

# 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](#)
- [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](#)
- [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. Eichler, *Nature*, in press, doi: [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](#)
- [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](#)
- [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](#)

- [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](#)
- 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](#)
- 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](#)
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- 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](#)
- D. Porubsky, [M. R. Vollger](#) , W. T. Harvey, A. N. Rozanski, P. Ebert, G. Hickey, P. Hasenfeld, A. D. Sanders, C. Stober, J. O. Korb, B. Paten, T. Marschall, E. E. Eichler, *Genome Research*, in press, doi: [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](#)
- S. Aganezov, S. M. Yan, D. C. Soto, M. Kirsche, S. Zarate, P. Avdeyev, D. J. Taylor, K. Shafin, A. Shumate, C. Xiao, J. Wagner, J. McDaniel, N. D. Olson, M. E. G. Sauria, [M. R. Vollger](#) , A. Rhie, M. Meredith, S. Martin, J. Lee, ... M. C. Schatz, A complete reference genome improves analysis of human genetic variation. *Science*. **376** (2022), doi: [10.1126/science.abl3533](#)
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- S. J. Hoyt, J. M. Storer, G. A. Hartley, P. G. S. Grady, A. Gershman, L. G. de Lima, C. Limouse, R. Halabian, L. Wojenski, M. Rodriguez, N. Altemose, A. Rhie, L. J. Core, J. L. Gerton, W. Makalowski, D. Olson, J. Rosen, A. F. A. Smit, A. F. Straight, ... R. J. O'Neill, From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. *Science*. **376** (2022), doi: [10.1126/science.abk3112](#)
- S. Nurk, S. Koren, A. Rhie, M. Rautiainen, A. V. Bzikadze, A. Mikheenko, [M. R. Vollger](#) , N. Altemose, L. Uralsky, A. Gershman, S. Aganezov, S. J. Hoyt, M. Diekhans, G. A. Logsdon, M. Alonge, S. E. Antonarakis, M. Borchers, G. G. Bouffard, S. Y. Brooks, ... A. M. Phillippy, *Science*, in press, doi: [10.1126/science.abj6987](#)
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- S. Nurk, B. P. Walenz, A. Rhie, [M. R. Vollger](#) , G. A. Logsdon, R. Grothe, K. H. Miga, E. E. Eichler, A. M. Phillippy, S. Koren, *Genome Research*, in press, doi: [10.1101/gr.263566.120](#)
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- 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)
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## Presentations

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### Fiber-seq and tools to understand the regulatory genome in a disease context

European Society of Human Genetics (ESHG)

May 2025

Allianz MiCo in Milan, Italy

### Computational tools for Fiber-seq and Fiber-seq Inferred Regulatory Elements

BBI Long-read Symposium

Oct 2024

Seattle Children's Research Institute

### Fiber-seq Inferred Regulatory Elements with diploid T2T genomes

Telomere-to-telomere face-to-face conference

Aug 2024

University of California Santa Cruz

### Comprehensive diploid genetic and epigenetic profiles with single-molecule precision

Division of Medical Genetics Seminar Series

Apr 2023

University of Washington

### Comprehensive diploid genetic and epigenetic profiles with single-molecule precision

AGBT 2023

Feb 2023

Hollywood, Florida

### A complete view of segmental duplications and their variation

Genome Sciences 20th anniversary symposium

Dec 2022

University of Washington

### Using a complete human reference to explore variation in segmental duplications

Long-Read, Long-Range scientific interest group

Oct 2022

NHGRI, remote

### Increased mutation rate and interlocus gene conversion within human segmental duplications

Telomere-to-telomere face-to-face conference

Aug 2022

University of California Santa Cruz

### Segmental duplications and their variation in a complete human genome

UCSC BME departmental seminar series

Mar 2022

University of California Santa Cruz, remote

### Segmental duplications and their variation in a complete human genome

NHGRI computational biology seminar series

Oct 2021

NHGRI, remote

### A complete view of segmental duplications and their variation

American Society of Human Genetics, Section talk

Sep 2021

remote

### A complete view of segmental duplications and their variation

T2T and HPRC conference

Sep 2020

University of Washington

### Improved Assembly of Segmental Duplications Using HiFi

Pacific Biosciences User Group Meeting

Sep 2019

University of Delaware

## Teaching Experience

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### Gene discovery and comparative genomics

Invited Lecture, Genomics and Proteomics, undergraduate course

October 2022

University of Washington

### Introduction to Statistical Genomics

Primary Instructor, Introduction to Statistical Genomics, graduate course

Spring 2022

University of Washington

### Introduction to Computational Molecular Biology

Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours

Winter 2020

University of Washington

### Fundamentals of Genetics and Genomics

Teaching Assistant, Lead weekly discussion sections, organized and graded assignments, and held office hours

Summer 2019

University of Washington

## Programming Languages

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

## Professional Organizations

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**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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**Advisor** [Andrew B. Stergachis](#) | [absterga@uw.edu](mailto:absterga@uw.edu)  
**Advisor** [Evan E. Eichler](#) | [eee@gs.washington.edu](mailto:eee@gs.washington.edu)  
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**Collaborator** [William Noble](#) | [wnoble@uw.edu](mailto:wnoble@uw.edu)  
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