UNIVERSITY OF PENNSYLVANIA - PERELMAN SCHOOL OF MEDICINE
Curriculum Vitae

Date: 11/02/2023

Shefali Setia Verma, Ph.D.

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Philadelphia, PA 19104 USA

If you are not a U.S. citizen or holder of a permanent visa, please indicate the type of visa you have:
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Education:

2008	B.Tech	Jaipur National University (Biotechnology)
2011	M.S.	New Jersey Institute of Technology (Bioinformatics)
2018	PhD	Penn State University (Bioinformatics and Genomics)

Postgraduate Training and Fellowship Appointments:

2018-2021	Lead Bioinformatics Scientist, University of Pennsylvania

Military Service:
[none]

Faculty Appointments:

2021-present	Instructor, Perelman School of Medicine

Hospital and/or Administrative Appointments:
[none]

Other Appointments:
[none]

Specialty Certification:
[none]

Licensure:
[none]

Awards, Honors and Membership in Honorary Societies:

2016	Travel Award, Pacific Symposium on Biocomputing
2016	Altman award, AMIA TBI Year in Review "Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR)"
2016	Reviewer's choice Award at ASHG for abstract titled "Identifying genetic associations with variability in metabolic health and blood count laboratory values: Diving into the

	quantitative traits in an EHR"
2017	Travel award Pacific Symposium of Biocomputing
2017	Altman award, AMIA TBI Year in Review to manuscript titled "Using knowledge-driven genomic interactions for multi-omics data analysis: meta-dimensional models for predicting clinical outcomes in ovarian carcinoma"
2021	COVID Dream Team Award, University of Pennsylvania
2022	Keystone Award, PSOM Center for Global Genome Health Equity

Memberships in Professional and Scientific Societies and Other Professional Activities:

National:

2018-Present American Society of Human Genetics (Member)

Editorial Positions:

2019-Present	ad-hoc reviewer, Bioinformatics
2019-Present	ad-hoc reviewer, GigaScience
2019-Present	ad-hoc reviewer, Frontiers in Genetics
2019-Present	ad-hoc reviewer, PLOS Computational Biology
2019-Present	ad-hoc reviewer, BioData Mining
2019-Present	ad-hoc reviewer, Nature Communications
2022-Present	Review Editor, Frontiers in Genetics
2023-Present	ad-hoc reviewer, PLOS Genetics
2023-Present	Special Issue Editor, Genes

Academic and Institutional Committees:

2021-2023	Committee Member (External) on Jiyan Zhou PhD thesis committee at Penn State University
2023-Present	Committee Member on Brenda Xiao's PhD thesis committee at Genomics and Computation Biology Graduate Program, University of Pennsylvania

Major Academic and Clinical Teaching Responsibilities:

2022	Grand Rounds talk at Department of Pathology and Laboratory Medicine Title: Use of Electronic Health Record linked BioBanks: Discovery to Implementation Science. Perelman School of Medicine University of Pennsylvania
2022	Lecture, Biomedical Data Science Series, University of Pennsylvania Title: Empowering Women's Health through Precision Medicine
2023	Multiomics in Precision Medicine, Philadelphia, PA Title: Multiomics in Women's Health. University of Pennsylvania Institute for Biomedical Informatics and

	Penn Center for Precision Medicine
2023	Human Genomic Diversity and Medicine: Challenges and Solutions to Reduce Health Disparities, Philadelphia, PA Title: Empowering Women's Health through Precision Medicine. University of Pennsylvania School of Arts and Sciences
2023	Penn IBI-GCB Retreat, Bear Creek Mountain Resort, PA Title: Journey though Academia

Lectures by Invitation (Last 5 years):

Feb, 2020	Challenge and Promise in Precision Medicine Meeting at Banbury Center, Cold Spring Harbor, New York Title: Groundwork for Precision Medicine: The role of electronic health records in discoveries and clinical implementation
Feb, 2020	Bortree Lecture Series at Pennsylvania State University Title: Groundwork for Precision Medicine: The role of electronic health records in discoveries and clinical implementation
Oct, 2020	American Society of Human Genetics, Extending Phenotype-Genotype Correlations to the Fetus: Integrating Genetics, Imaging, and the Electronic Health Record, Virtual Meeting Title: Bioinformatics methods for extracting genotype-phenotype information from electronic health records

Organizing Roles in Scientific Meetings:

Jan, 2018	Session co-organizer,Pacific Symposium on Biocomputing Kona, Hawaii
Nov, 2018	Abstract reviewer, American Medical Informatics Association Informatics Summit San Francisco, CA
Jan, 2019	Session co-organizer,Pacific Symposium on Biocomputing Kona, Hawaii
Mar, 2019	Abstract reviewer, American Medical Informatics Association Informatics Summit San Francisco, CA
Dec, 2019	Abstract reviewer, American Medical Informatics Association Informatics Summit Washington DC
Nov, 2020	Abstract reviewer, American Medical Informatics Association Informatics Summit Virtual
Jan, 2021	Session co-organizer,Pacific Symposium on Biocomputing Kona, Hawaii
Oct, 2022	Session co-organizer, American Society of Human Genetics Los Angeles, CA
Oct, 2022	Abstract reviewer, Mid Atlantic Bioinformatics Conference Philadelphia, PA
Jan, 2023	Session co-organizer,Pacific Symposium on Biocomputing

Kona, Hawaii
Jun, 2023 Co-organizer and Session Moderator, Precision Medicine Leaders Summit
Philadelphia, PA

Bibliography:

Research Publications, peer reviewed (print or other media):

1. Patel, Vandanaben; Wang, Jason TL; Setia, Shefali; Verma, Anurag; Warden, Charles D; Zhang, Kaizhong: On comparing two structured RNA multiple alignments. Journal of bioinformatics and computational biology 8(6): 967-980, December 2010.

2. Kent, Bethany N; Funkhouser, Lisa J; Setia, Shefali; Bordenstein, Seth R: Evolutionary genomics of a temperate bacteriophage in an obligate intracellular bacteria (Wolbachia). PLoS One 6(9): e24984, September 2011.

3. Brucker, Robert M; Funkhouser, Lisa J; Setia, Shefali; Pauly, Rini; Bordenstein, Seth R;: Insect Innate Immunity Database (IIID): an annotation tool for identifying immune genes in insect genomes. PLOS one 7(9): e45125, September 2012.

4. Ritchie MD, Verma SS, Hall MA, Goodloe RJ, Berg RL, Carrell DS, Carlson CS, Chen L, Crosslin DR, Denny JC, Jarvik G, Li R, Linneman JG, Pathak J, Peissig P, Rasmussen LV, Ramirez AH, Wang X, Wilke RA, Wolf WA, Torstenson ES, Turner SD, McCarty CA.: Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. Mol Vis 20(no issue): 1281-95, September 2014.

5. Crosslin DR, Tromp G, Burt A, Kim DS, Verma SS, Lucas AM, Bradford Y, Crawford DC, Armasu SM, Heit JA, Hayes MG, Kuivaniemi H, Ritchie MD, Jarvik GP, de Andrade M.: Controlling for population structure and genotyping platform bias in the eMERGE multi-institutional biobank linked to electronic health records. Front Genet 5(no issue): 352, November 2014 Notes: doi: 10.3389/fgene.2014.00352. eCollection 2014.

6. Namjou B, Marsolo K, Caroll RJ, Denny JC, Ritchie MD, Verma SS, Lingren T, Porollo A, Cobb BL, Perry C, Kottyan LC, Rothenberg ME, Thompson SD, Holm IA, Kohane IS, Harley JB.: Phenome-wide association study (PheWAS) in EMR-linked pediatric cohorts, genetically links PLCL1 to speech language development and IL5-IL13 to Eosinophilic Esophagitis. Front Genet 5: 401, November 2014.

7. Verma SS, Peissig P, Cross D, Waudby C, Brilliant M, McCarthy C, Ritchie MD: Benefits of accurate imputations in GWAS. European Conference on the Applications of Evolutionary Computation 8602(no issue): 71, November 2014 Notes: https://doi.org/10.1007/978-3-662-45523-4_71.

8. Verma SS, de Andrade M, Tromp G, Kuivaniemi H, Pugh E, Namjou-Khales B, Mukherjee S, Jarvik GP, Kottyan LC, Burt A, Bradford Y, Armstrong GD, Derr K, Crawford DC, Haines JL, Li R, Crosslin D, Ritchie MD.: Imputation and quality control steps for combining multiple genome-wide datasets. Front Genet 11(5): 370, December 2014 Notes: doi: 10.3389/fgene.2014.00370. eCollection 2014.

9. Moore CB, Verma A, Pendergrass S, Verma SS, Johnson DH, Daar ES, Gulick RM, Haubrich R, Robbins GK, Ritchie MD, Haas DW.: Phenome-wide Association Study Relating Pretreatment Laboratory Parameters With Human Genetic Variants in AIDS Clinical Trials Group Protocols. Open Forum Infect Dis 2(1): 113, January 2015.

10. Crosslin DR, Carrell DS, Burt A, Kim DS, Underwood JG, Hanna DS, Comstock BA, Baldwin E, de Andrade M, Kullo IJ, Tromp G, Kuivaniemi H, Borthwick KM, McCarty CA, Peissig PL, Doheny KF, Pugh E, Kho A, Pacheco J, Hayes MG, Ritchie MD, Verma SS, Armstrong G, Stallings S, Denny JC, Carroll RJ, Crawford DC, Crane PK, Mukherjee S, Bottinger E, Li R, Keating B, Mirel DB, Carlson CS, Harley JB, Larson EB, Jarvik GP: Genetic variation in the HLA region is associated with susceptibility to herpes zoster. Genes Immun. 16(1): 1-7, February 2015.

11. Pendergrass SA, Verma SS, Hall MA, Holzinger ER, Moore CB, Wallace JR, Dudek SM, Huggins W, Kitchner T, Waudby C, Berg R, Mccarty CA, Ritchie MD.: Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using biofilter, and gene-environment interactions using the Phenx Toolkit* Pac Symp Biocomput 20(no issue): 495-505, April 2015.

12. Hall MA, Verma SS, Wallace J, Lucas A, Berg RL, Connolly J, Crawford DC, Crosslin DR, de Andrade M, Doheny KF, Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Carrell DS, Tromp G, Vrabec TR, Pendergrass SA, McCarty CA, Ritchie MD.: Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. Genet Epidemiol 39(5): 376-384, July 2015.

13. Namjou B, Marsolo K, Lingren T, Ritchie MD, Verma SS, Cobb BL, Perry C, Kitchner TE, Brilliant MH, Peissig PL, Borthwick KM, Williams MS, Grafton J, Jarvik GP, Holm IA, Harley JB.: A GWAS Study on Liver Function Test Using eMERGE Network Participants. PLoS One 10(9): e0138677, September 2015 Notes: doi: 10.1371/journal.pone.0138677. eCollection 2015.

14. Li YR, van Setten J, Verma SS, Lu Y, Holmes MV, Gao H, Lek M, Nair N, Chandrupatla H, Chang B, Karczewski KJ, Wong C, Mohebnasab M, Mukhtar E, Phillips R, Tragante V, Hou C, Steel L, Lee T, Garifallou J, Guettouche T, Cao H, Guan W, Himes A, van Houten J, Pasquier A, Yu R, Carrigan E, Miller MB, Schladt D, Akdere A, Gonzalez A, Llyod KM, McGinn D, Gangasani A, Michaud

Z, Colasacco A, Snyder J, Thomas K, Wang T, Wu B, Alzahrani AJ, Al-Ali AK, Al-Muhanna FA, Al-Rubaish AM, Al-Mueilo S, Monos DS, Murphy B, Olthoff KM, Wijmenga C, Webster T, Kamoun M, Balasubramanian S, Lanktree MB, Oetting WS, Garcia-Pavia P, MacArthur DG, de Bakker PI, Hakonarson H, Birdwell KA, Jacobson PA, Ritchie MD, Asselbergs FW, Israni AK, Shaked A, Keating BJ.: Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Med 7(no issue): 90, October 2015 Notes: doi: 10.1186/s13073-015-0211-x.

15. De R, Verma SS, Drenos F, Holzinger ER, Holmes MV, Hall MA, Crosslin DR, Carrell DS, Hakonarson H, Jarvik G, Larson E, Pacheco JA, Rasmussen-Torvik LJ, Moore CB, Asselbergs FW, Moore JH, Ritchie MD, Keating BJ, Gilbert-Diamond D.: Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Min 14(8): 41, December 2015.

16. Kim D, Lucas A, Glessner J, Verma SS, Bradford Y, Li R, Frase AT, Hakonarson H, Peissig P, Brilliant M, Ritchie MD.: BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR COMMON AND RARE COPY NUMBER BURDEN. Pac Symp Biocomput 21: 357-368, January 2016.

17. Verma A, Leader JB, Verma SS, Frase A, Wallace J, Dudek S, Lavage DR, Van Hout CV, Dewey FE, Penn J, Lopez A, Overton JD, Carey DJ, Ledbetter DH, Kirchner HL, Ritchie MD, Pendergrass SA.: INTEGRATING CLINICAL LABORATORY MEASURES AND ICD-9 CODE DIAGNOSES IN PHENOME-WIDE ASSOCIATION STUDIES. Pac Symp Biocomput 21: 168-179, January 2016.

18. Verma SS, Frase AT, Verma A, Pendergrass SA, Mahony S, Haas DW, Ritchie MD.: PHENOME-WIDE INTERACTION STUDY (PheWIS) IN AIDS CLINICAL TRIALS GROUP DATA (ACTG). Pac Symp Biocomput 21(no issue): 57-68, January 2016.

19. Bailey JN, Loomis SJ, Kang JH, Allingham RR, Gharahkhani P, Khor CC, Burdon KP, Aschard H, Chasman DI, Igo RP Jr, Hysi PG, Glastonbury CA, Ashley-Koch A, Brilliant M, Brown AA, Budenz DL, Buil A, Cheng CY, Choi H, Christen WG, Curhan G, De Vivo I, Fingert JH, Foster PJ, Fuchs C, Gaasterland D, Gaasterland T, Hewitt AW, Hu F, Hunter DJ, Khawaja AP, Lee RK, Li Z, Lichter PR, Mackey DA, McGuffin P, Mitchell P, Moroi SE, Perera SA, Pepper KW, Qi Q, Realini T, Richards JE, Ridker PM, Rimm E, Ritch R, Ritchie M, Schuman JS, Scott WK, Singh K, Sit AJ, Song YE, Tamimi RM, Topouzis F, Viswanathan AC, Verma SS, Vollrath D, Wang JJ, Weisschuh N, Wissinger B, Wollstein G, Wong TY, Yaspan BL, Zack DJ, Zhang K, Study EN; ANZRAG Consortium, Weinreb RN, Pericak-Vance MA, Small K, Hammond CJ, Aung T, Liu Y, Vithana EN, MacGregor S, Craig JE, Kraft P, Howell G, Hauser MA, Pasquale LR, Haines JL, Wiggs JL.: Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle

glaucoma. Nat Genet 48(2): 189-194, February 2016.

20. Simonti CN, Vernot B, Bastarache L, Bottinger E, Carrell DS, Chisholm RL, Crosslin DR, Hebbring SJ, Jarvik GP, Kullo IJ, Li R, Pathak J, Ritchie MD, Roden DM, Verma SS, Tromp G, Prato JD, Bush WS, Akey JM, Denny JC, Capra JA.: The phenotypic legacy of admixture between modern humans and Neandertals. Science 351(6274): 737-41, February 2016.

21. Mosley JD, Shaffer CM, Van Driest SL, Weeke PE, Wells QS, Karnes JH, Velez Edwards DR, Wei WQ, Teixeira PL, Bastarache L, Crawford DC, Li R, Manolio TA, Bottinger EP, McCarty CA, Linneman JG, Brilliant MH, Pacheco JA, Thompson W, Chisholm RL, Jarvik GP, Crosslin DR, Carrell DS, Baldwin E, Ralston J, Larson EB, Grafton J, Scrol A, Jouni H, Kullo IJ, Tromp G, Borthwick KM, Kuivaniemi H, Carey DJ, Ritchie MD, Bradford Y, Verma SS, Chute CG, Veluchamy A, Siddiqui MK, Palmer CN, Doney A, MahmoudPour SH, Maitland-van der Zee AH, Morris AD, Denny JC, Roden DM: A genome-wide association study identifies variants in KCNIP4 associated with ACE inhibitor-induced cough. Pharmacogenomics J 16(3): 231-237, June 2016.

22. van 't Hof FN, Ruigrok YM, Lee CH, Ripke S, Anderson G, de Andrade M, Baas AF, Blankensteijn JD, Böttinger EP, Bown MJ, Broderick J, Bijlenga P, Carrell DS, Crawford DC, Crosslin DR, Ebeling C, Eriksson JG, Fornage M, Foroud T, von Und Zu Fraunberg M, Friedrich CM, Gaál EI, Gottesman O, Guo DC, Harrison SC, Hernesniemi J, Hofman A, Inoue I, Jääskeläinen JE, Jones GT, Kiemeney LA, Kivisaari R, Ko N, Koskinen S, Kubo M, Kullo IJ, Kuivaniemi H, Kurki MI, Laakso A, Lai D, Leal SM, Lehto H, LeMaire SA, Low SK, Malinowski J, McCarty CA, Milewicz DM, Mosley TH, Nakamura Y, Nakaoka H, Niemelä M, Pacheco J, Peissig PL, Pera J, Rasmussen-Torvik L, Ritchie MD, Rivadeneira F, van Rij AM, Santos-Cortez RL, Saratzis A, Slowik A, Takahashi A, Tromp G, Uitterlinden AG, Verma SS, Vermeulen SH, Wang GT; Aneurysm Consortium; Vascular Research Consortium of New Zealand, Han B, Rinkel GJ, de Bakker PI.: Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. J Am Heart Assoc 5(7): e002603, July 2016.

23. Verma A*, Verma SS*, Pendergrass SA, Crawford DC, Crosslin DR, Kuivaniemi H, Bush WS, Bradford Y, Kullo I, Bielinski SJ, Li R, Denny JC, Peissig P, Hebbring S, De Andrade M, Ritchie MD, Tromp G.: eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. BMC Med Genomics 9(Suppl 1): 32, August 2016.

24. Verma SS, Cooke Bailey JN, Lucas A, Bradford Y, Linneman JG, Hauser MA, Pasquale LR, Peissig PL, Brilliant MH, McCarty CA, Haines JL, Wiggs JL, Vrabec TR, Tromp G, Ritchie MD; eMERGE Network; NEIGHBOR Consortium.: Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. PLoS Genet 12(9): e1006186, September 2016.

25. Jones GT, Tromp G, Kuivaniemi H, Gretarsdottir S, Baas AF, Giusti B, Strauss E, Van't Hof FN, Webb TR, Erdman R, Ritchie MD, Elmore JR, Verma A, Pendergrass S, Kullo IJ, Ye Z, Peissig PL, Gottesman O, Verma SS, Malinowski J, Rasmussen-Torvik LJ, Borthwick KM, Smelser DT, Crosslin DR, de Andrade M, Ryer EJ, McCarty CA, Böttinger EP, Pacheco JA, Crawford DC, Carrell DS, Gerhard GS, Franklin DP, Carey DJ, Phillips VL, Williams MJ, Wei W, Blair R, Hill AA, Vasudevan TM, Lewis DR, Thomson IA, Krysa J, Hill GB, Roake J, Merriman TR, Oszkinis G, Galora S, Saracini C, Abbate R, Pulli R, Pratesi C, Saratzis A, Verissimo AR, Bumpstead S, Badger SA, Clough RE, Cockerill G, Hafez H, Scott DJ, Futers TS, Romaine SP, Bridge K, Griffin KJ, Bailey MA, Smith A, Thompson MM, van Bockxmeer FM, Matthiasson SE, Thorleifsson G, Thorsteinsdottir U, Blankensteijn JD, Teijink JA, Wijmenga C, de Graaf J, Kiemeney LA, Lindholt JS, Hughes A, Bradley DT, Stirrups K, Golledge J, Norman PE, Powell JT, Humphries SE, Hamby SE, Goodall AH, Nelson CP, Sakalihasan N, Courtois A, Ferrell RE, Eriksson P, Folkersen L, Franco-Cereceda A, Eicher JD, Johnson AD, Betsholtz C, Ruusalepp A, Franzén O, Schadt EE, Björkegren JL, et al.: Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circ Res 120(2): 341-353, January 2017.

26. Verma SS, Lucas AM, Lavage DR, Leader JB, Metpally R, Krishnamurthy S, Dewey F, Borecki I, Lopez A, Overton J, Penn J, Reid J, Pendergrass SA, Breitwieser G, Ritchie MD.: IDENTIFYING GENETIC ASSOCIATIONS WITH VARIABILITY IN METABOLIC HEALTH AND BLOOD COUNT LABORATORY VALUES: DIVING INTO THE QUANTITATIVE TRAITS BY LEVERAGING LONGITUDINAL DATA FROM AN EHR. Pac Symp Biocomput 22(no issue): 533-544, January 2017.

27. De R, Verma SS, Holzinger E, Hall M, Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, Ritchie MD, Keating B, Gilbert-Diamond D.: Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Hum Genet 136(2): 165-178, February 2017.

28. Verma A, Bradford Y, Verma SS, Pendergrass SA, Daar ES, Venuto C, Morse GD, Ritchie MD, Haas DW.: Multiphenotype association study of patients randomized to initiate antiretroviral regimens in AIDS Clinical Trials Group protocol A5202. Pharmacogenet Genomics 27(3): 101-111, March 2017.

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30. Kim D, Li R, Lucas A, Verma SS, Dudek SM, Ritchie MD.: Using knowledge-driven genomic interactions for multi-omics data analysis: metadimensional models for predicting clinical outcomes in ovarian carcinoma. J Am Med Inform Assoc 24(3): 577-587, May 2017.

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32. Kim D, Volk H, Girirajan S, Pendergrass S, Hall MA, Verma SS, Schmidt RJ, Hansen RL, Ghosh D, Ludena-Rodriguez Y, Kim K, Ritchie MD, Hertz-Picciotto I, Selleck SB.: The joint effect of air pollution exposure and copy number variation on risk for autism. Autism Res 10(9): 1470-1480, September 2017.

33. Hall MA, Wallace J, Lucas A, Kim D, Basile AO, Verma SS, McCarty CA, Brilliant MH, Peissig PL, Kitchner TE, Verma A, Pendergrass SA, Dudek SM, Moore JH, Ritchie MD.: PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nat Commun 8(1): 1167, October 2017.

34. Li B, Verma SS, Veturi YC, Verma A, Bradford Y, Haas DW, Ritchie MD: Evaluation of PrediXcan for prioritizing GWAS associations and predicting gene expression. Pac Symp Biocomput 23(no issue): 448-459, January 2018.

35. Verma SS, Josyula N, Verma A, Zhang X, Veturi Y, Dewey FE, Hartzel DN, Lavage DR, Leader J, Ritchie MD, Pendergrass SA.: Rare variants in drug target genes contributing to complex diseases, phenome-wide. Sci Rep 8(1): 4624, March 2018.

36. Verma A, Bradford Y, Dudek S, Lucas AM, Verma SS, Pendergrass SA, Ritchie MD.: A simulation study investigating power estimates in phenome-wide association studies. BMC Bioinformatics 19(1): 120, April 2018.

37. Verma A, Lucas A, Verma SS, Zhang Y, Josyula N, Khan A, Hartzel DN, Lavage DR, Leader J, Ritchie MD, Pendergrass SA.: PheWAS and Beyond: The Landscape of Associations with Medical Diagnoses and Clinical Measures across 38,662 Individuals from Geisinger. Am J Hum Genet 102(4): 592-608, April

2018.

38. Verma SS, Lucas A, Zhang X, Veturi Y, Dudek S, Li B, Li R, Urbanowicz R, Moore JH, Kim D, Ritchie MD.: Collective feature selection to identify crucial epistatic variants. BioData Min 11(no issue): 5, April 2018 Notes: doi: 10.1186/s13040-018-0168-6. eCollection 2018.

39. Haas DW, Bradford Y, Verma A, Verma SS, Eron JJ, Gulick RM, Riddler SA, Sax PE, Daar ES, Morse GD, Acosta EP, Ritchie MD.: Brain neurotransmitter transporter/receptor genomics and efavirenz central nervous system adverse events. Pharmacogenet Genomics 28(7): 179-187, July 2018.

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Patents:

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