Mitchell R. **Vollger**

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Assistant Professor, Department of Human Genetics, University of Utah

Education

Ph.D. in Genome Sciences at University of Washington *Sep. 2016 - Mar. 2021*
Dissertation: Assembly of segmental duplications and their variation in humans *Seattle, Washington*

- Advisor: Evan E. Eichler
- Completed the Advanced Data Science Option

B.S.E. in Computer Science Engineering at Princeton University *Sep. 2011 - June 2015*
Departments of Computer Science and Quantitative and Computational Biology *Princeton, New Jersey*

- Student of the Integrated Science Curriculum
- Certificate in Quantitative and Computational Biology

Associate of Arts Degrees at College of the Redwoods *Sep. 2008 - June 2011*
AA in Mathematics | AA in Science *Eureka, California*

Positions and Employment

Assistant Professor, Department of Human Genetics *Jan. 2026 - Present*
Principal Investigator, Vollger Lab *University of Utah*

Postdoctoral Scholar in the Division of Medical Genetics *Apr. 2022 - Dec. 2025*
In the lab of Andrew B. Stergachis *University of Washington*

Postdoctoral Scholar in the Department of Genome Sciences *Mar. 2021 - Apr. 2022*
In the lab of Evan E. Eichler *University of Washington*

Funding and Awards

K99/R00 Pathway to Independence Award *Summer 2024 - Present*
National Institute of General Medical Sciences, 1K99GM155552-01 *University of Washington / University of Utah*

NIH/NHGRI T32 Genome Training Grant *Fall 2022 - Fall 2024*
Division of Medical Genetics at University of Washington *University of Washington*

BDGN, Big Data in Genomics and Neuroscience *Fall 2017 - Fall 2019*
Genome Sciences at University of Washington *University of Washington*

NIH/NHGRI T32 Genome Training Grant *Fall 2016 - Fall 2017*
Genome Sciences at University of Washington *University of Washington*

Publications

- **M. R. Vollger**†, E. G. Swanson, S. J. Neph, J. Ranchalis, K. M. Munson, C.-H. Ho, Y. H. H. Cheng, A. E. Sedeno-Cortes, W. E. Fondrie, S. C. Bohaczuk, M. A. Dippel, Y. Mao, N. L. Parmalee, B. J. Mallory, W. T. Harvey, Y. Kwon, G. H. Garcia, K. Hoekzema, J. G. Meyer, … A. B. Stergachis, Somatic epimutations cap genetic determinism in the human diploid chromatin epigenome. *Cell* (2026) (Accepted in principle), doi: 10.1101/2024.06.14.599122 .
- **M. R. Vollger**†, rustybam: a composable toolkit for alignment analysis and visualization with SafFire (2026), doi: 10.64898/2026.02.16.706142 .
- X. Guitart, J. W. Brunner, L. Ren, H. Jeong, D. Yoo, D. Porubsky, K. Hoekzema, K. M. Munson, K. A. Sun, M. Ayllon, K. Hoglin, R. McMullen, B. Pavlovic, M. R. Vollger, A. A. Pollen, E. E. Eichler, NPEPPS segmental duplication drives position effect expression of TBC1D3 in the human brain (2026), doi: 10.64898/2026.01.14.699559 .
- E. G. Swanson, Y. Mao, B. J. Mallory, M. R. Vollger, S. C. Bohaczuk, C. B. Oliveira, D. B. Lyon, J. Ranchalis, N. L. Parmalee, B. A. Cohen, J. T. Bennett, A. B. Stergachis, Mapping single-cell diploid chromatin fiber architectures using DAF-seq. *Nature Biotechnology* (2025), doi: 10.1038/s41587-025-02914-3 .
- Y.-H. H. Cheng, A. E. Sedeño-Cortés, J. E. Ranchalis, K. M. Munson, M. R. Vollger, E. Balton, C. A. Genetti, M. H. Wojcik, A. H. Beggs, M. J. Bamshad, C.-L. Wei, K. M. Dipple, R. D. Kumar, E. E. Blue, G. Jarvik, J. X. Chong, D. M. Witten, A. O'Donnell-Luria, A. B. Stergachis, Long-read transcriptome analysis using IsoRanker for identifying pathogenic variants in Mendelian conditions (2025), doi: 10.1101/2025.11.07.25339764 .

- M.-H. Sohn, D. Dubocanin, M. R. Vollger, Y. Kwon, A. Minkina, K. M. Munson, S. F. Hart, J. E. Ranchalis, N. L. Parmalee, A. E. Sedeño-Cortés, J. Ou, N. Y. Au, S. Bohaczuk, B. Carroll, C. D. Frazar, W. T. Harvey, K. Hoekzema, M.-F. Huang, C. N. Jacques, … A. B. Stergachis, A telomere-to-telomere map of somatic mutation burden and functional impact in cancer (2025), doi: 10.1101/2025.10.10.681725 .
- N. F. Hansen, N. Dwarshuis, H. J. Ji, A. Rhie, H. Loucks, G. A. Logsdon, M. R. Vollger, J. M. Storer, J. Kim, E. Adam, N. Altemose, D. Antipov, M. Asri, S. Barreira, S. C. Bohaczuk, A. V. Bzikadze, S. A. Carioscia, A. Carroll, K.-H. Chao, … A. M. Phillippy, A complete diploid human genome benchmark for personalized genomics (2025), doi: 10.1101/2025.09.21.677443 .
- K. L. Bubb, M. O. Hamm, T. W. Tullius, J. K. Min, B. Ramirez-Corona, N. A. Mueth, J. Ranchalis, Y. Mao, E. J. Bergstrom, M. R. Vollger, C. Trapnell, J. T. Cuperus, A. B. Stergachis, C. Queitsch, The regulatory potential of transposable elements in maize. *Nature Plants*. **11**, 1181–1192 (2025), doi: 10.1038/s41477-025-02002-z .
- T. D. Real, P. Hebbar, D. Yoo, F. Antonacci, I. Pačar, M. Diekhans, G. J. Mikol, O. G. Popoola, B. J. Mallory, M. R. Vollger, P. C. Dishuck, X. Guitart, A. N. Rozanski, K. M. Munson, K. Hoekzema, J. E. Ranchalis, S. J. Neph, A. E. Sedeño-Cortes, B. Paten, … E. E. Eichler, Genetic diversity and regulatory features of human-specific NOTCH2NL duplications (2025), doi: 10.1101/2025.03.14.643395 .
- D. Dubocanin, A. Kalygina, J. M. Franklin, C. Chittenden, M. R. Vollger, S. Neph, A. B. Stergachis, N. Altemose, Integrating Single-Molecule Sequencing and Deep Learning to Predict Haplotype-Specific 3D Chromatin Organization in a Mendelian Condition (2025), doi: 10.1101/2025.02.26.640261 .
- **M. R. Vollger** , J. Korlach, K. C. Eldred, E. Swanson, J. G. Underwood, S. C. Bohaczuk, Y. Mao, Y.-H. H. Cheng, J. Ranchalis, E. E. Blue, U. Schwarze, K. M. Munson, C. T. Saunders, A. M. Wenger, A. Allworth, S. Chanprasert, B. L. Duerden, I. Glass, M. Horike-Pyne, … A. B. Stergachis, Synchronized long-read genome, methylome, epigenome and transcriptome profiling resolve a Mendelian condition. *Nature Genetics*. **57**, 469–479 (2025), doi: 10.1038/s41588-024-02067-0 .
- S. C. Bohaczuk, Z. J. Amador, C. Li, B. J. Mallory, E. G. Swanson, J. Ranchalis, M. R. Vollger, K. M. Munson, T. Walsh, M. O. Hamm, Y. Mao, A. Lieber, A. B. Stergachis, Resolving the chromatin impact of mosaic variants with targeted Fiber-seq (2024), doi: 10.1101/2024.07.09.602608 .
- A. Jha, S. C. Bohaczuk, Y. Mao, J. Ranchalis, B. J. Mallory, A. T. Min, M. O. Hamm, E. Swanson, D. Dubocanin, C. Finkbeiner, T. Li, D. Whittington, W. S. Noble, A. B. Stergachis, **M. R. Vollger**†, DNA-m6A calling and integrated long-read epigenetic and genetic analysis with fibertools. *Genome Research*. **34**, 1976–1986 (2024), doi: 10.1101/gr.279095.124 .
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- **M. R. Vollger** , P. C. Dishuck, W. T. Harvey, W. S. DeWitt, X. Guitart, M. E. Goldberg, A. N. Rozanski, J. Lucas, M. Asri, H. J. Abel, L. L. Antonacci-Fulton, G. Baid, C. A. Baker, A. Belyaeva, K. Billis, G. Bourque, S. Buonaiuto, A. Carroll, M. J. P. Chaisson, … E. E. Eichler, Increased mutation and gene conversion within human segmental duplications. *Nature*. **617**, 325–334 (2023), doi: 10.1038/s41586-023-05895-y .
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- **M. R. Vollger** , X. Guitart, P. C. Dishuck, L. Mercuri, W. T. Harvey, A. Gershman, M. Diekhans, A. Sulovari, K. M. Munson, A. P. Lewis, K. Hoekzema, D. Porubsky, R. Li, S. Nurk, S. Koren, K. H. Miga, A. M. Phillippy, W. Timp, M. Ventura, E. E. Eichler, Segmental duplications and their variation in a complete human genome. *Science*. **376** (2022), doi: 10.1126/science.abj6965 .
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- **M. R. Vollger** , P. Kerpedjiev, A. M. Phillippy, E. E. Eichler, StainedGlass: Interactive visualization of massive tandem repeat structures with identity heatmaps. *Bioinformatics* (2022), doi: 10.1093/bioinformatics/btac018 .
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- **M. R. Vollger** , G. A. Logsdon, P. A. Audano, A. Sulovari, D. Porubsky, P. Peluso, A. M. Wenger, G. T. Concepcion, Z. N. Kronenberg, K. M. Munson, C. Baker, A. D. Sanders, D. C. Spierings, P. M. Lansdorp, U. Surti, M. W. Hunkapiller, E. E. Eichler, Improved assembly and variant detection of a haploid human genome using single-molecule, high-fidelity long reads. *Annals of Human Genetics*. **84**, 125–140 (2019), doi: 10.1111/ahg.12364 .
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- **M. R. Vollger** , P. C. Dishuck, M. Sorensen, A. E. Welch, V. Dang, M. L. Dougherty, T. A. Graves-Lindsay, R. K. Wilson, M. J. P. Chaisson, E. E. Eichler, Long-read sequence and assembly of segmental duplications. *Nature Methods*. **16**, 88–94 (2018), doi: 10.1038/s41592-018-0236-3 .

Presentations

Genetic and functional characterization of segmental duplications *Oct. 2025*
Seminar at the Department of Human Genetics *University of Utah*

Evaluating the genetic drivers of gene regulation heterogeneity across the human pangenome *Oct. 2025*
Human Pangenome Reference Consortium *Memphis, Tennessee, United States*

Computational tools for epigenetic characterization of the human pangenome *Jul. 2025*
All Hands Call for the Human Pangenome Reference Consortium *remote*

Fiber-seq and tools to understand the regulatory genome in a disease context
May 2025
European Society of Human Genetics (ESHG)
Allianz MiCo in Milan, Italy

Working towards genetic and functional characterization of segmental duplications
Mar. 2025
Seminar at the Department of Biomedical Engineering
Johns Hopkins University

Working towards genetic and functional characterization of segmental duplications
Feb. 2025
Seminar at the Department of Genetics, Cell Biology and Development
University of Minnesota

Working towards genetic and functional characterization of segmental duplications
Feb. 2025
Seminar at the Department of Human Genetics
University of Utah

Computational tools for Fiber-seq and Fiber-seq Inferred Regulatory Elements
Oct. 2024
BBI Long-read Symposium
Seattle Children's Research Institute

Tooling for accurately studying the epigenome along the human pangenome reference
Aug. 2024
Human Pangenome Reference Consortium face-to-face conference
University of California Santa Cruz

Fiber-seq Inferred Regulatory Elements with diploid T2T genomes
Aug. 2024
Telomere-to-telomere face-to-face conference
University of California Santa Cruz

Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
Apr. 2023
Division of Medical Genetics Seminar Series
University of Washington

Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
Feb. 2023
AGBT 2023
Hollywood, Florida

A complete view of segmental duplications and their variation
Dec. 2022
Genome Sciences 20th anniversary symposium
University of Washington

Using a complete human reference to explore variation in segmental duplications
Oct. 2022
Long-Read, Long-Range scientific interest group
NHGRI, remote

Increased mutation rate and interlocus gene conversion within human segmental duplications
Aug. 2022
Telomere-to-telomere face-to-face conference
University of California Santa Cruz

Segmental duplications and their variation in a complete human genome
Mar. 2022
UCSC BME departmental seminar series
University of California Santa Cruz, remote

Segmental duplications and their variation in a complete human genome
Oct. 2021
NHGRI computational biology seminar series
NHGRI, remote

A complete view of segmental duplications and their variation
Sep. 2021
American Society of Human Genetics, Section talk
remote

A complete view of segmental duplications and their variation
Sep. 2020
T2T and HPRC conference
University of Washington

Improved Assembly of Segmental Duplications Using HiFi
Sep. 2019
Pacific Biosciences User Group Meeting
University of Delaware

Teaching Experience

Gene discovery and comparative genomics
Oct. 2022
Invited Lecture, Genomics and Proteomics, undergraduate course
University of Washington

Introduction to Statistical Genomics
Spring 2022
Primary Instructor, Introduction to Statistical Genomics, graduate course
University of Washington

Introduction to Computational Molecular Biology
Winter 2020
Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours
University of Washington

Fundamentals of Genetics and Genomics
Summer 2019
Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours
University of Washington

Professional Organizations

2023-Present	Somatic Mosaicism Across Human Tissues consortium (SMaHT)
2021-Present	American Society of Human Genetics (ASHG)
2020-Present	Telomere to Telomere consortium (T2T)
2020-Present	Human Pangenome Reference Consortium (HPRC)

References

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