

# Mitchell R. Vollger

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## *Curriculum Vitae*

### Personal Information

Legal name      Mitchell Robert Vollger  
Place of Birth      Carson City, Nevada, USA

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### Education

Sep 2016 – **Ph.D. in Genome Sciences**, *University of Washington*, Seattle, Washington, GPA  
March 2021 – 3.86  
Sep. 2011 – **B.S.E. in Computer Science Engineering**, *Princeton University*, Princeton, New  
June 2015 Jersey, GPA – 3.13. Student of the [Integrated Science Curriculum](#)  
Sep. 2011 – **Certificate in Quantitative and Computational Biology**, *Princeton University*,  
June 2015 Princeton, New Jersey, GPA – 3.48  
Sep. 2008 – **Associate of Arts Degree in Mathematics**, *College of the Redwoods*, Eureka,  
June 2011 California, GPA – 4.00  
Sep. 2008– **Associate of Arts Degree in Science**, *College of the Redwoods*, Eureka, California,  
June 2011 GPA – 4.00

### Postdoctoral Experience

April 2022 – **Postdoctoral Scholar in Medical Genetics**, *University of Washington*, Seattle,  
Present Washington, Lab of Andrew B. Stergachis  
March 2021 – **Postdoctoral Scholar in Genome Sciences**, *University of Washington*, Seattle,  
April 2022 Washington, Lab of Evan E. Eichler

## Professional Organizations

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

## Research Funding

- Summer 2024 - Summer 2031 K99/R00 Pathway to Independence Award from the National Institute of General Medical Sciences.  
Fall 2022 - Fall 2024 NIH/NHGRI T32 Genome Training Grant through the Division of Medical Genetics at University of Washington.  
Fall 2017 - Fall 2019 BDGN, Big Data in Genomics and Neuroscience. Awarded for two years.  
Fall 2016 - Fall 2017 NIH/NHGRI T32 Genome Training Grant through Genome Sciences at University of Washington. Awarded for two years.

## Bibliography

### First author

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- **Mitchell R. Vollger**, Jonas Korlach, Kiara C. Eldred, Elliott Swanson, Jason G. Underwood, Yong-Han H. Cheng, et al. Synchronized long-read genome, methylome, epigenome, and transcriptome for resolving a Mendelian condition. *Nature Genetics, accepted in principle. Online*. 2024. [10.1101/2023.09.26.559521](https://doi.org/10.1101/2023.09.26.559521)
- **Mitchell R. Vollger**, Philip C. Dishuck, William T. Harvey, William S. DeWitt, Xavi Guitart, Michael E. Goldberg, et al. Increased mutation and gene conversion within human segmental duplications. *Nature*. 325–334,7960,617. 2023. [10.1038/s41586-023-05895-y](https://doi.org/10.1038/s41586-023-05895-y)
- **Mitchell R. Vollger**, Xavi Guitart, Philip C. Dishuck, Ludovica Mercuri, William T. Harvey, Ariel Gershman, et al. Segmental duplications and their variation in a complete human genome. *Science*. 6588,376. 2022. [10.1126/science.abj6965](https://doi.org/10.1126/science.abj6965)
- **Mitchell R. Vollger**, Peter Kerpedjiev, Adam M Phillippy, Evan E Eichler. Stained-Glass: Interactive visualization of massive tandem repeat structures with identity heatmaps. *Bioinformatics. Online*. 2022. [10.1093/bioinformatics/btac018](https://doi.org/10.1093/bioinformatics/btac018)
- **Mitchell R. Vollger**, Glennis A. Logsdon, Peter A. Audano, Arvis Sulovari, David Porubsky, Paul Peluso, et al. Improved assembly and variant detection of a haploid human genome using single-molecule, high-fidelity long reads. *Annals of Human Genetics*. 125–140,2,84. 2019. [10.1111/ahg.12364](https://doi.org/10.1111/ahg.12364)

- **Mitchell R. Vollger**, Philip C. Dishuck, Melanie Sorensen, AnneMarie E. Welch, Vy Dang, Max L. Dougherty, et al. Long-read sequence and assembly of segmental duplications. *Nature Methods*. 88–94,1,16. 2018. [10.1038/s41592-018-0236-3](https://doi.org/10.1038/s41592-018-0236-3)

#### Corresponding author

- Anupama Jha, Stephanie C. Bohaczuk, Yizi Mao, Jane Ranchalis, Benjamin J. Mallory, Alan T. Min, ... **Mitchell R. Vollger**. DNA-m6A calling and integrated long-read epigenetic and genetic analysis with fibertools. *Genome Research*. gr.279095.124. 2024. [10.1101/gr.279095.124](https://doi.org/10.1101/gr.279095.124)

#### Collaborative author

- Kerry L. Bubb, Morgan O. Hamm, Joseph K. Min, Bryan Ramirez-Corona, Nicholas A. Mueth, Jane Ranchalis, **Mitchell R. Vollger**, et al. The regulatory potential of transposable elements in maize. *bioRxiv. Online*. 2024. [10.1101/2024.07.10.602892](https://doi.org/10.1101/2024.07.10.602892)
- Stephanie C. Bohaczuk, Zachary J. Amador, Chang Li, Benjamin J. Mallory, Elliott G Swanson, Jane Ranchalis, **Mitchell R. Vollger**, et al. Resolving the chromatin impact of mosaic variants with targeted Fiber-seq. *bioRxiv. Online*. 2024. [10.1101/2024.07.09.602608](https://doi.org/10.1101/2024.07.09.602608)
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- William S. DeWitt, Luke Zhu, **Mitchell R. Vollger**, Michael E. Goldberg, Andrea Talenti, Annabel C. Beichman, et al. mutyper: assigning and summarizing mutation types for analyzing germline mutation spectra. *Journal of Open Source Software*. 5227,85,8. 2023. [10.21105/joss.05227](https://doi.org/10.21105/joss.05227)
- David Porubsky, **Mitchell R. Vollger**, William T. Harvey, Allison N. Rozanski, Peter Ebert, Glenn Hickey, et al. Gaps and complex structurally variant loci in phased genome assemblies. *Genome Research*. 496–510,4,33. 2023. [10.1101/gr.277334.122](https://doi.org/10.1101/gr.277334.122)
- Xiangyu Yang, Xuankai Wang, Yawen Zou, Shilong Zhang, Manying Xia, **Mitchell R. Vollger**, et al. A refined characterization of large-scale genomic differences in the first complete human genome. *bioRxiv. Online*. 2022. [10.1101/2022.12.17.520860](https://doi.org/10.1101/2022.12.17.520860)
- Sergey Aganezov, Stephanie M. Yan, Daniela C. Soto, Melanie Kirsche, Samantha Zarate, Pavel Avdeyev, ... **Mitchell R. Vollger**..., et al. A complete reference genome improves analysis of human genetic variation. *Science*. 6588,376. 2022. [10.1126/science.abl3533](https://doi.org/10.1126/science.abl3533)
- Nicolas Altemose, Glennis A. Logsdon, Andrey V. Bzikadze, Pragma Sidhwani, Sasha A. Langley, Gina V. Caldas, ... **Mitchell R. Vollger**..., et al. Complete genomic and epigenetic maps of human centromeres. *Science*. 6588,376. 2022. [10.1126/science.abl4178](https://doi.org/10.1126/science.abl4178)
- Ariel Gershman, Michael E. G. Sauria, Xavi Guitart, **Mitchell R. Vollger**, Paul W. Hook, Savannah J. Hoyt, et al. Epigenetic patterns in a complete human genome. *Science*. 6588,376. 2022. [10.1126/science.abj5089](https://doi.org/10.1126/science.abj5089)

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- Sergey Nurk, Sergey Koren, Arang Rhie, Mikko Rautiainen, Andrey V. Bzikadze, Alla Mikheenko, **Mitchell R. Vollger**, et al. The complete sequence of a human genome. *Science*. 44–53,6588,376. 2022. [10.1126/science.abj6987](https://doi.org/10.1126/science.abj6987)
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## Invited Talks

- May 2025 **Speaker**, *European Society of Human Genetics (ESHG)*, Allianz MiCo in Milan  
Fiber-seq and tools to understand the regulatory genome in a disease context
- Summer 2024 **Speaker**, *Telomere to telomere face to face*, University of California Santa Cruz  
Fiber-seq Inferred Regulatory Elements with diploid T2T genomes
- April 2023 **Speaker**, *Division of Medical Genetics Seminar Series*, University of Washington  
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
- Feb 2023 **Speaker**, *AGBT 2023*, Hollywood Florida, National  
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
- Dec 2022 **Lighting talk**, *Genome Sciences 20th anniversary symposium*, University of Washington  
A complete view of segmental duplications and their variation
- Oct 2022 **Invited talk**, *Long-Read, Long-Range scientific interest group*, NIH  
Using a complete human reference to explore variation in segmental duplications
- Aug 2022 **Plenary talk**, *T2T-F2F conference, National*, University of California Santa Cruz  
Increased mutation rate and interlocus gene conversion within human segmental duplications
- March 2022 **Speaker**, *UCSC BME departmental seminar series, Local*  
Segmental duplications and their variation in a complete human genome
- Oct 2021 **Speaker**, *NHGRI computational biology seminar series, Local*  
Segmental duplications and their variation in a complete human genome
- Sep 2021 **Section talk**, *American Society of Human Genetics, National*  
A complete view of segmental duplications and their variation
- Sep 2020 **Plenary talk**, *T2T and HPRC conference, National*, University of Washington  
A complete view of segmental duplications and their variation
- Sep 2019 **Plenary talk**, *Pacific Biosciences User Group Meeting, National*, University of Delaware  
Improved Assembly of Segmental Duplications Using HiFi
- Feb 2015 **Speaker**, *The Princeton High Throughput Sequencing Group, Local*, Princeton University  
Computational methods to quantify DNA damage done to *Saccharomyces cerevisiae* by UV and Cisplatin

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## Posters

- September 2022 **Fibertools: computational methods for chromatin accessibility with long-reads**, *Genome Sciences Annual Retreat*, Washington University
- May 2021 **A complete view of segmental duplications and their variation**, *Biology of genomes*, Cold Spring Harbor Laboratory
- December 2019 **Improved Assembly of Human Genomes Using HiFi**, *Annual Scientific Meeting*, Howard Hughes Medical Institute  
Presented a poster on my research on assembly of human genomes using accurate long reads.
- October 2018 **Resolving segmental duplications using long reads and correlation clustering**, *Collaborative Seminar Series*, Allen Institute, Fred Hutch, and UW Medicine  
Presented a poster on my thesis research on developing and applying methods that use paralog specific variants (PSVs) to resolve collapsed duplications to improve genome assembly.
- September 2017/2018 **Resolving Segmental Duplications with PSV based Community Detection**, *Genome Sciences Annual Retreat*, Washington University  
Presented a poster on my thesis research on developing and applying methods that use paralog specific variants (PSVs) to resolve collapsed duplications to improve genome assembly.
- April 2017 **Identifying Multiple Charge States of Peptides in Mass Spectrometry**, *2017 NHGRI Annual Meeting*, Washington University in St. Louis  
Presented a poster on the research I did with William Noble. A description of the research can be found in the Independent Work and Research section.

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## Teaching Responsibilities

- October 2022 **Invited Lecture**, *Genomics and Proteomics (Genome 372)*, Gene discovery and comparative genomics  
University of Washington, Department of Genome Sciences
- Spring 2022 **Primary Lecturer**, *Introduction to Statistical Genomics (Genome 560)*  
University of Washington, Department of Genome Sciences
- Winter 2020 **Teaching Assistant**, *Introduction to Computational Molecular Biology*, Lead weekly discussion sections, organized and graded assignments, and held weekly office hours  
University of Washington, Department of Genome Sciences
- Summer 2019 **Teaching Assistant**, *Fundamentals of Genetics and Genomics*, Lead weekly discussion sections, graded assignments, and held weekly office hours  
University of Washington, Department of Genome Sciences

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## Programming Languages

- Daily Rust, Python, R
- Weekly Snakemake
- As needed C, C++, Java, L<sup>A</sup>T<sub>E</sub>X

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## References

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