, Kilpeläinen TO, Vojinovic D, Aschard H, Bartz TM, Bielak LF, Brown MR, Chitrala K, Hartwig FP, Horimoto ARVR, Liu Y, Manning AK, Noordam R, et al. (2021) Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. *HGG Advances*. 2(1):100013.
50. Mikhaylova AV, McHugh CP, Polfus LM, Raffield LM, Boorgula MP, Blackwell TW, Brody JA, Broome J, Chami N, Chen MH, Conomos MP, Cox C, Curran JE, Daya M, Ekunwe L, Glahn DC, Heard-Costa N, Highland HM, Hobbs BD, Ilboudo Y,et al. (2021) Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*. 108(10):1836-1851.
51. Little A, Hu Y, Sun Q, Jain D, Broome J, Chen MH, Thibord F, McHugh C, Surendran P, Blackwell TW, Brody JA, Bhan A, Chami N, **de Vries PS**, Ekunwe L, Heard-Costa N, Hobbs BD, Manichaikul A, Moon JY, Preuss MH, et al. (2021) Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. *Human Molecular Genetics*. 31(3):347-361.
52. Folsom AR, **de Vries PS**, Cushman M (2021) No prospective association of a polygenic risk score for coronary artery disease with venous thromboembolism incidence. Journal of *Thrombosis and Haemostasis*. 19(11):2841-2844.
53. Nayor M, Shen L, Hunninghake GM, Kochunov P, Barr RG, Bluemke DA, Broeckel U, Caravan P, Cheng S, **de Vries PS**, Hoffmann U, Kolossváry M, Li H, Luo J, McNally EM, Thanassoulis G, Arnett DK, Vasan RS. (2021) Progress and Research Priorities in Imaging Genomics for Heart and Lung Disease: Summary of an NHLBI Workshop. *Circulation Cardiovascular Imaging.* 14(8):e012943.
54. Murdock DR, Venner E, Muzny DM, Metcalf GA, Murugan M, Hadley TD, Chander V, **de Vries PS**, Jia X, Hussain A, Agha AM, Sabo A, Li S, Meng Q, Hu J, Tian X, Cohen M, Yi V, Kovar CL, Gingras MC, et al. (2021) Genetic testing in ambulatory cardiology clinics reveals high rate of findings with clinical management implications. *Genetics in Medicine*. 23(12):2404-2414.
55. Guo Y, Rist PM, Sabater-Lleal M, **de Vries PS**, Smith N, Ridker PM, Kurth T, Chasman DI. (2021) Association between hemostatic profile and migraine: a Mendelian randomization analysis. *Neurology*. 96(20):e2481-2487.

56. Ellervik C, Mora S, Kuś A, Åsvold B, Marouli E, Deloukas P, Sterenborg RBTM, Teumer A, Burgess S, Sabater-Lleal M, Huffman J, Johnson AD, Trégouet DA, Smith NL, Medici M, **de Vries PS**, Chasman DI, Kjaergaard AD. (2021) Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. *Thyroid.* 31(9):1305-1315.
57. Hu Y, Stilp AM, McHugh CP, Rao S, Jain D, Zheng X, Lane J, Méric de Bellefon S, Raffield LM, Chen MH, Yanek LR, Wheeler M, Yao Y, Ren C, Broome J, Moon JY, **de Vries PS**, Hobbs BD, Sun Q, Surendran P, et al. (2021) Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*. 108(5):874-893.
58. Tortolero GA, Brown MR, Sharma SV, de Oliveira Otto MC, Yamal JM, Aguilar D, Gunther MD, Mofleh DI, Harris RD, John JC, **de Vries PS**, Ramphul R, Serbo DM, Kiger J, Banerjee D, Bonvino N, Merchant A, Clifford W, Mikhail J, Xu H, et al. (2021) Leveraging a health information exchange for analyses of COVID-19 outcomes including an example application using smoking history and mortality. *PLoS One*. 16(6):e0247235.
59. Cornelissen A, Fuller DT, Fernandez R, Zhao X, Kutys R, Binns-Roemer E, Delsante M, Sakamoto A, Paek KH, Sato Y, Kawakami R, Mori M, Kawai K, Yoshida T, Latt KZ, Miller CL, **de Vries PS**, Kolodgie FD, Virmani R, et al. (2021) APOL1 Genetic Variants Are Associated With Increased Risk of Coronary Atherosclerotic Plaque Rupture in the Black Population. *ATVB*. 41(7):2201-2214.
60. Thibord F, Song C, Pattee J, Rodriguez BAT, Chen MH, O'Donnell CJ, Kleber ME, Delgado GE, Guo X, Yao J, Taylor KD, Ozel AB, Brody JA, McKnight B, Gyorgy B, Simonsick E, Leonard HL, Carrasquilla GD, Guindo-Martinez M, Silveira A, et al. (2021) FGL1 as a modulator of plasma D-dimer levels: Exome-wide marker analysis of plasma tPA, PAI-1, and D-dimer. *Journal of Thrombosis and Haemostasis*. 19(8):2019-2028.
61. 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, et al. (2021) A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. *American Journal of Epidemiology*. 190(10):1977-1992.
62. Wang H, Noordam R, Cade BE, Schwander K, Winkler TW, Lee J, Sung YJ, Bentley AR, Manning AK, Aschard H, Kilpeläinen TO, Ilkov M, Brown MR, Horimoto AR, Richard M, Bartz TM, Vojinovic D, Lim E, Nierenberg JL, Liu Y, et al. (2021) Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*. 26(11):6293-6304.
63. Natarajan P, Pampana A, Graham SE, Ruotsalainen SE, Perry JA, **de Vries PS**, Broome JG, Pirruccello JP, Honigberg MC, Aragam K, Wolford B, Brody JA, Antonacci-Fulton L, Arden M, Aslibekyan S, Assimes TL, Ballantyne CM, Bielak LF, Bis JC, Cade BE, Do R, et al. (2021) Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communication*. 12;12(1):2182.
64. Goumidi L, Thibord F, Wiggins KL, Li-Gao R, Brown MR, van Hylckama Vlieg A, Souto JC, Soria JM, Ibrahim-Kosta M, Saut N, Daian D, Olaso R, Amouyel P, Debette S, Boland A, Bailly P, Morrison AC, Mook-Kanamori DO, Deleuze JF, Johnson A, **de Vries PS**, et al. (2021) Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. *Blood*. 137(17):2394-2402.
65. Xu H, Schwander K, Brown MR, Wang W, Waken RJ, Boerwinkle E, Cupples LA, de Las Fuentes L, van Heemst D, Osazuwa-Peters O, de Vries PS, van Dijk KW, Sung YJ, Zhang X, Morrison AC, Rao DC, Noordam R, Liu CT. (2021) Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. *European Journal of Human Genetics*. 29(5):839-850.
66. Bennett JA, Mastrangelo MA, Ture SK, Smith CO, Loelius SG, Berg RA, Shi X, Burke RM, Spinelli SL, Cameron SJ, Carey TE, Brookes PS, Gerszten RE, Sabater-Lleal M, **de Vries PS**, Huffman JE, Smith NL,

Morrell CN, Lowenstein CJ. (2020) The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. *Nature Communications*. 11(1):3479.

67. Laville V, Majarian T, **de Vries PS**, Bentley AR, Feitosa MF, Sung YJ, Rao DC, Manning A, Aschard H, CHARGE Gene-Lifestyle Interactions Working Group. (2020) Deriving stratified effects from joint models investigating gene-environment interactions. *BMC Bioinformatics*. 21(1):251.
68. Wang Z, Chen H, Bartz TM, Bielak LF, Chasman DI, Feitosa MF, Franceschini N, Guo X, Lim E, Noordam R, Richard MA, Wang H, Cade B, Cupples LA, **de Vries PS**, Giulanini F, Lee J, Lemaitre RN, Martin LW, Reiner AP, et al. (2020) Role of rare and low-frequency variants in gene-alcohol interactions on plasma lipid levels. *Circulation: Genomic and Precision Medicine*. 13(4):e002772.
69. de Las Fuentes L, Sung YJ, Noordam R, Winkler T, Feitosa MF, Schwander K, Bentley AR, Brown MR, Guo X, Manning A, Chasman DI, Aschard H, Bartz TM, Bielak LF, Campbell A, Cheng CY, Dorajoo R, Hartwig FP, Horimoto ARVR, Li C, et al. (2020) Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*. 26(6):2111-2115.
70. Osazuwa-Peters OL, Waken RJ, Schwander KL, Sung YJ, **de Vries PS**, Hartz SM, Chasman DI, Morrison AC, Bierut LJ, Xiong C, de Las Fuentes L, Rao DC. (2020) Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. *Genetic Epidemiology*. 44(6):629-641.
71. Kowalski MH, Qian H, Hou Z, Rosen JD, Tapia AL, Shan Y, Jain D, Argos M,
72. Arnett DK, Avery C, Barnes KC, Becker LC, Bien SA, Bis JC, Blangero J, Boerwinkle E, Bowden DW, Buyske S, Cai J, Cho MH, Choi SH, et al. (2019) Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. *PLOS Genetics*. 15(12):e1008500.
73. Noordam R, Bos MM, Wang H, Winkler TW, Bentley AR, Kilpeläinen TO, **de Vries PS**, Sung YJ, Schwander K, Cade BE, Manning A, Aschard H, Brown MR, Chen H, Franceschini N, Musani SK, Richard M, Vojinovic D, Aslibekyan S, Bartz TM, et al. (2019) Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*. 10(1):5121.
74. Sarnowski C, Leong A, Raffield LM, Wu P, **de Vries PS**, DiCorpo D, Guo X, Xu H, Liu Y, Zheng X, Hu Y, Brody JA, Goodarzi MO, Hidalgo BA, Highland HM, Jain D, Liu CT, Naik RP, O'Connell JR, Perry JA, et al. (2019) Impact of rare and common genetic variants on type 2 diabetes diagnosis by hemoglobin A1c in multi-ancestry populations from the Trans-Omics for Precision Medicine (TOPMed) Program. *American Journal of Human Genetics*. 105(4):706-718.
75. Lindström S, Wang L, Smith EN, Gordon W, van Hylckama Vlieg A, de Andrade M, Brody JA, Pattee JW, Haessler J, Brumpton BM, Chasman DI, Suchon P, Chen MH, Turman C, Germain M, Wiggins KL, MacDonald J, Braekkan SK, Armasu SM, Pankratz N, et al. (2019) Genomic and Transcriptomic Association Studies Identify 16 Novel Susceptibility Loci for Venous Thromboembolism: the INVENT Consortium. *Blood*. 134(19):1645-1657.
76. Flannick J, Mercader JM, Fuchsberger C, Udler MS, Mahajan A, Wessel J, Teslovich TM, Caulkins L, Koesterer R, Barajas-Olmos F, Blackwell TW, Boerwinkle E, Brody JA, Centeno-Cruz F, Chen L, Chen S, Contreras-Cubas C, Córdova E, Correa A, Cortes M, et al. (2019) Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries. *Nature*. 570(7759):71-76.
77. Tzoulaki I, Castagné R, Boulangé CL, Karaman I, Chekmeneva E, Evangelou E, Ebbels TMD, Kaluarachchi MR, Chadeau-Hyam M, Mosen D, Dehghan A, Moayyeri A, Ferreira DLS, Guo X, Rotter JI, Taylor KD, Kavousi M, **de Vries PS**, Lehne B, Loh M, et al. (2019) Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. *European Heart Journal*. 40(34):2883-2896.

78. Ward-Caviness CK, **de Vries PS**, Wiggins KL, Huffman JE, Yanek LR, Bielak LF, Giulianini F, Guo X, Kleber ME, Kacprowski T, Groß S, Petersman A, Davey Smith G, Hartwig FP, Bowden J, Hemani G, Müller-Nuraysid M, Strauch K, Koenig W, Waldenberger M, et al. (2019) Evaluation of causal associations between fibrinogen and incident coronary heart disease: a meta-analysis of Mendelian Randomization studies. *PLOS One*. 14(5):e0216222.
79. Bentley AR, Sung YJ, Brown MR, Winkler TW, Kraja AT, Ntalla I, Schwander K, Chasman DI, Lim E, Deng X, Guo X, Liu J, Lu Y, Cheng CY, Sim X, Vojinovic D, Huffman JE, Musani SK, Li C, Feitosa MF, et al. (2019) Multi-ancestry genome-wide smoking interaction study of 387,283 individuals identifies novel lipid loci. *Nature Genetics*. 51(4):636-648.
80. He KY, Li X, Kelly TN, Liang J, Cade BE, Assimes TL, Becker LC, Beitelshees AL, Bress AP, Chang YC, Chen YI, **de Vries PS**, Fox ER, Franceschini N, Furniss A, Gao Y, Guo X, Haessler J, Hwang SJ, Irvin MR, et al. (2019) Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. *Human Genetics*. 138(2):199-210.
81. läinen TO, Bentley AR, Noordam R, Sung YJ, Schwander K, Winkler TW, Jakupović H, Chasman DI, Manning A, Ntalla I, Aschard H, Brown MR, de Las Fuentes L, Franceschini N, Guo X, Vojinovic D, Aslibekyan S, Feitosa MF, Kho M, Musani SK, et al. (2019) Multi-Ancestry Study of Blood Lipid Levels Identifies Four Loci Interacting with Physical Activity. *Nature Communications*. 10(1):376.
82. Chen H, Huffman JE, Brody JA, Wang C, Lee S, Li Z, Gogarten SM, Sofer T, Bielak LF, Bis JC, Blangero J, Bowler RP, Cade BE, Cho MH, Correa A, Curran JE, **de Vries PS**, Glahn DC, Guo X, Johnson AD, et al. (2019) Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies. *American Journal of Human Genetics*. 104(2):260-274.
83. Petty LE, Highland HM, Gamazon ER, Hu H, Karhade M, Chen HH, **de Vries PS**, Grove ML, Aguilar D, Bell GI, Huff CD, Hanis CL, Doddapaneni H, Munzy DM, Gibbs RA, Ma J, Parra EJ, Cruz M, Valladares-Salgado A, Arking DE, et al. (2019) Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. *Human Molecular Genetics*. 28(7):1212-1224.
84. Franceschini N, Giambartolomei C, **de Vries PS**, Finan C, Bis JC, Huntley RP, Lovering RC, Tajuddin SM, Winkler TW, Graff M, Kavousi M, Dale C, Smith AV, Hofer E, van Leeuwen EM, Nolte IM, Lu L, Scholz M, Sargurupremraj M, Pitkänen N, et al. (2018) GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*. 9(1):5141.
85. Ligthart S, Vaez A, Võsa U, Stathopoulou MG, **de Vries PS**, Prins BP, Van der Most PJ, Tanaka T, Naderi E, Rose LM, Wu Y, Karlsson R, Barbalic M, Lin H, Pool R, Zhu G, Macé A, Sidore C, Trompet S, Mangino M, et al. (2018) Genome-wide association analyses of >200,000 subject identifies 42 novel genetic loci for chronic inflammation and highlights causal pathways that link inflammation and complex disorders. *American Journal of Human Genetics*. 103(5):691-706.
86. Ward-Caviness CK, Huffman JE, Everett K, Germain M, van Dongen J, Hill WD, Jhun MA, Brody JA, Ghanbari M, Du L, Roetker NS, **de Vries PS**, Waldenberger M, Gieger C, Wolf P, Prokisch H, Koenig W, O'Donnell CJ, Levy D, Liu C, et al. (2018) DNA methylation age is associated with an altered hemostatic profile in a multi-ethnic meta-analysis. *Blood*. 132(17):1842-1850.
87. Merino J, Dashti HS, Li SX, Sarnowski C, Justice AE, Graff M, Papoutsakis C, Smith CE, Dedoussis GV, Lemaitre RN, Wojczynski MK, Männistö S, Ngwa JS, Kho M, Ahluwalia TS, Pervjakova N, Houston DK, Bouchard C, Huang T, Orho-Melander M, et al. (2018) Genome-wide Meta-Analysis of Macronutrient Intake Identifies Two Novel Loci: Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. *Molecular Psychiatry*. 24(12):1920-1932.
88. Wolters FJ, Boender J, **de Vries PS**, Sonneveld MA, Koudstaal PJ, de Maat MP, Franco OH, Ikram MK, Leebeek FW, Ikram MA. (2018) Von Willebrand factor and ADAMTS13 activity in relation to risk of dementia: a population-based study. *Scientific Reports*. 8(1):5474.

89. Guo L, Akahori H, Harari E, Smith SL, Polavarapu R, Karmali V, Otsuka F, Gannon RL, Braumann RE, Dickinson MH, Gupta A, Jenkins AL, Lipinski MJ, Kim J, Chhour P, **de Vries PS**, Jinnouchi H, Kutys R, Mori H, Kutyna MD, Torii S, et al. (2018) Alternative CD163 Macrophages Promote Intraplaque Angiogenesis, Vascular Permeability and Inflammation, and Plaque Progression in Atherosclerosis. *Journal of Clinical Investigation.* 128(3):1106-1124.
90. Ghanbari M, Peters MJ, **de Vries PS**, Boer CG, van Rooij JGJ, Lee YC, Kumar V, Uitterlinden AG, Ikram MA, Wijmenga C, Ordovas JM, Smith CE, van Meurs JBJ, Erkeland SJ, Franco OH, Dehghan A. (2018) A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. *Journal of Human Genetics.* 63(4):431-446.
91. Smith CE, Follis JL, Dashti HS, Tanaka T, Graff M, Fretts AM, Kilpeläinen TO, Wojczynski MK, Richardson K, Nalls MA, Schulz CA, Liu Y, Frazier-Wood AC, van Eekelen E, Wang C, **de Vries PS**, Mikkilä V, Rohde R, Psaty BM, Hansen T, et al. (2018) Genome-wide interactions with dairy intake for body mass index in adults of European descent. *Molecular Nutrition & Food Research.* 62(3).
92. Pirastu N, Joshi PK, **de Vries PS**, Cornelis MC, Keum N, Franceschini N, Colombo M, Giovannucci EL, Spiliopoulou A, Franke L, North KE, Kraft P, Morrison AC, Esko T, Wilson JF. (2017) GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nature Communications.* 8(1):1584.
93. Nano J, Ghanbari M, Wang W, **de Vries PS**, Dhana K, Muka T, Uitterlinden AG, van Meurs JBJ, Hofman A, BIOS consortium, Franco OH, Pan Q, Murad SD, Dehghan A. (2017) Epigenome-wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. *Gastroenterology*. 153(4):1096-1106.
94. Braun KVE, Dhana K, **de Vries PS**, Voortman T, van Meurs JBJ, Uitterlinden AG, BIOS consortium, Hofman A, Hu FB, Franco OH, Dehghan A. (2017) Epigenome-wide association study (EWAS) on lipids: The Rotterdam Study. *Clinical Epigenetics*. 9:15.
95. Karaman I, Ferreira DL, Boulangé CL, Kaluarachchi MR, Herrington D, Dona AC, Castagné R, Moayyeri A, Lehne B, Loh M, **de Vries PS**, Dehghan A, Franco OH, Hofman A, Evangelou E, Tzoulaki I, Elliott P, Lindon JC, Ebbels TM. (2016). Workflow for Integrated Processing of Multicohort Untargeted ^{1}H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. *Journal of Proteome Research.* 15(12):4188-4194.
96. Nikpay M, Goel A, Won HH, Hall LM, Willenborg C, Kanoni S, Saleheen D, Kyriakou T, Nelson CP, Hopewell JC, Webb TR, Zeng L, Dehghan A, Alver M, Armasu SM, Auro K, Bjonnes A, Chasman DI, Chen S, Ford I, et al. (2015) A comprehensive 1000 genomes-based GWAS meta-analysis of coronary artery disease. *Nature Genetics.* 47(10):1121-30.
97. Huffman JE, **de Vries PS**, Morrison AC, Sabater-Lleal M, Kacprowski T, Auer PL, Brody JA, Chasman DI, Chen MH, Guo X, Lin LA, Marioni RE, Müller-Nurasyid M, Yanek LR, Pankratz N, Grove ML, de Maat MP, Cushman M, Wiggins KL, Qi L, et al. (2015) Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood.* 126(11):e19-29.
98. Hägg S, Fall T, Ploner A, Mägi R, Fischer K, Draisma HH, Kals M, **de Vries PS**, Dehghan A, Willems SM, Sarin AP, Kristiansson K, Nuotio ML, Havulinna AS, de Bruijn RF, Ikram MA, Kuningas M, Stricker BH, Franco OH, Benyamin B, et al. (2015) Adiposity as a cause of cardiovascular disease: a mendelian randomization study. *International Journal of Epidemiology.* 44(2):578-86.
99. Ligthart S, **de Vries PS**, Uitterlinden AG, Hofman A; CHARGE Inflammation working group, Franco OH, Chasman DI, Dehghan A. (2015) Pleiotropy among common genetic loci identified for cardiometabolic disorders and C-reactive protein. *PLOS One*. 10 (3):e0118859.
100. Fall T, Hägg S, Ploner A, Mägi R, Fischer K, Draisma HH, Sarin AP, Benyamin B, Ladenvall C, Åkerlund M, Kals M, Esko T, Nelson CP, Kaakinen M, Huikari V, Mangino M, Meirhaeghe A, Kristiansson K, Nuotio ML, Kobl M, et al. (2015) Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. *Diabetes.* 64(5):1841-51.

101. Yu B, Li AH, Muzny D, Veeraraghavan N, **de Vries PS**, Bis JC, Musani SK, Alexander D, Morrison AC, Franco OH, Uitterlinden A, Hofman A, Dehghan A, Wilson JG, Psaty BM, Gibbs R, Wei P, Boerwinkle E. (2015) Association of Rare Loss-Of-Function Alleles in HAL, Serum Histidine Levels and Incident Coronary Heart Disease. *Circ Cardiovasc Genet.* 8(2):351-5.
102. Ghanbari M, **de Vries PS**, de Looper H, Peters MJ, Schurmann C, Yaghootkar H, Dörr M, Frayling TM, Uitterlinden AG, Hofman A, van Meurs JB, Erkeland SJ, Franco OH, Dehghan A. (2014) A genetic variant in the seed region of miR-4513 shows pleiotropic effects on lipid and glucose homeostasis, blood pressure, and coronary artery disease. *Hum Mutation.* 35(12):1524-31.

Published Invited Editorials

1. **de Vries PS** (2024) Early life cardiovascular risk factors and midlife epigenetic aging: an enduring legacy. *JACC: Basic to Translational Science*. 9(5):5901-592.
2. **de Vries PS**. (2023) Genetics of predicted platelet activity. *Blood*. 142(22):1851-1852.
3. **de Vries PS**. (2023) Polygenic risk, lifestyle and the lifetime risk of coronary artery disease. *Heart*. 109(10):730-731.
4. Assimes T, **de Vries PS.** (2018) Making the most out of Mendel's laws in complex coronary artery disease. *Journal of the American College of Cardiology*. 72(3):311-313.

Invited Presentations

1. Genetics of hemostasis and thrombosis. *Cardiovascular Epidemiology Seminar. University of Minnesota Twin Cities School of Public Health*. Virtual. September 26th 2025.
2. Harmonization and analysis of atherosclerosis phenotypes in the Trans-Omics for Precision Medicine (TOPMed) program. *COnsortium of METabolomics Studies (COMETS) Cardiovascular Working Group*. Virtual. November 9th 2023.
3. Grants as a junior principal investigator in CHARGE. *CHARGE Investigator Meeting*. San Antonio. October 10th 2023.
4. Using results from genome-wide association studies for genetic risk prediction. *Center for Heart Care Data Team Inservice Seminar Series, Department of Management, Policy, and Community Health, The University of Texas Health Science Center at Houston*. Houston. July 12th 2023.
5. Opportunities and challenges in researching the genomics of hemostasis and thrombosis. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston. November 7th 2022.
6. Whole genome sequencing study of coronary artery calcification: the Trans-Omics for Precision Medicine (TOPMed) program. *Human Genome Sequencing Center Virtual Seminar Series, Baylor College of Medicine*. Virtual. June 17th 2021.
7. Genome-wide association studies of coronary artery calcification. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston. September 14th 2020.
8. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Framingham Heart Study OMICS Conference Series*. Virtual. November 5th 2019.
9. Multi-ancestry whole genome sequencing analysis of coronary artery calcification in the Trans-Omics for Precision Medicine (TOPMed) program. *NHLBI's Harnessing the New Frontier of Imaging Genomics for Heart, Lung, Blood, and Sleep Disorders workshop*. Bethesda, October 25th 2019.

10. Genetics of hemostasis: new biology and links to cardiovascular disease. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston, October 9th 2017.
11. Mendelian randomization for precision medicine: causal effect of fibrinogen on coronary heart disease. *Precision Medicine Day*. *Center for Precision Health, School of Biomedical Informatics, The University of Texas Health Science Center at Houston.* Houston, April 13th 2017.
12. Exploring the role of genetic variation in hemostasis: updates from the CHARGE Hemostasis Working Group. *Framingham Heart Study OMICS Conference Series*. Virtual. November 1st 2016.

Conference Presentations

1. Cross-population meta-analysis of 1 million participants identifies variant-by-alcohol consumption interactions at 3 new and 10 known lipid loci. *CHARGE Investigator Meeting*. Denver, May 22nd–24th 2024 (working group presentation).
2. Whole genome sequencing study of coagulation factor VIII and von Willebrand factor reveals new genetic associations. *International Society of Thrombosis and Haemostasis*. Virtual, July 12th–14th 2020 (poster).
3. Multi-ancestry whole genome sequencing analysis of coronary artery calcification. *American Heart Association Scientific Sessions*. Philadelphia, November 16th–18th 2019 (moderated digital poster).
4. Whole genome sequencing and associations with coagulation factors VII and VIII and von Willebrand factor: the Trans-Omics for Precision Medicine (TOPMed) program. *American Society of Human Genetics Meeting*. Houston, October 15th–19th 2019 (poster).
5. Genetically Determined Fibrinogen, Gamma Prime Fibrinogen and Risk of Venous Thromboembolism and Ischemic Stroke: Evidence From Mendelian Randomization. *American Heart Association Epidemiology, Prevention, Lifestyle & Cardiometabolic Health*. Houston, March 5th–8th 2019 (poster).
6. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Trans-Omics for Precision Medicine (TOPMed) Investigator Meeting*. Tysons, December 5th–7th 2018 (platform).
7. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Investigator Meeting*. Baltimore, October 11th–12th 2018 (poster).
8. Multi-ancestry genome-wide association study of incident coronary heart disease. *CHARGE Investigator Meeting*. Rotterdam, April 18th–19th 2018 (poster).
9. Association of rare variants specific to pancreatic islets with type 2 diabetes. *Trans-Omics for Precision Medicine (TOPMed) Investigator Meeting*. Tysons, November 29th–December 1st 2017 (platform).
10. Multi-ancestry genome-wide association study incorporating gene-alcohol intake interactions identifies 18 new lipid loci. *American Society of Human Genetics Meeting.* Orlando, October 17th–21st 2017 (platform).
11. Multi-ethnic genome-wide association study of hemostasis phenotypes. *CHARGE Investigator Meeting*. New York City, March 23rd–24th 2017 (poster).
12. Whole-genome sequencing study of serum peptides: the Atherosclerosis Risk in Communities (ARIC) study. *American Society of Human Genetics Meeting.* Vancouver, October 18th–22nd 2016 (platform).
13. Multi-ethnic genome-wide association study of incident coronary heart disease. *CHARGE Investigator Meeting.* Charlottesville, September 28th–29th 2016 (poster).
14. GWAS of circulating fibrinogen using 1000 genomes imputed data. *CHARGE Investigator Meeting.* Los Angeles, January 22nd–24th 2014 (poster).

Trainee Conference Presentations

Mentored trainees from UTHealth are underlined.
Manuscripts with > 3 authors are shown with condensed author lists.

1. Johnston AC, Lowenstein CJ, Sabater-Lleal M, [...], **de Vries PS**. Genome-wide association studies including measures from multiplex assays identify new genetic loci for circulating Factor VIII, von Willebrand Factor, and ADAMTS13 levels. *American Society of Human Genetics Meeting*. Boston. October 14th-18th 2025 (poster).
2. Hahn J, Hasbani NR, Heath A, […], **de Vries PS**. Multi-ancestry genome-wide association study of Factor VIII and von Willebrand Factor levels incorporating variant by ABO blood group interactions. *CHARGE Consortium Investigator Meeting*. Washington DC. May 6th–8th 2025 (working group presentation).
3. Cornelius A, Heath AS, Sabater-Lleal M, […], **de Vries PS**. A genetic association study of circulating factor VIII, von Willebrand factor, and ADAMTS13. *CHARGE Consortium Investigator Meeting*. Rotterdam. October 15-17th 2024 (working group presentation).
4. Heath AS, Brown MR, Sabater-Lleal M, […] **de Vries PS**. A genome-wide association study of coagulation Factor VII levels uncovers 14 new loci and provides evidence for regulation by lipid levels. *CHARGE Consortium Investigator Meeting*. Denver. May 22nd-24th 2024 (working group presentation).
5. Braendle SS, Heath A, **de Vries PS**. Longitudinal fasting glucose trajectories in type 2 diabetes patients: associations with polygenic score and atherosclerotic cardiovascular disease. *CHARGE Consortium Investigator Meeting*. San Antonio. October 10th–12th 2023 (poster).
6. Godbole, AR, Heath A, **de Vries PS**. Genome-wide association study of circulating ADAMTS13 levels leveraging publicly available proteomics summary statistics. *Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Investigator Meeting*. Boston. May 9th–11th 2023 (poster).
7. Hahn J, Bressler J, Fornage M, […], **de Vries PS**. Epigenome-wide association study of DNA methylation in blood and coagulation factor VIII and von Willebrand factor plasma levels. *European Society of Human Genetics Meeting*. Glasgow, Scotland. June 10th–13th 2023 (poster).
8. Hahn J, Bressler J, Fornage M, […], **de Vries PS**. Epigenome-wide association study of DNA methylation in blood and coagulation factor VIII and von Willebrand factor plasma levels. *CHARGE Consortium Investigator Meeting*. Boston. May 9th–11th 2023 (poster).
9. Braendle SS, Hasbani NR, Morrison AC, […], **de Vries PS**. Polygenic scores and longitudinal trajectories of cardiometabolic phenotypes. *American Heart Association Scientific Sessions*. Chicago. November 5th–7th 2022 (poster).
10. Hasbani NR, Hahn J, Heath AS, […], **de Vries PS**. Multi-trait analysis genome-wide association study of atherosclerosis phenotypes. *American Society of Human Genetics Meeting*. Los Angeles. October 25th–29th 2022 (poster).
11. Hasbani NR, Hahn J, Heath AS, […], **de Vries PS**. Multi-trait analysis genome-wide association study of atherosclerosis phenotypes. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (platform).
12. Friedman R, Heath AS, Johnsen JM, […] **de Vries PS**. Genome-wide association study of low von Willebrand factor levels. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (poster and poster blitz).
13. Braendle SS, Hasbani NR, Morrison AC, […], **de Vries PS**. Polygenic scores and longitudinal trajectories of cardiometabolic phenotypes. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (poster and working group presentation).

14. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *International Fibrinogen Research Society Workshop*. Vevey, Switzerland. June 12th–16th 2022 (platform).
15. Hasbani NR, Ligthart S, Brown, MR, [...], **de Vries PS**. Lifetime risk of coronary heart disease: American Heart Association's Life's Simple 7 lifestyle recommendations and polygenic risk. *CHARGE Consortium Investigator Meeting*. Philadelphia. April 27th–29th 2022 (poster and working group presentation).
16. Hahn J, Temprano-Sagrera G, Smith NL, […], **de Vries PS**. Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein (CRP) levels. *American Society of Human Genetics Meeting*. Virtual. October 18th–22nd 2021 (poster).
17. Hasbani NR, Meigs J, Kwak SH, **de Vries PS**. The genetics of coronary artery calcification in individuals with type 2 diabetes. *American Society of Human Genetics*. Virtual. October 18th–22nd 2021 (poster).
18. Hahn J, Temprano-Sagrera G, Smith NL, […], **de Vries PS**. Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein (CRP) levels. *CHARGE Consortium Investigator Meeting*. Virtual. October 7th–8th 2021 (poster, and poster blitz: awarded "best poster").
19. Hasbani NR, Meigs J, Kwak SH, **de Vries PS**. The genetics of coronary artery calcification in individuals with type 2 diabetes. *CHARGE Consortium Investigator Meeting*. Virtual. October 7th–8th 2021 (poster and poster blitz).
20. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *Congress of the International Society on Thrombosis and Haemostasis (ISTH)*. Virtual. July 17th–21st 2021 (poster).
21. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *CHARGE Consortium Investigator Meeting*. Virtual. May 6th–7th 2021 (poster and poster blitz).
22. Hasbani NR, Ligthart S, Brown MR, [...], **de Vries PS**. Lifetime risk of coronary heart disease: American Heart Association's Life's Simple 7 lifestyle recommendations and polygenic risk. *Program in Quantitative Genomics Conference*. Virtual. November 5th–6th 2020. (poster).
23. Hasbani NR, Broome JG, Terry JG, [...], **de Vries PS**. Multi-ancestry whole genome sequencing study of carotid intima media thickness and carotid plaque. *American Society of Human Genetics*, Houston. October 15th–19th 2019 (poster).

Active Research Support

NIH/NHLBI: R01 HL173974 (Wolberg/Leiderman) 05/15/24-05/30/28
Interdisciplinary approach to elucidate modifiers of bleeding phenotype in factor XI deficiency
Our long-term goals are to: 1) characterize mechanisms that promote hemostasis in FXI deficiency, and 2) translate these mechanisms into clinically-accessible methods to predict bleeding.
Role: Subcontract PI (subcontract) Total Subcontract Amount: $68,290

NIH/NHLBI: R01 HL141291 (Morrison/Wolberg) 02/01/24-01/31/28
Using genomics and functional biology to understand fibrinogen and its effect on thrombotic and atherosclerotic outcomes

Fibrinogen and factor XIII (FXIII) are essential components of the blood coagulation cascade and major determinants of both bleeding and clotting. We will expand our knowledge of the genetics of total and γ' fibrinogen levels and FXIIIa activity in diverse populations, and assess the complex regulatory mechanisms influencing these blood coagulation proteins. The goal of this project is to leverage our multidisciplinary expertise in genomic studies and functional biology to generate new biological knowledge about the genomic

regulation of these factors and their relationship with thrombotic diseases.
Role: Co-investigator Total Award Amount: $2,045,660

NIH/NIA: R01 AG079108 (Sedaghat) 04/01/23-03/31/27
Early onset Alzheimer's disease and related dementias: a population-based approach to identify characteristics and risk factors.
We propose here to pool and rigorously harmonize data to create a cohort with a sizable number of early onset dementia events to estimate its incidence in the general population, identify predisposing or protective physiologic and behavioral risk factors, and study whether a favorable midlife risk profile in the presence of genetic predisposition delays its occurrence.
Role: Subcontract PI Total Subcontract Amount: $273,880

NIH/NHLBI: R01 HL139553 (Morrison/de Vries/Smith) 04/01/23-03/31/27
Analysis of whole genome sequence and hemostasis phenotypes.
We will expand our knowledge of the genetics of FVIII and VWF levels in multi-ethnic populations, and explore complex regulatory mechanisms influencing FVIII and VWF levels such as epistasis and epigenetics.
Role: Multi-PI Total Award Amount: $2,205,101

NIH/NHLBI: R01 HL162928 (Malhotra/de Vries) 04/01/23-03/31/27
Role of Arylsulfatase in vascular calcification.
This proposal aims to enhance our mechanistic insights of vascular disease by focusing on a novel biological pathway, the sulfatase family, that contributes to the development of calcified arteries and plaque development in the blood vessels of humans.
Role: Multi-PI Total Subcontract Amount: $347,248

NIH/NIDDK: U01DK078616 (Meigs) 09/01/20-08/31/25 (NCE)
TOPMed Omics of Type 2 Diabetes and Quantitative Traits
We will investigate type 2 diabetes and quantitative traits by leveraging (1) the biracial Atherosclerosis Risk in Communities Study (ARIC) phenotype, omics, and genetic data; (2) strong TOPMed analytic expertise and leadership, and (3) an ongoing track record of successful collaboration with all investigators that are a part of this competing renewal.
Role: Co-investigator (subcontract) Total Subcontract Amount: $234,000

NIH/NHLBI: R01 HL105756 (Psaty) 07/01/22-06/30/25 (NCE)
CHARGE Consortium: gene discovery for CVD and aging phenotypes
The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.
Role: Co-investigator Total Subcontract Amount: $93,600

NIH/NHLBI: R01 HL156991 (Rao) 04/27/21-03/31/25 (NCE)
A Multi-Ancestry Study of Gene-Lifestyle Interactions and Multi-Omics in Cardiometabolic Traits
The primary goal of the proposed research is to leverage existing genomic and –omic data from large multi-ethnic cohorts to discover additional genetic loci for cardiovascular traits by modeling gene-lifestyle interactions.
Role: Co-investigator (subcontract) Total Award Amount: $436,800

NIH/NHLBI: R01 HL146860 (de Vries) 3/17/20-02/28/26 (NCE)
Whole-genome sequencing analysis of coronary atherosclerosis and related traits
This project aims to integrate whole-genome sequence information to study subclinical atherosclerosis and coronary heart disease (CHD). Aims include discovering novel associated genetic variants, studying the underlying genetic architecture, determining the genetic correlation among the phenotypes, and exploring the use of rare variants in genetic risk prediction.
Role: PI Total Award Amount: $2,483,493

Completed Research Support

NIH/NHLBI: R01 HL151855 (Meigs) 07/01/20-06/30/25 (NCE)
TOPMed Omics of Cardiovascular Disease in Diabetes
We will utilize large-scale whole genome sequence variation, whole blood DNA methylation, transcription, proteomics, and metabolomics to elucidate pathways that contribute to the increased risk of cardiovascular disease in people with type 2 diabetes.
Role: Subcontract PI Total Subcontract Amount: $291,968

NIH/NHLBI: R01 HL141291 (Morrison/Wolberg) 02/01/19-01/31/24
Using genomics and functional biology to understand fibrinogen and its effect on thrombotic and atherosclerotic outcomes
Through this interdisciplinary collaboration between genetic epidemiologists and functional biologists, we will investigate fibrinogen-associated loci to characterize the genomic regulation of fibrinogen, assess epigenetic association with fibrinogen levels, and translate results of genomic studies into a clear understanding of fibrinogen's role in thrombotic and atherosclerotic disease.
Role: Co-investigator Total Award Amount: $3,152,180

NIH/NHLBI: R01 HL134894 (Smith) 08/19/17-07/31/23
Population Genomic Variation, Functional Biology, and the Risk of Venous Thrombosis
The goals of this project are a) to coordinate and advance new genetic discovery in the setting of two international consortia on hemostasis and venous thrombosis, and b) to integrate population work with functional biology work.
Role: Co-investigator (subcontract) Total Subcontract Amount: $344,376

NIH/NHLBI: R01 HL139553 (Morrison/Smith) 02/05/18-01/31/23
Analysis of Whole Genome Sequence and Hemostasis Phenotypes
To expand our knowledge of the genetic factors contributing to the plasma levels of 7 hemostasis phenotypes, we aim to use whole genome sequence data and imputed genotypes to facilitate new genomic discovery for these measured traits and to determine how genetic variation influencing these traits affects susceptibility to clinical outcomes such as venous thromboembolism and cardiovascular events.
Role: Co-investigator Total Award Amount: $2,205,101

NIH/NHLBI: R56 HL155528 (Newman) 09/20/21-08/31/22
Molecular predictors of resistance and vulnerability to cardiovascular events in stable ischemic heart disease
The objective of the proposed research is to determine which molecular assays could help predict cardiovascular disease events in stable ischemic heart disease patient and to better identify and treat high-risk patients.
Role: Subcontract PI Total Subcontract Amount: $23,111

NIH/NHLBI: R01 HL105756 (Psaty) 07/01/18-06/30/22

CHARGE Consortium: gene discovery for CVD and aging phenotypes

The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.

Role: Co-investigator Total Subcontract Amount: $291,947

AHA: 18CDA34110116 (de Vries) 07/01/18-06/30/21

Genomic discoveries for understanding and predicting coronary heart disease incidence and prognosis

Using the results of ongoing GWAS of incident CHD, incident myocardial infarction (MI), and incident mortality after MI, we will use whole-genome sequencing to study regions highlighted by our GWAS in more detail and to see whether these findings improve risk prediction of CHD. We will also perform Mendelian randomization analyses to estimate the causal effect of hemostatic factors on CHD and MI, and of traditional cardiovascular risk factors, hemostatic factors, and inflammatory factors on mortality after incident MI.

Role: PI Total Award Amount: $231,000

UTHealth School of Public Health: PRIME award (de Vries) 09/01/18-09/01/19

Multi-ancestry whole-genome sequencing analysis of atherosclerosis phenotypes

This is an internal award of the School of Public Health meant to help early stage investigators gather and analyze pilot data in preparation for a R01 submission.

Role: PI Total Award Amount: $24,940

AHA: 17POST3335004 (de Vries) 01/01/17-07/31/17

Genomic discovery for improved risk prediction of coronary heart disease

The goal of this study was to identify new genomic determinants of coronary heart disease and translate these findings into improved risk prediction.

Role: PI Total Award Amount: $95,450

Awards

2023	UTHealth-SPH: Research Mentor-Mentee Award
2018	CHARGE Consortium: Travel Award for the 2018 Investigator Meeting in Baltimore
2017	American Society of Human Genetics: Charles J. Epstein Trainee Award for Excellence in Human Genetics Research, Semifinalist
2017	CHARGE Consortium: Early Career Award
2017	CHARGE Consortium: Travel Award for the 2017 Investigator Meeting in New York City
2016	American Society of Human Genetics: Charles J. Epstein Trainee Award for Excellence

	in Human Genetics Research, Semifinalist
2014	Erasmus Trust Fund: Travel Award
2013	Erasmus Trust Fund: Travel Award

Teaching Experience

2021 – present	*Guest Lecturer* Molecular Epidemiology (Instructor: Abbas Dehghan) Imperial College London, London, UK
2019 – present	*Co-instructor (50%)* Epidemiology 1 (Online) Department of EHGES, UTHealth-SPH, Houston, TX, USA
2017 – present	*Course Coordinator and sole instructor* Foundations of Public Health Genetics (Online since 2019) Department of Epidemiology, UTHealth-SPH, Houston, TX, USA
2018	*Guest Lecturer* Epidemiology 1 (Instructor: Alan Nyitray) Department of Epidemiology, UTHealth-SPH, Houston, TX, USA
2016 & 2018	*Guest Lecturer* Applied Genetic Methods in Public Health (Instructor: Bing Yu) Department of Epidemiology, UTHealth-SPH, Houston, TX, USA
2013 – 2015	*Teaching Assistant* Study Design Netherlands Institute of Health Sciences Erasmus Medical Center, Rotterdam, the Netherlands
2013 – 2015	*Teaching Assistant* Methodological Topics in Epidemiologic Research Netherlands Institute of Health Sciences Erasmus Medical Center, Rotterdam, the Netherlands
2013	*Organizer and Lecturer* Exome Chip Analysis Workshop Erasmus Medical Center, Rotterdam, the Netherlands

---

Current Mentoring Experiences

Student	Program	Role
Natalie Hasbani	PhD	Dissertation supervisor
Benjamin Cristol	PhD	Dissertation committee member
Emily Mason	PhD	Dissertation committee member
Jessica Rodriguez	PhD	Dissertation committee member
Julie Hahn	PhD	Dissertation committee member
Morrigan Madady	PhD	Thesis supervisor
Preston Lee	MPH	Academic advisor
Amber Henry	MPH	Academic advisor
Sambridhi Bhujel	MPH	Academic advisor
Janaina De Queiroz Carvalho	MPH	Academic advisor
Parul Biswas	MPH	Academic advisor
Rinitha Rajan	MPH	Academic advisor
Phi-Christopher Ly	MPH	Academic advisor
Felix Lara	MPH	Academic advisor
Ermina Ali	MPH	Academic advisor
Adewale Adebayo	MPH	Academic advisor
Sydney Gholston	MPH	Academic advisor
Phi-Christopher Ly	MPH	Academic advisor
Adewale Adebayo	MPH	Academic advisor
Ermina Ali	MPH	Academic advisor
Lara Felix	MPH	Academic advisor
Rinitha Rajan	MPH	Academic advisor
Odinakachukwu Dimgba	MPH	Academic advisor

Previous Mentoring Experiences

Student	Program	Role	Graduation
Jamie Rose	MPH	Academic advisor	2025
Dharmiben Patel	MPH	Academic advisor	2025
Lauren Mignogna	MPH	Academic advisor	2025
Annmaria Joseph	MPH	Academic advisor	2025
Emily Mason	PhD	Dissertation committee member	2025
Julie Hahn	PhD	Dissertation committee member	2025
Hanxiao Sun	PhD	External reviewer	2024
Suha Soni	MPH	Academic advisor	2024
Alondra Cueto Valadez	MPH	Academic advisor	2024
Kiana Hunte	MPH	Academic advisor	2024
Alexandra Jordan	MPH	Academic advisor	2023

Aisha Mahmoud	MPH	Academic advisor	2023
Rachel Friedman	MPH	Thesis supervisor and academic advisor	2023
Anuja Godbole	MPH	Independent integrative learning experience advisor	2023
MacIntosh Cornwell	PhD	External reviewer at NYU Grossman School of Medicine	2023
Stephen Thomas	MPH	Academic advisor	2023
Audrey-Carelle Wandji	MPH	Academic advisor	2023
Sara Butt	MPH	Academic advisor	2023
Timothy Cruz	MPH	Academic advisor	2023
Iain Forrest	PhD	External reviewer at Icahn School of Medicine at Mt Sinai	2022
Chandler Childress	MPH	Academic advisor	2022
Nicole Linnard	MPH	Academic advisor	2022
Allison Bebo	MS	Thesis supervisor	2021
Xinyu Wang	PhD	External reviewer	2021
Kalen Blackburn	MPH	Academic advisor	2021
Mrinalini Buddha	MPH	Academic advisor	2021
Ricardo Gutierrez	MPH	Academic advisor	2021
Justin Muller	MPH	Academic advisor	2021
Hayley Snider	MPH	Academic advisor	2021
Andy Castaneda	MPH	Thesis supervisor	2020
Rahema Aman	MPH	Academic advisor	2020
Gregory Ware	MPH	Academic advisor	2020
Jillian Maners	MPH	Thesis supervisor	2019

Professional Memberships

National Associations

2016 – Present	American Heart Association, Council of Epidemiology and Prevention
2016 – Present	American Society of Human Genetics

Research Consortia

2022 – Present	Co-convener, TOPMed Atherosclerosis Working Group
2021 – Present	Co-convener, TOPMed-CHARGE Hemostasis Working Group
2017 – Present	Investigator, Centers for Common Disease Genomics (CCDG) Program
2016 – Present	Investigator, Trans-Omics for Precision Medicine (TOPMed) Program
2016 – Present	Investigator, ARIC Study

2012 – Present	Investigator, CHARGE

Institutional Service at UTHealth-SPH

2025	Judge for the UTHealth-SPH Student Association Research Day
2025	Reviewer for the UTHealth-SPH Doctoral Student Dissertation Award
2024 – Present	Convener of the Doctoral Student Experience Committee. Member of the Compensation subcommittee and the Research and Collaboration subcommittee.
2024 – 2025	Member, Human Genetics Center Search Committee (2 positions)
2022	Reviewer, UTHealth-SPH PRIME award
2020 – 2024	Member, Epidemiology Preliminary Exam Committee
2019 – 2020	External Reviewer, Epidemiology Preliminary Exam Committee
2019 – 2020	Member, Human Genetics Center Search Committee (2 positions)
2018 – Present	Epidemiology Representative, Faculty Council

Professional Service

2022 – Present	Co-convener of the TOPMed Atherosclerosis Working Group
2021 – Present	Co-convener of the TOPMed-CHARGE Hemostasis Working Group
2022	Session moderator at the 2022 CHARGE investigator meeting in Seattle
2020	Member of the organizing committee of the 2020 CHARGE investigator meeting in Houston

Grant Reviews

2025	Ad hoc reviewer in the NIH Neurological, Mental and Behavrioural Health (NMBH) study section (7 grants)
2025	Reviewer for NHLBI TOPMed Fellowships (3 grants)
2024	Ad hoc reviewer in the NIH NMBH study section (7 grants)
2023	Ad hoc reviewer in the NIH Hemostasis, Thrombosis, Blood Cells and

	Transfusion (HTBT) study section (7 grants)
2020	Reviewer for the Austrian Science Fund (1 grant)

Abstract and Manuscript Reviews

-Served as Guest Editor for a special issue in Genome Biology.

-Served as abstract reviewer for the American Diabetes Association meeting in 2021 and 2022.

-Served as a reviewer for the following journals:

Cardiology journals: Circulation, JACC, JACC: Basic to Translational Science, Heart, Journal of the American Heart Association, JAMA Cardiology, Circulation Genomics and Precision Medicine, Circulation Cardiovascular Genetics.

Hemostasis journals: Blood, Blood advances, Journal of Thrombosis and Haemostasis, Research and Practice in Thrombosis and Haemostasis, Thrombosis Update.

Genetics journals: American Journal of Human Genetics, Cell Genomics, Bioinformatics, PLOS Genetics, Genetic Epidemiology, and Human Molecular Genetics.

Other journals: JAMA, Nature Medicine, Nature Communication, Diabetes Care, Med, Communications Biology, eBioMedicine, Journal of Diabetes and Its Complications, Hypertension Research, European Journal of Clinical Investigation, PLOS One, Scientific Reports, and European Journal of Epidemiology.