

Mitchell R. Vollger

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Postdoctoral Scholar in the Division of Medical Genetics at the University of Washington

Education

Ph.D. in Genome Sciences at University of Washington

Dissertation: Assembly of segmental duplications and their variation in humans

Sep 2016 - March 2021

Seattle, Washington

- Advisor: Evan E. Eichler
- Completed the [Advanced Data Science Option](#)

B.S.E. in Computer Science Engineering at Princeton University

Departments of Computer Science and Quantitative and Computational Biology

Sep. 2011 - June 2015

Princeton, New Jersey

- Student of the [Integrated Science Curriculum](#)
- Certificate in Quantitative and Computational Biology

Associate of Arts Degrees at College of the Redwoods

AA in Mathematics | AA in Science

Sep. 2008 - June 2011

Eureka, California

Postdoctoral Experience

Postdoctoral Scholar in the Division of Medical Genetics

In the lab of Andrew B. Stergachis

April 2022 - Present

University of Washington

Postdoctoral Scholar in the Department of Genome Sciences

In the lab of Evan E. Eichler

March 2021 - April 2022

University of Washington

Funding and Awards

K99/R00 Pathway to Independence Award

National Institute of General Medical Sciences, 1K99GM155552-01

Summer 2024 - present

University of Washington

NIH/NHGRI T32 Genome Training Grant

Division of Medical Genetics at University of Washington

Fall 2022 - Fall 2024

University of Washington

BDGN, Big Data in Genomics and Neuroscience

Genome Sciences at University of Washington

Fall 2017 - Fall 2019

University of Washington

NIH/NHGRI T32 Genome Training Grant

Genome Sciences at University of Washington

Fall 2016 - Fall 2017

University of Washington

Publications

- First Author** [M. R. Vollger](#), E. G. Swanson, S. J. Neph, J. Ranchalis, K. M. Munson, C.-H. Ho, A. E. Sedeño-Cortés, W. E. Fondrie, S. C. Bohaczuk, Y. Mao, N. L. Parmalee, B. J. Mallory, W. T. Harvey, Y. Kwon, G. H. Garcia, K. Hoekzema, J. G. Meyer, M. Cicek, E. E. Eichler, ... A. B. Stergachis, A haplotype-resolved view of human gene regulation (2024), doi: [10.1101/2024.06.14.599122](https://doi.org/10.1101/2024.06.14.599122)
- [M. R. Vollger](#), J. Korlach, K. C. Eldred, E. Swanson, J. G. Underwood, Y.-H. H. Cheng, J. Ranchalis, Y. Mao, 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, M. Kim, ... A. B. Stergachis, Synchronized long-read genome, methylome, epigenome, and transcriptome for resolving a Mendelian condition. *Nature Genetics*, *accepted in principle* (2024), doi: [10.1101/2023.09.26.559521](https://doi.org/10.1101/2023.09.26.559521)
- [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. P. R. Consortium, K. M. Munson, A. P. Lewis, K. Hoekzema, G. A. Logsdon, D. Porubsky, B. Paten, K. Harris, P. Hsieh, E. E. Eichler, *Nature*, in press, doi: [10.1038/s41586-023-05895-y](https://doi.org/10.1038/s41586-023-05895-y)
- [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](https://doi.org/10.1126/science.abj6965)
- [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](https://doi.org/10.1093/bioinformatics/btac018)
- [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, *Annals of Human Genetics*, in press, doi: [10.1111/ahg.12364](https://doi.org/10.1111/ahg.12364)

- [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, *Nature Methods*, in press, doi: [10.1038/s41592-018-0236-3](https://doi.org/10.1038/s41592-018-0236-3)
- Corresponding** 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](#) , *Genome Research*, in press, doi: [10.1101/gr.279095.124](https://doi.org/10.1101/gr.279095.124)
- Collaborative** K. L. Bubb, M. O. Hamm, J. K. Min, B. Ramirez-Corona, N. A. Mueth, J. Ranchalis, [M. R. Vollger](#) , C. Trapnell, J. T. Cuperus, C. Queitsch, A. B. Stergachis, The regulatory potential of transposable elements in maize (2024), doi: [10.1101/2024.07.10.602892](https://doi.org/10.1101/2024.07.10.602892)
- 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](https://doi.org/10.1101/2024.07.09.602608)
- W.-W. Liao, M. Asri, J. Ebler, D. Doerr, M. Haukness, G. Hickey, S. Lu, J. K. Lucas, J. Monlong, H. J. Abel, S. Buonaiuto, X. H. Chang, H. Cheng, J. Chu, V. Colonna, J. M. Eizenga, X. Feng, C. Fischer, R. S. Fulton, ... B. Paten, *Nature*, in press, doi: [10.1038/s41586-023-05896-x](https://doi.org/10.1038/s41586-023-05896-x)
- W. S. DeWitt, L. Zhu, [M. R. Vollger](#) , M. E. Goldberg, A. Talenti, A. C. Beichman, K. Harris, *Journal of Open Source Software*, in press, doi: [10.21105/joss.05227](https://doi.org/10.21105/joss.05227)
- D. Porubsky, [M. R. Vollger](#) , W. T. Harvey, A. N. Rozanski, P. Ebert, G. Hickey, P. Hasenfeld, A. D. Sanders, C. Stober, J. O. Korbel, B. Paten, T. Marschall, E. E. Eichler, *Genome Research*, in press, doi: [10.1101/gr.277334.122](https://doi.org/10.1101/gr.277334.122)
- X. Yang, X. Wang, Y. Zou, S. Zhang, M. Xia, [M. R. Vollger](#) , N.-C. Chen, D. J. Taylor, W. T. Harvey, G. A. Logsdon, D. Meng, J. Shi, R. C. McCoy, M. C. Schatz, W. Li, E. E. Eichler, Q. Lu, Y. Mao, A refined characterization of large-scale genomic differences in the first complete human genome (2022), doi: [10.1101/2022.12.17.520860](https://doi.org/10.1101/2022.12.17.520860)
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- G. A. Logsdon, [M. R. Vollger](#) , P. Hsieh, Y. Mao, M. A. Liskovych, S. Koren, S. Nurk, L. Mercuri, P. C. Dishuck, A. Rhie, L. G. de Lima, T. Dvorkina, D. Porubsky, W. T. Harvey, A. Mikheenko, A. V. Bzikadze, M. Kremitzki, T. A. Graves-Lindsay, C. Jain, ... E. E. Eichler, *Nature*, in press, doi: [10.1038/s41586-021-03420-7](https://doi.org/10.1038/s41586-021-03420-7)
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- K. H. Miga, S. Koren, A. Rhie, [M. R. Vollger](#) , A. Gershman, A. Bzikadze, S. Brooks, E. Howe, D. Porubsky, G. A. Logsdon, V. A. Schneider, T. Potapova, J. Wood, W. Chow, J. Armstrong, J. Fredrickson, E. Pak, K. Tigyi, M. Kremitzki, ... A. M. Phillippy, *Nature*, in press, doi: [10.1038/s41586-020-2547-7](https://doi.org/10.1038/s41586-020-2547-7)

- K. Shafin, T. Pesout, R. Lorig-Roach, M. Haukness, H. E. Olsen, C. Bosworth, J. Armstrong, K. Tigyi, N. Maurer, S. Koren, F. J. Sedlazeck, T. Marschall, S. Mayes, V. Costa, J. M. Zook, K. J. Liu, D. Kilburn, M. Sorensen, K. M. Munson, ... B. Paten, *Nature Biotechnology*, in press, doi: [10.1038/s41587-020-0503-6](https://doi.org/10.1038/s41587-020-0503-6)
- A. Sulovari, R. Li, P. A. Audano, D. Porubsky, [M. R. Vollger](#), G. A. Logsdon, W. C. Warren, A. A. Pollen, M. J. P. Chaisson, E. E. Eichler, *Proceedings of the National Academy of Sciences*, in press, doi: [10.1073/pnas.1912175116](https://doi.org/10.1073/pnas.1912175116)
- P. Hsieh, [M. R. Vollger](#), V. Dang, D. Porubsky, C. Baker, S. Cantsilieris, K. Hoekzema, A. P. Lewis, K. M. Munson, M. Sorensen, Z. N. Kronenberg, S. Murali, B. J. Nelson, G. Chiatante, F. A. M. Maggiolini, H. Blanché, J. G. Underwood, F. Antonacci, J.-F. Deleuze, E. E. Eichler, Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. *Science*. **366** (2019), doi: [10.1126/science.aax2083](https://doi.org/10.1126/science.aax2083)
- F. A. M. Maggiolini, S. Cantsilieris, P. D'Addabbo, M. Manganeli, B. P. Coe, B. L. Dumont, A. D. Sanders, A. W. C. Pang, [M. R. Vollger](#), O. Palumbo, P. Palumbo, M. Accadia, M. Carella, E. E. Eichler, F. Antonacci, *PLOS Genetics*, in press, doi: [10.1371/journal.pgen.1008075](https://doi.org/10.1371/journal.pgen.1008075)

Presentations

Fiber-seq and tools to understand the regulatory genome in a disease context European Society of Human Genetics (ESHG)	<i>May 2025</i> <i>Allianz MiCo in Milan, Italy</i>
Computational tools for Fiber-seq and Fiber-seq Inferred Regulatory Elements BBI Long-read Symposium	<i>Oct 2024</i> <i>Seattle Children's Research Institute</i>
Fiber-seq Inferred Regulatory Elements with diploid T2T genomes Telomere-to-telomere face-to-face conference	<i>Aug 2024</i> <i>University of California Santa Cruz</i>
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision Division of Medical Genetics Seminar Series	<i>Apr 2023</i> <i>University of Washington</i>
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision AGBT 2023	<i>Feb 2023</i> <i>Hollywood, Florida</i>
A complete view of segmental duplications and their variation Genome Sciences 20th anniversary symposium	<i>Dec 2022</i> <i>University of Washington</i>
Using a complete human reference to explore variation in segmental duplications Long-Read, Long-Range scientific interest group	<i>Oct 2022</i> <i>NHGRI, remote</i>
Increased mutation rate and interlocus gene conversion within human segmental duplications Telomere-to-telomere face-to-face conference	<i>Aug 2022</i> <i>University of California Santa Cruz</i>
Segmental duplications and their variation in a complete human genome UCSC BME departmental seminar series	<i>Mar 2022</i> <i>University of California Santa Cruz, remote</i>
Segmental duplications and their variation in a complete human genome NHGRI computational biology seminar series	<i>Oct 2021</i> <i>NHGRI, remote</i>
A complete view of segmental duplications and their variation American Society of Human Genetics, Section talk	<i>Sep 2021</i> <i>remote</i>
A complete view of segmental duplications and their variation T2T and HPRC conference	<i>Sep 2020</i> <i>University of Washington</i>
Improved Assembly of Segmental Duplications Using HiFi Pacific Biosciences User Group Meeting	<i>Sep 2019</i> <i>University of Delaware</i>

Teaching Experience

Gene discovery and comparative genomics Invited Lecture, Genomics and Proteomics, undergraduate course	<i>October 2022</i> <i>University of Washington</i>
Introduction to Statistical Genomics Primary Instructor, Introduction to Statistical Genomics, graduate course	<i>Spring 2022</i> <i>University of Washington</i>
Introduction to Computational Molecular Biology Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours	<i>Winter 2020</i> <i>University of Washington</i>
Fundamentals of Genetics and Genomics Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours	<i>Summer 2019</i> <i>University of Washington</i>

Programming Languages

Daily Use Rust | Python | R | Snakemake | Bash
As needed C++ | LaTeX | typst

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

- Advisor** [Andrew B. Stergachis](#) | absterga@uw.edu
- Advisor** [Evan E. Eichler](#) | eee@gs.washington.edu
- Collaborator** [Adam Phillippy](#) | adam.phillippy@nih.gov
- Collaborator** [William Noble](#) | wnoble@uw.edu
- Collaborator** [Winston Timp](#) | wtimp@jhu.edu