

Mitchell R. Vollger

Curriculum Vitae

Personal Information

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

Email

Primary mvollger[at]uw.edu
Secondary mrvollger[at]gmail.com

Phone

Mobile (707) 407-8732

Address

Primary 1214 141st PL SW, Lynnwood Washington, 98087

Education

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

Postdoctoral Experience

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

- **Mitchell R. Vollger**, Elliott G. Swanson, Shane J. Neph, Jane Ranchalis, Katherine M. Munson, Ching-Huang Ho, et al. A haplotype-resolved view of human gene regulation. *bioRxiv. Online.* 2024. [10.1101/2024.06.14.599122](https://doi.org/10.1101/2024.06.14.599122)
- **Mitchell R. Vollger**, Jonas Korf, 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. *bioRxiv. Online.* 2023. [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)
- Wen-Wei Liao, Mobin Asri, Jana Ebler, Daniel Doerr, Marina Haukness, Glenn Hickey, ... **Mitchell R. Vollger**..., et al. A draft human pangenome reference. *Nature*. 312–324,7960,617. 2023. [10.1038/s41586-023-05896-x](https://doi.org/10.1038/s41586-023-05896-x)
- 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, Pragya 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)
- Savannah J. Hoyt, Jessica M. Storer, Gabrielle A. Hartley, Patrick G. S. Grady, Ariel Gershman, Leonardo G. de Lima, ... **Mitchell R. Vollger**..., et al. From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. *Science*. 6588,376. 2022. [10.1126/science.abk3112](https://doi.org/10.1126/science.abk3112)
- 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)

- PingHsun Hsieh, Vy Dang, **Mitchell R. Vollger**, Yafei Mao, Tzu-Hsueh Huang, Philip C. Dishuck, et al. Evidence for opposing selective forces operating on human-specific duplicated TCAF genes in Neanderthals and humans. *Nature Communications*. 1,12. 2021. [10.1038/s41467-021-25435-4](https://doi.org/10.1038/s41467-021-25435-4)
- Glennis A. Logsdon, **Mitchell R. Vollger**, PingHsun Hsieh, Yafei Mao, Mikhail A. Liskovych, Sergey Koren, et al. The structure, function and evolution of a complete human chromosome 8. *Nature*. 101–107,7857,593. 2021. [10.1038/s41586-021-03420-7](https://doi.org/10.1038/s41586-021-03420-7)
- David Porubsky, Peter Ebert, Peter A. Audano, **Mitchell R. Vollger**, William T. Harvey, Pierre Marijon, et al. Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. *Nature Biotechnology*. Online. 2020. [10.1038/s41587-020-0719-5](https://doi.org/10.1038/s41587-020-0719-5)
- Wesley C. Warren, R. Alan Harris, Marina Haukness, Ian T. Fiddes, Shwetha C. Murali, Jason Fernandes, ... **Mitchell R. Vollger**..., et al. Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. *Science*. eabc6617,6523,370. 2020. [10.1126/science.abc6617](https://doi.org/10.1126/science.abc6617)
- Glennis A. Logsdon, **Mitchell R. Vollger**, Evan E. Eichler. Long-read human genome sequencing and its applications. *Nature Reviews Genetics*. 597–614,10,21. 2020. [10.1038/s41576-020-0236-x](https://doi.org/10.1038/s41576-020-0236-x)
- Sergey Nurk, Brian P. Walenz, Arang Rhie, **Mitchell R. Vollger**, Glennis A. Logsdon, Robert Grothe, et al. HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. *Genome Research*. 1291–1305,9,30. 2020. [10.1101/gr.263566.120](https://doi.org/10.1101/gr.263566.120)
- Karen H. Miga, Sergey Koren, Arang Rhie, **Mitchell R. Vollger**, Ariel Gershman, Andrey Bzikadze, et al. Telomere-to-telomere assembly of a complete human X chromosome. *Nature*. 79–84,7823,585. 2020. [10.1038/s41586-020-2547-7](https://doi.org/10.1038/s41586-020-2547-7)
- Kishwar Shafin, Trevor Pesout, Ryan Lorig-Roach, Marina Haukness, Hugh E. Olsen, Colleen Bosworth, ... **Mitchell R. Vollger**..., et al. Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*. 1044–1053,9,38. 2020. [10.1038/s41587-020-0503-6](https://doi.org/10.1038/s41587-020-0503-6)
- Arvis Sulovari, Ruiyang Li, Peter A. Audano, David Porubsky, **Mitchell R. Vollger**, Glennis A. Logsdon, et al. Human-specific tandem repeat expansion and differential gene expression during primate evolution. *Proceedings of the National Academy of Sciences*. 23243–23253,46,116. 2019. [10.1073/pnas.1912175116](https://doi.org/10.1073/pnas.1912175116)
- PingHsun Hsieh, **Mitchell R. Vollger**, Vy Dang, David Porubsky, Carl Baker, Stuart Cantsilieris, et al. Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. *Science*. 6463,366. 2019. [10.1126/science.aax2083](https://doi.org/10.1126/science.aax2083)
- Flavia A. M. Maggolini, Stuart Cantsilieris, Pietro D'Addabbo, Michele Manganelli, Bradley P. Coe, Beth L. Dumont, ... **Mitchell R. Vollger**..., et al. Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. *PLOS Genetics*. e1008075,3,15. 2019. [10.1371/journal.pgen.1008075](https://doi.org/10.1371/journal.pgen.1008075)

Invited Talks

- 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

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.

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

Programming Languages

- Daily Rust, Python, R
- Weekly Snakemake
- As needed C, C++, Java, \LaTeX

References

- A. Stergachis absterga@uw.edu
- E. Eichler eee@gs.washington.edu
- A. Phillippy adam.phillippy@nih.gov
- W. Noble wnoble@uw.edu
- W. Timp wtimp@jhu.edu