

Curriculum Vitae

Rajiv C. McCoy

December 10, 2025

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Professional experience

2025–Present	Associate Professor
2018–2025	Assistant Professor Department of Biology Johns Hopkins University, Baltimore, MD
2015–2018	Postdoctoral Fellow Advisor: Joshua Akey
2017–2018	Department of Ecology and Evolutionary Biology Princeton University, Princeton, NJ
2015–2017	Department of Genome Sciences University of Washington, Seattle, WA

Education

2015	PhD in Biology Stanford University, Stanford, CA Advisors: Dmitri Petrov & Carol Boggs
2010	BS in Biology; Ecosystem Science & Policy, <i>summa cum laude</i> University of Miami, Coral Gables, FL

Affiliations

SECONDARY APPOINTMENTS

2025–Present	Department of Genetic Medicine, Johns Hopkins University
2024–Present	Department of Earth and Planetary Sciences, Johns Hopkins University

GRADUATE PROGRAMS

2022–Present	Faculty Preceptor, Predoctoral Training Program in Human Genetics and Genomics, Johns Hopkins School of Medicine
2018–Present	Training Faculty, Predoctoral Training Program in Cell, Molecular, Developmental Biology and Biophysics (CMDB), Johns Hopkins University

CENTERS AND INSTITUTES

2024–Present	Member, Institute for Data Intensive Engineering and Science, Johns Hopkins University
2023–Present	Member, Epigenome Sciences Cluster, Johns Hopkins University
2022–Present	Member, Center for Computational Biology, Johns Hopkins University

Awards

Awards since starting faculty position:

2025 & 2022	Discovery Award, Johns Hopkins University
2024	Catalyst Award, Johns Hopkins University
2024	Graduate Education Award, CMDB Graduate Program, Johns Hopkins University
2021–2023	Technology Fellowship, Center for Educational Resources, Johns Hopkins University

Awards prior to starting faculty position:

2015–2017	Genome Training Grant (NIH/NHGRI T32), U. of Washington, Dept. of Genome Sciences
2015	Epstein Trainee Award for Excellence in Human Genetics Research – Finalist, ASHG
2014	Office of Graduate Education Travel Award, Stanford University
2013 & 2012	Excellence in Teaching Award, Stanford University, Department of Biology
2012	Rosemary Grant Award, Society for the Study of Evolution
2012	Arthropod Genomics Consortium i5K Workshop Fellowship Award
2010–2013	Stanford University Graduate Fellowship in Science & Engineering
2010	Phi Beta Kappa Society
2010	Abess Center for Ecosystem Science and Policy Award, University of Miami

Research support

ACTIVE

2025–2028	NSF DBI 2504115 Infrastructure Innovation for Biological Research; Standard Grant Role: Co-I PI: Liliana Florea, Johns Hopkins University Title: “Characterizing transposable element contributions to the transcriptome with evidence-based and inferential methods” Total award: \$875,379; Total award to McCoy Lab: \$147,841
2025–2029	NIH/NCI R01CA292812 Research Project Grant Program Role: Co-I PI: Mary Armanios, Johns Hopkins University Title: “Cancer genetics of long telomere syndromes” Total award: \$3,872,849; Total award to McCoy Lab: \$55,475
2025–2027	Johns Hopkins University Discovery Award Role: PI Co-PIs: Yumi Kim and Philip Jordan, Johns Hopkins University Title: “Combining statistical and experimental genetics to understand the basis of variation in human fertility” Total award: \$150,000; Total award to McCoy Lab: \$50,000

2023–2028	NIH/NICHD R01HD091331 Research Project Grant Program Role: Co-I PI: Karen Schindler, Rutgers University Title: “Understanding genetic risk for aneuploid conception” Total award: \$2,474,125; Total award to JHU / McCoy Lab: \$55,928
2019–2029	NIH/NIGMS R35GM133747 Maximizing Investigators’ Research Award Role: PI Title: “Functional and fitness consequences of human genetic variation” Total award: \$4,186,700 (\$427,965 per year)
	COMPLETED
2024–2025	Johns Hopkins University Catalyst Award Role: PI Title: “Genomic sources of variability in human embryonic aneuploidy” Total award: \$75,000
2023–2025	NIH OT2OD034190 Cloud Platform Interoperability Program Role: Co-I PI: Michael Schatz, Johns Hopkins University Title: “AnVIL/Velsera-CGC interoperability project to study the genetic and transcriptomic contributions towards Hispanic colorectal cancer health disparities” Total award to JHU: *\$786,221; Total award to McCoy Lab: *\$335,752 *Original award; budget subsequently reduced due to change in NIH funding priorities; Dispersed award to McCoy Lab: \$54,603
2022–2024	Johns Hopkins University Discovery Award Role: PI Co-PIs: Alexis Battle and Winston Timp, Johns Hopkins University Title: “A high-resolution view of human gene expression and splicing diversity with single-molecule long-read sequencing” Total award: \$100,000; Total award to McCoy Lab: \$35,069

Publications

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- * denotes co-first authors
- † denotes co-corresponding authors
- § denotes lab members or rotation students

Publications since starting faculty position:

RESEARCH ARTICLES (PEER REVIEWED; 10 as corresponding author [gray], 20 as co-author)

- 2025 30 *[§]Carioscia, S. A., *[§]Biddanda, A., [§]Starostik, M. R., Tang, X., Hoffmann, E. R., Demko, Z. P., **McCoy, R. C.** Common variation in meiosis genes shapes human recombination phenotypes and aneuploidy risk. *Nature*: in press.
- 2025 29 [§]Yang, Q., [§]Carioscia, S. A., [§]Isada, M., **McCoy, R. C.** Approximate Bayesian computation supports a high incidence of chromosomal mosaicism in blastocyst-stage human embryos. *Genetics*, 231(2): iyaf149.
- 2025 28 McDaniel, J. H., Patel, V., Olson, N. D., He, H. J., He, Z., Cole, K. D., Schmitt, A., Sikkink, K., Sedlazeck, F. J., Doddapaneni, H., Jhangiani, S. N., Muzny, D. M., Gingras, M. C., Mehta, H., Paulin, L. F., Hastie, A. R., Yu, H. C., Weigman, V., Rojas, A., Kennedy, K., Remington, J., Gonzalez, I., Sudkamp, M., Wiseman, K., Lajoie, B. R., Levy, S., Jain, M., Akesson, S., Narzisi, G., Steinsnyder, Z., Reeves, C., Shelton, J., Kingan, S. B., Lambert, C., Bayabian, P., Wenger, A. M., McLaughlin, I. J., Adamson, A., Kingsley, C., Wescott, M., Kim, Y., Paten, B., Park, J., Violich, I., Miga, K. H., Gardner, J., McNulty, B., Rosen, G., **McCoy, R. C.**, Brundu, F., Sayyari, E., Scheffler, K., Truong, S., Catreux, S., Hannah, L. C., Lipson, D., Benjamin, H., Iremadze, N., Soifer, I., Eacker, S., Wood, M., Cross, E., Husar, G., Gross, S., Vernich, M., Kolmogorov, M., Ahmad, T., Keskus, A., Bryant, A., Thibaud-Nissen, F., Trow, J., Proszynski, J., Hirschberg, J. W., Ryon, K., Mason, C. E., Wagner, J., Xiao, C., Liss, A. S., Zook, J. M. Development and extensive sequencing of a broadly-consented Genome in a Bottle matched tumor-normal pair for somatic benchmarks. *Scientific Data*, 12: 1195.
- 2025 27 Wang, D., Cearlock, A., Lane, K., Jan, I., **McCoy, R. C.**, Yang, M. (2025), Chromosomal instability in human trophoblast stem cells and placentas. *Nature Communications*, 16: 3918.
- 2025 26 Yoo, D., Rhie, A., Hebbar, P., Antonacci, F., Logsdon, G. A., Solar, S. J., Antipov, D., Pickett, B. D., Safonova, Y., Montinaro, F., Luo, Y., Malukiewicz, J., Storer, J. M., Lin, J., Sequeira, A. N., Mangan, R. J., Hickey, G., Anez, G. M., Balachandran, P., Bankevich, A., Beck, C. R., [§]Biddanda, A., Borchers, M., Bouffard, G. G., Brannan, E., Brooks, S. Y., Carbone, L., Carrel, L., Chan, A. P., Crawford, J., Diekhans, M., Engelbrecht, E., Feschotte, C., Formenti, G., Garcia, G. H., de Gennaro, L., Gilbert, D., Green, R. E., Guarracino, A., Gupta, I., Haddad, D., Han, J., Harris, R. S., Hartley, G. A., Harvey, W. T., Hiller, M., Hoekzema, K., Houck, M. L., Jeong, H., Kamali, K., Kellis, M., Kille, B., Lee, C., Lee, Y., Lees, W., Lewis, A. P., Li, Q., Loftus, M., Loh, Y. H. E., Loucks, H., Ma, J., Mao, Y., Martinez, J. F. I., Masterson, P., **McCoy, R. C.**, McGrath, B., McKinney, S., Meyer, B. S., Miga, K. H., Mohanty, S. K., Munson, K. M., Pal, K., Pennell, M., Pevzner, P. A., Porubsky, D., Potapova, T., Ringeling, F. R., Rocha, J. L., Ryder, O. A., Sacco, S., Saha, S., Sasaki, T., Schatz, M. C., Schork, N. J., Shanks, C., Smeds, L., Son, D. R., Steiner, C., Sweeten, A. P., [§]Tassia, M. G., Thibaud-Nissen, F., Torres-Gonzalez, E., Trivedi, M., Wei, W., Wertz, J., Yang, M., Zhang, P., Zhang, S., Zhang, Y., Zhang, Z., Zhao, S. A., Zhu, Y., Jarvis, E. D., Gerton, J. L., Rivas-Gonzalez, I., Paten, B., Szpiech, Z. A., Huber, C. D., Lenz, T. L., Konkel, M. K., Yi, S. V., Canzar, S., Watson, C. T., Sudmant, P. H., Molloy, E., Garrison, E., Lowe, C. B., Ventura, M., O'Neill, R. J., Koren, S., Makova, K. D., Phillippy, A. M., Eichler, E. E. (2025), Complete sequencing of ape genomes. *Nature*, 641: 401-418.
- 2025 25 Liang, S., Ren, T., Zhang, J., He, J., Wang, X., Jiang, X., He, Y., **McCoy, R. C.**, Fu, Q., Akey, J. M., Mao, Y., Chen, L. (2025), A refined analysis of Neanderthal-introgressed sequences in modern humans with a complete reference genome. *Genome Biology*, 26: 32.
- 2024 24 [§]Taylor, D. J., Chhetri, S. B., [§]Tassia, M. G., [§]Biddanda, A., [§]Yan, S. M., Wojcik, G. L., Battle, A., **McCoy, R. C.** (2024), Sources of gene expression variation in a globally diverse human

cohort. *Nature*, 632: 122–130.

Also see editorial: [§]Taylor, D. J., [§]Yan, S. M. (2024), A broader view of the diversity of human gene expression. *Nature*.

- 2024 (23) Xiang, G., He, X., Giardine, B. M., [§]Weaver, K. J., [§]Taylor, D. J., **McCoy, R. C.**, Jansen, C., Keller, C. A., Wixom, A., Cockburn, A., Miller, A., Qi, Q., He, Y., Li, Y., Lichtenberg, J., Heuston, E. F., Anderson, S. M., Luan, J., Vermunt, M. W., Yue, F., Sauria, M. E. G., Schatz, M. C., Taylor, J., Gottgens, B., Hughes, J. R., Higgs, D. R., Weiss, M. J., Cheng, Y., Blobel, G. A., Bodine, D., Zhang, Y., Li, Q., Mahony, S., Hardison, R. C. (2024), Interspecies regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. *Genome Research*, 34: 1089-1105.
- 2024 (22) Makova, K. D., Pickett, B. D., Harris, R. S., Hartley, G. A., Cechova, M., Pal, K., Nurk, S., Yoo, D., Li, Q., Hebbard, P., McGrath, B. C., Antonacci, F., Aubel, M., [§]Biddanda, A., Borchers, M., Bomberg, E., Bouffard, G. G., Brooks, S. Y., Carbone, L., Carrel, L., Carroll, A., Chang, P. C., Chin, C. S., Cook, D. E., Craig, S. J. C., de Gennaro, L., Diekhans, M., Dutra, A., Garcia, G. H., Grady, P. G. S., Green, R. E., Haddad, D., Hallast, P., Harvey, W. T., Hickey, G., Hillis, D. A., Hoyt, S. J., Jeong, H., Kamali, K., Kosakovsky Pond, S. L., LaPolice, T. M., Lee, C., Lewis, A. P., Loh, Y. E., Masterson, P., **McCoy, R. C.**, Medvedev, P., Miga, K. H., Munson, K. M., Pak, E., Paten, B., Pinto, B. J., Potapova, T., Rhie, A., Rocha, J. L., Ryabov, F., Ryder, O. A., Sacco, S., Shafin, K., Shepelev, V. A., Slon, V., Solar, S. J., Storer, J. M., Sudmant, P. H., Sweetalana, Sweeten, A., [§]Tassia, M. G., Thibaud-Nissen, F., Ventura, M., Wilson, M. A., Young, A. C., Zeng, H., Zhang, X., Szpiech, Z. A., Huber, C. D., Gerton, J. L., Yi, S. V., Schatz, M. C., Alexandrov, I. A., Koren, S., O'Neill, R. J., Eichler, E., Phillippy, A. M. (2024), The complete sequence and comparative analysis of ape sex chromosomes. *Nature*, 630: 401–411.
- 2024 (21) Hadyniak, S. E., Eldred, K. C., Brennerman, B., Hussey, K. A., **McCoy, R. C.**, Sauria, M. E. G., Kuchenbeker, J. A., Neitz, M., Neitz, J., Taylor, J., Johnston, R. J. (2024), Retinoic acid signaling regulates spatiotemporal specification of human green and red cones. *PLoS Biology*, 22(1): e3002464.
- 2024 (20) [§]Ariad, D., Madjunkova, S., Madjunkov, M., Chen, S., Abramov, R., Librach, C., **McCoy, R. C.** (2023). Aberrant landscapes of maternal meiotic crossovers contribute to aneuploidies in human embryos. *Genome Research*, 34: 70-84.
- 2023 (19) Sun, S., Aboelenain, M., [§]Ariad, D., Haywood, M. E., Wageman, C. R., Duke, M., Bag, A., Viotti, M., Katz-Jaffe, M., **McCoy, R. C.**, Schindler, K., Xing, J. (2023), Identifying risk variants for embryo aneuploidy using ultra-low coverage whole-genome sequencing from preimplantation genetic testing. *American Journal of Human Genetics*, 110(12): 2092–2102.
- 2023 (18) **McCoy, R. C.**, Summers, M. C., McCollin, A., Ottolini, C. S., Ahuja, K., Handyside, A. H. (2023), Meiotic and mitotic aneuploidies drive arrest of in vitro fertilized human preimplantation embryos. *Genome Medicine*, 15: 77.
- 2023 (17) *Rhie, A., *Nurk, S., *Cechova, M., *Hoyt, S., [§]Taylor, D., Altemose, N., Hook, P. W., Koren, S., Rautiainen, M., Alexandrov, I. A., McNulty, B. M., Bzikadze, A. V., Chen, N.-C., Chin, C.-S., Diekhans, M., Formenti, G., Flicek, P., ..., **McCoy, R. C.** (44/81), ..., Eichler, E. E., O'Neill, R., Schatz, M. C., Miga, K. H., Makova, K. D., Phillippy, A. M. (2023), The complete sequence of a human Y chromosome. *Nature*, 621(7978): 344-354.
- 2023 (16) Yang, X., Wang, X., Zou, Y., Zhang, S., Xia, M., Vollger, M. R., Chen, N.-C., [§]Taylor, D. J., Harvey, W. T., Logsdon, G. A., Meng, D., Shi, J., **McCoy, R. C.**, Schatz, M. C., Li, W., Eichler, E. E., Lu, Q., Mao, Y. (2023), Characterization of large-scale genomic differences in the first complete human genome. *Genome Biology*, 24(1): 157.
- 2023 (15) Giraldo, D., Rankin-Turner, S., Corver, A., Tauxe, G. M., Gao, A. L., Jackson, D. M.,

- Simubali, L., Book, C., Stevenson, J. C., Thuma, P. E., **McCoy, R. C.**, Gordus, A., Mburu, M. M., Simulundu, E., McMeniman, C. J. (2023), Human scent guides mosquito thermotaxis and host selection under naturalistic conditions. *Current Biology*, 33(12): 2367-2382.e7.
- 2023 (14) *DeBoy, E. A., *[§]Tassia, M. G., Schratz, K. E., [§]Yan, S. M., Cosner, Z. L., McNally, E. J., Gable, D. L., Xiang, Z., Lombard, D. B., Antonarakis, E. S., Gocke, C. D., **McCoy, R. C.**, Armanios, M. (2023), Familial clonal hematopoiesis in a long telomere syndrome. *New England Journal of Medicine*, 388(26): 2422-2433.
- Also see editorial: Vassiliou, G. (2023), Telomere length and clonal hematopoiesis. *New England Journal of Medicine*, 388(26): 2481-2484.
- 2022 (13) *[§]Carioscia, S. A., *[§]Weaver, K. J., [§]Bortvin, A. N., [§]Pan, H., [§]Ariad, D., Bell, A. D., **McCoy, R. C.** (2022), A method for low-coverage single-gamete sequence analysis demonstrates adherence to Mendel's first law across a large sample of human sperm. *eLife*, 11: e76383.
- 2022 (12) Griffin, D. K., Brezina, P. R., Tobler, K., Silvestri, G., **McCoy, R. C.**, Anchan, R., Benner, A., Cutting, G. R., Kearns, W. G. (2022), The human embryonic genome is karyotypically complex, with chromosomally abnormal cells preferentially located away from the developing fetus. *Human Reproduction*, 38(1): 180-188.
- 2022 (11) *Aganezov, S., *[§]Yan, S. M., *Soto, D. C., *Kirsche, M., *Zarate, S., Avdeyev, P., [§]Taylor, D. J., Shafin, K., Shumate, A., Xiao, C., Wagner, J., McDaniel, J., Olson, N. D., Sauria, M. E. G., Vollger, M. R., Meredith, M., Martin, S., Koren, S., Rosenfeld, J. A., Paten, B., Layer, R., Chin, C., Sedlazeck, F. J., Hansen, N. F., Miller, D. E., Phillippy, A., Miga, K., [†] **McCoy, R. C.**, [†] Dennis, M. Y., [†] Zook, J. M., [†] Schatz, M. C. (2022), A complete reference genome improves analysis of human genetic variation. *Science*, 376(6588): eabl3533.
- 2022 (10) Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A. V., Mikheenko, A., Vollger, M. R., Altemose, N., Uralsky, L., Gershman, A., Aganezov, S., Hoyt, S. J., Diekhans, M., Logsdon, G. A., Alonge, M., Antonarakis, S. E., Borchers, M., Bouffard, G. G., Brooks, S. Y., ..., [§]Yan, S. M., ..., **McCoy, R. C.** (89/99), ..., Eichler, E. E., Miga, K. H., Phillippy, A. M. (2022), The complete sequence of a human genome. *Science*, 376(6588): eabj6987.
- 2021 (9) [§]Ariad, D., [§]Yan, S. M., Victor, A. R., Barnes, F. L., Zouves, C. G., Viotti, M., **McCoy, R. C.** (2021), Haplotype-aware inference of human chromosome abnormalities. *Proceedings of the National Academy of Sciences USA*, 118(46): e2109307118.
- 2021 (8) [§]Yan, S. M., Sherman, R. M., [§]Taylor, D. J., [§]Nair, D. R., [§]Bortvin, A. N., Schatz, M. C., **McCoy, R. C.** (2021), Local adaptation and archaic introgression shape global diversity at human structural variant loci. *eLife*, 10, e67615.
- 2021 (7) Ranallo-Benavidez, T. R., Lemmon, Z. H., Soyk, S., Aganezov, S., Salerno, W. J., **McCoy, R. C.**, Lippman, Z. B., Schatz, M. C., Sedlazeck, F. J. (2021), SVCollector: Optimized sample selection for cost-efficient long-read population sequencing. *Genome Research*, 31(5): 910-918.
- 2020 (6) [§]Starostik, M. R., Sosina, O. A., **McCoy, R. C.** (2020), Single-cell analysis of human embryos reveals diverse patterns of aneuploidy and mosaicism. *Genome Research*, 30(6): 814-825.
- 2020 (5) Tyc, K. M., **McCoy, R. C.**, Schindler, K., Xing, J. (2020), Mathematical modeling of human oocyte aneuploidy. *Proceedings of the National Academy of Sciences USA*, 117(19): 10455-10464.
- 2020 (4) Sharma, R., Singh, P., **McCoy, R. C.**, Lenz, S. M., Donovan, K., Ochoa, M. T., Estrada-Garcia, I., Silva-Miranda, M., Jurado-Santa Cruz, F., Balagon, M. F., Stryjewska, B., Scollard, D. M., Pena, M. T., Lahiri, R., Williams, D. L., Truman, R. W., Adams, L. B. (2020), Isolation of *Mycobacterium lepromatosis* and development of molecular diagnostic assays to distinguish *M. leprae* and *M. lepromatosis*. *Clinical Infectious Diseases*, 71(8): e262-e269.

- 2019 (3) Gruhn, J. R., Zielinska, A., Shukla, V., ..., **McCoy, R. C.** (23/28), ..., Hoffmann, E. R. (2019), Chromosome errors in human eggs shape natural fertility over reproductive lifespan. *Science*, 365(6460): 1466-1469.
- 2019 (2) Victor, A. R., Tyndall, J. C., Brake, A. J., Lepkowski, L. T., Murphy, A., Griffin, D. K., **McCoy, R. C.**, Barnes, F. L., Zouves, C. G., Viotti, M. (2019), One hundred mosaic embryos transferred prospectively in a single clinic: exploring when and why they result in normal pregnancies. *Fertility & Sterility*, 111(2): 280-293.
- 2019 (1) Victor, A. R., Griffin, D. K., Brake, A. J., Tyndall, J. C., Murphy, A., Lepkowski, L. T., Lal, A., Zouves, C. G., Barnes, F. L., **McCoy, R. C.**, Viotti, M. (2019), Assessment of aneuploidy concordance between clinical trophoctoderm biopsy and blastocyst. *Human Reproduction*, 34(1): 181-192.

REVIEW ARTICLES (PEER REVIEWED; 3 as corresponding author [gray], 5 as co-author)

- 2025 (8) *Moya, N., *[§]Yan, S. M., [†] **McCoy, R. C.**, [†] Andersen, E. C. (2025), The long and short of hyperdivergent regions. *Trends in Genetics*, 41(4): 303-314.
- 2024 (7) [§]Taylor, D. J., Eizenga, J. M., Li, Q., Das, A., Jenike, K. M., Kenny, E. E., Miga, K. H., [†]Monlong, J., [†]**McCoy, R. C.**, [†]Paten, B., [†]Schatz, M. C. (2024), Beyond the Human Genome Project: The Age of Complete Human Genome Sequences and Pangenome References. *Annual Review of Genomics and Human Genetics*, 25: 77-104.
- 2023 (6) Muter, J., Lynch, V. J., **McCoy, R. C.**, Brosens, J. J. (2023), Human embryo implantation. *Development*, 150(10): dev201507.
- 2022 (5) Brosens, J. J., Bennett, P. R., Abrahams, V., Ramhorst, R., Coomarasamy, A., Quenby, S., Lucas, E. S., **McCoy, R. C.** (2022), Maternal selection of human embryos in early gestation: insights from recurrent miscarriage. *Seminars in Cell and Developmental Biology*, 131: 14-24.
- 2021 (4) Quenby, S., Gallos, I. D., Dhillon-Smith, R. K., Podsek, M., Stephenson, M. D., Fisher, J., Brosens, J., Brewin, J., Ramhorst, R., Lucas, E. S., **McCoy, R. C.**, Anderson, R., Daher, S., Regan, L., Al-Memar, M., Bourne, T., MacIntyre, D. A., Rai, R., Christiansen, O. B., Sugiura-Ogasawara, M., Odendaal, J., Devall, A. J., Bennett, P. R., Petrou, S., Coomarasamy, A. (2021), Miscarriage matters: the epidemiological, physical, psychological, and economic costs of early pregnancy loss. *The Lancet*, 397(10285): 1658-1667.
- 2021 (3) Levy, B., Hoffmann, E. R., **McCoy, R. C.**, Grati, F. R. (2021), Chromosomal mosaicism: origins and clinical implications in preimplantation and prenatal diagnosis. *Prenatal Diagnosis*, 41(5): 631-641.
- 2021 (2) Wartosch, L., Schindler, K., Schuh, M., Gruhn, J. R., Hoffmann, E. R., **McCoy, R. C.**, Xing, J. (2021), Origins and mechanisms leading to aneuploidy in human eggs. *Prenatal Diagnosis*, 41(5), 620-630.
- 2020 (1) [§]Yan, S. M., **McCoy, R. C.** (2020), Archaic hominin genomics provides a window into gene expression evolution. *Current Opinion in Genetics & Development*, 62: 44-49.

EDITORIALS AND COMMENTARIES (2 as corresponding author [gray], 2 as co-author)

- 2024 (4) [§]Carioscia, S., **McCoy, R. C.** (2024), A rare genetic variant biases maternal meiotic recombination toward risk of pregnancy loss. *Nature Structural & Molecular Biology*, 31: 584-585.

- 2021 (3) Viotti, M., **McCoy, R. C.**, Griffin, D. K., Spinella, F., Greco, E., Madjunkov, M., Madjunkova, S., Librach, C. L., Victor, A. R., Barnes, F. L., Zouves, C. G. (2021), Let the data do the talking: the need to consider mosaicism during embryo selection. *Fertility & Sterility*, 116(5): 1212-1219.
- 2019 (2) ^SYan, S. M., **McCoy, R. C.** (2019), Functional divergence among hominins. *Nature Ecology & Evolution*, 3(11): 1507-1508.
- 2019 (1) **McCoy, R. C.**, Kort, J. D. (2019), Quantifying the transcriptional impacts of aneuploidy in human blastocysts. *Fertility & Sterility*, 111(5): 888-889.

ARTICLES UNDER REVIEW (1 as corresponding author [gray], 2 as co-author)

- (3) Das, A., ^SBiddanda, A., **McCoy, R. C.**, Schatz, M. C. Assembling unmapped reads reveals hidden variation in South Asian genomes. *bioRxiv*: 2025.05.14.653340.
- (2) Lalli, J. L., ^SBortvin, A. N., [†] **McCoy, R. C.**, [†] Werling, D. M. A T2T-CHM13 recombination map and globally diverse haplotype reference panel improves phasing and imputation. *bioRxiv*: 2025.02.24.639687.
- (1) DeGorter, M. K., Goddard, P. C., Karakoc, E., Kundu, S., ^SYan, S. M., Nachun, D., Abell, N., Aguirre, M., Carstensen, T., Chen, Z., Durrant, M., Dwaracherla, V. R., Feng, K., Gloudemans, M. J., Hunter, N., Moorthy, M. P. S., Pomilla, C., Rodrigues, K. B., Smith, C., Smith, K. S., Ungar, R. A., Balliu, B., Fellay, J., Flicek, P., McLaren, P. J., Henn, B., **McCoy, R. C.**, Sugden, L., Kundaje, A., Sandu, M. S., Gurdasani, D., Montgomery, S. B. Transcriptomics and chromatin accessibility in multiple African population samples. *bioRxiv*: 2023.11.04.564839.

Publications prior to starting faculty position:

- 2018 Tucci, S., Vohr, S. H., **McCoy, R. C.**, Vernot, B., Robinson, M., Barbieri, C., Fu, W., Purnomo, G. A., Sudoyo, H., Barbujani, G., Visscher, P. M., Akey, J. M., Green, R. E. (2018), Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. *Science*, 361(6401): 511-516.
- 2018 Press, M. O., **McCoy, R. C.**, Hall, A. N., Akey, J. M., Queitsch, C. (2018), Short tandem repeats with massive variation and functional consequences across strains of *Arabidopsis thaliana*. *Genome Research*, 28(8): 1169-1178.
- 2018 ***McCoy, R. C.**, *Newnham, L. J., Ottolini, C. S., Hoffmann, E. R., Chatzimeletiou, K., Cornejo, O. E., Zhan, Q., Zaninovic, N., Rosenwaks, Z., Petrov, D. A., Demko, Z. P., Sigurjonsson, S., Handyside, A. H. (2018), Tripolar chromosome segregation drives the association between maternal genotype at variants spanning *PLK4* and aneuploidy in human preimplantation embryos. *Human Molecular Genetics*, 27(14): 2573-2585.
- 2018 Kort, J. D., **McCoy, R. C.**, Demko, Z. P., Lathi, R. B. (2018), Are blastocyst aneuploidy rates different between fertile and infertile populations? *Journal of Assisted Reproduction and Genetics*, 35(3): 403-408.
- 2017 **McCoy, R. C.** (2017), Mosaicism in preimplantation human embryos: when chromosomal abnormalities are the norm. *Trends in Genetics*, 33(7): 448-463.
- 2017 **McCoy, R. C.**, Akey, J. M. (2017), Selection plays the hand it was dealt: evidence that human adaptation commonly targets standing genetic variation. *Genome Biology*, 18(1): 139.
- 2017 Adashi, E. Y., **McCoy, R. C.** (2017), Technology versus biology: the limits of pre-implantation genetic screening. *EMBO Reports*, 18(5): 670-672.

- 2017 McCoy, R. C., Wakefield, J., Akey, J. M. (2017), Impacts of Neanderthal-introgressed sequences on the landscape of human gene expression. *Cell*, 168(5): 916-927.e12.
- 2016 Vernot, B., Tucci, S., Kelso, J., Schraiber, J. G., Wolf, A. B., Gittelman, R. M., Dannemann, M., Grote, S., McCoy, R. C., Norton, H., Scheinfeldt, L. B., Merriwether, D. A., Koki, G., Friedlaender, J. S., Wakefield, J., Pääbo, S., Akey, J. M. (2016), Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. *Science*, 352(6282): 235–239.
- 2016 McCoy, R. C., Akey, J. M. (2016), Patterns of deleterious variation between human populations reveal an unbalanced load. *Proceedings of the National Academy of Sciences USA*, 113(4): 809–811.
- 2016 Demko, Z. P., Simon, A. L., McCoy, R. C., Petrov, D. A., Rabinowitz, M. (2016), Effects of maternal age on euploidy in a large cohort of embryos analyzed with 24 chromosome single nucleotide polymorphism-based preimplantation genetic screening. *Fertility & Sterility*, 105(5): 1307-1313.
- 2015 McCoy, R. C., Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Petrov, D. A. (2015), Evidence of selection against complex mitotic-origin aneuploidy during preimplantation development. *PLoS Genetics*, 11(10): e1005601.
- 2015 McCoy, R. C., Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Fraser, H. B., Petrov, D. A. (2015), Common variants spanning *PLK4* are associated with mitotic-origin aneuploidy in human embryos. *Science*, 348(6231): 235-238.
- Also see editorial: Vohr, S. H., Green, R. E. (2015), Aneuploidy and mother's genes. *Science*, 348(6231): 180-181.
- 2014 Ahola, V., Lehtonen, R., Somervou, P., ..., McCoy, R. C. (18/45) , ..., Hanski, I. (2014), The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. *Nature Communications*, 5: 4737.
- 2014 McCoy, R. C., Taylor, R., Blauwkamp, T. A., Kelley, J. L., Kertesz, M., Pushkarev, D., Petrov, D. A., Fiston-Lavier, A. S. (2014), Illumina TruSeq synthetic long reads empower *de novo* assembly and resolve complex, highly repetitive transposable elements. *PLoS ONE*, 9(9): e106689.
- 2014 McCoy, R. C., Garud, N. R., Kelley, J. L., Boggs, C. L., Petrov, D. A. (2014), Genomic inference accurately predicts the timing and severity of a recent bottleneck in a non-model insect population. *Molecular Ecology*, 23(1): 136-150.

Patents

- 2025 Ariad, D., McCoy, R. C., Viotti, M. Methods and related aspects for analyzing chromosome number status. US Patent #12,322,509.

Oral presentations

- ‡ denotes presentations postponed or cancelled due to COVID-19 or personal reasons
 # denotes plenary or keynote presentations

Oral presentations since starting faculty position:

INVITED ORAL PRESENTATIONS (54)

Mar. 2026	Interurban Clinical Club, Baltimore, MD
Mar. 2026	Department of Genetics, University of Alabama at Birmingham, Birmingham, AB
Jan. 2026	Department of Ecology and Evolutionary Biology, Brown University, Providence, RI
Jan. 2026	Department of Human Genetics, University of Utah, Salt Lake City, UT
2025	Key Aspects of Reproductive Medicine, Interdisciplinary Clinical Association for Reproductive Medicine, Moscow, Russia (Online)
2025	Department of Human Genetics, University of Michigan, Ann Arbor, MI
2025	Artificial Intelligence and the Study of Life Symposium, Johns Hopkins University, Baltimore, MD
2025	[#] Annual International Conference on Preimplantation Genetics (PGDIS), Leuven, Belgium
2025	Biological Anthropology Colloquium Series, Department of Anthropology, Yale University, New Haven, CT
2024	Ctr. for Theoretical and Evolutionary Genetics, Univ. of California, Berkeley, CA (Online)
2024	Lieber Institute for Brain Development, Maltz Research Laboratories, Baltimore, MD
2024	Consequences of Aneuploidy Meeting, Federation of American Societies for Experimental Biology, Melbourne, FL
2024	Center for Genetic Epidemiology, University of Southern California, CA (Online)
2024	Department of Genome Sciences, University of Washington, Seattle, WA
2024	Biology of Genomes, Cold Spring Harbor Laboratory, NY
2024	Department of Genetics, University of Pennsylvania, Philadelphia, PA
2024	Department of Molecular Biology and Genetics, Johns Hopkins Univ., Baltimore, MD
2024	Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX (Online)
2023	World Congress on Controversies in Preconception, Preimplantation and Prenatal Genetic Diagnosis, Online
2023	International IVF Initiative (i3) Webinar, Online
2023	[‡] Origins of Human Aneuploidy Meeting, Florence, Italy
2023	[#] National Association of Biology Teachers Conference, Baltimore, MD
2023	Johns Hopkins University Graduate Program in Cell, Molecular, Developmental Biology, and Biophysics Retreat, Hershey, PA
2023	Statistical Genetics Working Group, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD (Online)
2023	Department of Genetics, Cell Biology and Development, University of Minnesota, Minneapolis, MN
2023	Joint audience of the Department of Cellular and Molecular Medicine, University of Copenhagen & ReproUnion, Copenhagen, Denmark
2023	Globe Institute, University of Copenhagen, Denmark
2023	Max Planck Institute for Evolutionary Biology, Plön, Germany
2023	Annual International Conference on Preimplantation Genetics (PGDIS), Paris, France
2023	Department Colloquium, Department of Biology, Johns Hopkins University
2022	Origins of Human Aneuploidy Meeting, Paris, France
2022	Department of Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD

2022 Joint Didactic Session, Reproductive Endocrinology & Infertility / Medical Genetics Fellowship Program, Johns Hopkins School of Medicine, Baltimore, MD

2022 Maimon M. Cohen Genetics Colloquium, Greater Baltimore Medical Center, Towson, MD (Online)

2021 Cell Bio Virtual, American Society of Cell Biology / European Molecular Biology Organization, Online

2021 Howard and Georgeanna Jones Endowed Symposium on Assisted Reproductive Technology, Annual Meeting of the American Society for Reproductive Medicine, Baltimore, MD

2021 Origins of Human Aneuploidy Meeting, Online

2021 Division of Biomedical Sciences, Warwick Medical School, Coventry, United Kingdom (Online)

2021 Center for Reproductive Medicine, Weill Medical College of Cornell University (Online), New York, NY

2020 Zouves Foundation for Reproductive Medicine, Foster City, CA (Online)

2020 World Congress on Controversies in Obstetrics, Gynecology and Infertility, Online

2020 [‡]Department of Molecular and Cellular Biology, Harvard University, Cambridge, MA

2020 Origins of Human Aneuploidy Meeting, Online

2020 Department of Embryology, Carnegie Institution, Baltimore, MD

2020 Computational Biology Department, Carnegie Mellon University, Pittsburgh, PA

2020 CReATe Fertility Centre, Toronto, Canada

2019 Annual Conference of the Foundation for Reproductive Medicine, New York, NY

2019 Origins of Human Aneuploidy Meeting, Paris, France

2019 Department of Genetics, Rutgers University, Piscataway, NJ

2019 Department of Biology, Catholic University, Washington, DC

2018 Annual Conference of the Foundation for Reproductive Medicine, New York, NY

2018 Genomics & Bioinf. Symposium, Johns Hopkins University, Baltimore, MD

2018 Johns Hopkins University Graduate Program in Cell, Molecular, Developmental Biology, and Biophysics Retreat, Rocky Gap State Park, MD

2018 Origins of Human Aneuploidy Meeting, Toronto, Canada

CONTRIBUTED ORAL PRESENTATIONS (5)

2024 [#]Annual Meeting of the American Society of Human Genetics, Denver, CO

2022 Annual Meeting of the American Society of Human Genetics, Los Angeles, CA

2022 [#]Annual Meeting of the American Society for Reproductive Medicine, Anaheim, CA (presented by co-author, Michael Summers, due to scheduling conflict with ASHG)

2021 Chromatin, Chromosomes, and Epigenomes Workshop, Johns Hopkins University, Baltimore, MD (Online)

2019 Annual Meeting of the American Society of Human Genetics, Houston, TX

SENIOR AUTHORSHIP OF TRAINEE ORAL PRESENTATIONS (25)

2025 Tassia, M.G., American Soc. of Hematology (Abstract Achievement Award), Orlando, FL

2025 Starostik, M.R., Industry Workshop, American Society of Human Genetics, Boston, MA

2025 Carioscia, S. A., Mutations in Time and Space, Broad Institute, Cambridge, MA

2025 Biddanda, A., Origins of Human Aneuploidy Meeting, Leuven, Belgium

2024 Carioscia, S. A., Chromatin, Chromosomes, and Epigenomes Workshop, Johns Hopkins University, Baltimore, MD

2024 Carioscia, S. A., JHU CMDDB Program Retreat, Fairfield, PA

2024 Tassia, M. G., Biology of Genomes, Cold Spring Harbor Laboratory, NY

2024 Carioscia, S. A., Biology of Genomes, Cold Spring Harbor Laboratory, NY

2023 Tassia, M. G., SBE Satellite Meeting on Mechanisms of Cellular Evolution, Tempe, AZ

2023 Biddanda, A., Annual Meeting of the Am. Society of Human Genetics, Washington, DC

2023 Taylor, D. J., Center for Bioinf. and Comp. Biology, Univ. of Maryland, College Park, MD

2022 Yan, S. M., JHU CMDDB Program Retreat, Harpers Ferry, VA

2022 Yan, S. M., Telomere-to-Telomere Face-to-Face, Santa Cruz, CA

2022 Taylor, D. J., Telomere-to-Telomere Face-to-Face, Santa Cruz, CA

2022 Yan, S. M., Advances in Genome Biology and Technology (AGBT), Orlando, FL

2022 Tassia, M. G., Evolution, Cleveland, OH (Online)

2022 Ariad, D., Biology of Genomes, Cold Spring Harbor Laboratory, NY

2021 Yan, S. M., *eLife* Virtual Symposium on Evolutionary Medicine (Online)

2021 Zarate, S., Annual Meeting of the American Society of Human Genetics (Online)

2021 Ariad, D., Genomics & Bioinf. Symposium, Johns Hopkins University (Online)

2021 Ariad, D., RECOMB-Genetics Satellite Meeting (Online)

2021 Yan, S. M., Biology of Genomes, Cold Spring Harbor Laboratory (Online)

2020 Yan, S. M., Annual Meeting of the American Society of Human Genetics (Online)

2020 ‡Yan, S. M., Society for Molecular Biology & Evolution, Québec City, Canada

2019 Seyedian, A., RECOMB-Genetics Satellite Mtg., George Wash. Univ., Washington, DC

Oral presentations prior to starting faculty position:

2017 Marabou Symposium on Nutrition and Human Development, Stockholm, Sweden

2017 Origins of Human Aneuploidy Meeting, Barcelona, Spain

2017 Annual International Conference on Preimplantation Genetics (PGDIS), Valencia, Spain

2017 Department of Genomes Sciences / Computational Molecular Biology Program Combi Seminar, University of Washington, Seattle, WA

2016 Genotype-Tissue Expression (GTEx) Project Community Meeting, Stanford, CA

2015 Annual Meeting of the American Society of Human Genetics, Baltimore, MD

2014 Illumina Long-Reads Applications Symposium, University of California, Davis, CA

2014 Presentation to Management Team at Natera, Inc., San Carlos, CA

2014 Bay Area Population Genomics Meeting, University of California, Davis, CA

Poster presentations

Poster presentations since starting faculty position:

POSTER PRESENTATIONS AS PRESENTING AUTHOR (5)

2025	Annual Meeting of the American Society of Human Genetics (Reviewers' Choice Abstract Award), Boston, MA
2023	Annual Meeting of the American Society of Human Genetics, Washington, DC
2020	‡Society for Molecular Biology & Evolution, Québec City, Canada
2020	‡The Allied Genetics Conference, Genetics Society of America
2019	Society for Molecular Biology & Evolution, Manchester, England

SENIOR AUTHORSHIP OF TRAINEE POSTER PRESENTATIONS (37)

2025	Biddanda, A., Annual Meeting of the American Society of Human Genetics, Boston, MA
2025	Starostik, M. R., Annual Meeting of the American Society of Human Genetics, Boston, MA
2025	Carioscia, S. A., Biology of Genomes, Cold Spring Harbor Laboratory, NY
2025	Tassia, M. A., Mutations in Time and Space, Broad Institute, Cambridge, MA
2024	Yang, Q., DREAMS Symposium, Hopkins Office of Undergraduate Research, Johns Hopkins University, Baltimore, MD
2024	Yang, Q., Chromatin, Chromosomes, and Epigenomes Workshop, Johns Hopkins University, Baltimore, MD
2024	Biddanda, A., Maryland Genetics, Epidemiology, and Medicine (MD-GEM) Research Day, Johns Hopkins University, Baltimore, MD
2024	Carioscia, S. A., Maryland Genetics, Epidemiology, and Medicine (MD-GEM) Research Day, Johns Hopkins University, Baltimore, MD
2024	Bortvin, A. N., Biology of Genomes, Cold Spring Harbor Laboratory, NY
2024	Biddanda, A., Biology of Genomes, Cold Spring Harbor Laboratory, NY
2024	Yan, S. M., Biology of Genomes, Cold Spring Harbor Laboratory, NY
2024	Taylor, D. J., The Allied Genetics Conference, Genetics Soc. of America, Washington, DC
2024	Yang, Q., The Allied Genetics Conference, Genetics Society of America, Washington, DC
2024	Carioscia, S. A., The Allied Genet. Conference, Genet. Soc. of America, Washington, DC
2023	Taylor, D. J., Annual Mtg. of the American Society of Human Genetics, Washington, DC
2023	Tassia, M. G., Annual Mtg. of the American Society of Human Genetics, Washington, DC
2023	Carioscia, S., Annual Mtg. of the American Society of Human Genetics, Washington, DC
2023	Yan, S. M., Annual Meeting of the American Society of Human Genetics, Washington, DC
2023	Tassia, M. G., Society for Molecular Biology & Evolution (Online)
2023	Yan, S. M., Society for Molecular Biology & Evolution (Online)
2022	Ariad, D., RECOMB, La Jolla, CA
2022	Taylor, D. J., Biology of Genomes, Cold Spring Harbor Laboratory, NY
2021	Weaver, K. J., RegSys COSI, International Society for Computational Biology / European Conference on Computational Biology (Online)
2021	Ariad, D., RECOMB (Online)

2021 Ariad, D., Annual Meeting of the American Society of Human Genetics (Online)
 2021 Carioscia, S. A., Genomics & Bioinf. Symposium, Johns Hopkins University (Online)
 2021 *Weaver, K. J., *Bortvin, A. N., Genomics & Bioinformatics Symposium, Johns Hopkins University (Online)
 2021 *Carioscia, S. A., *Weaver, K. J., Biology of Genomes, Cold Spring Harbor Lab. (Online)
 2021 Ariad, D., Biology of Genomes, Cold Spring Harbor Laboratory (Online)
 2020 Ariad, D., Annual Meeting of the American Society of Human Genetics (Online)
 2020 Taylor, D. J., Annual Meeting of the American Society of Human Genetics (Online)
 2020 Yan, S. M., The Allied Genetics Conference, Genetics Society of America (Online)
 2020 Carioscia, S. A., The Allied Genetics Conference, Genetics Society of America (Online)
 2019 Yan, S. M., Genomics & Bioinf. Symposium, Johns Hopkins University, Baltimore, MD
 2019 Carioscia, S. A., Genomics & Bioinf. Symposium, Johns Hopkins Univ., Baltimore, MD
 2019 Yan, S. M., Society for Molecular Biology & Evolution, Manchester, England
 2018 Farney, S., Genomics & Bioinf. Symposium, Johns Hopkins University, Baltimore, MD

Poster presentations prior to starting faculty position:

2017 Annual Meeting of the American Society of Human Genetics (Reviewers' Choice Abstract Award), Orlando, FL
 2017 NHGRI Annual Training and Career Development Meeting, St. Louis, MO
 2016 Annual Meeting of the American Society of Human Genetics, Vancouver, Canada
 2016 NHGRI Annual Training and Career Development Meeting, Bethesda, MD
 2014 Bay Area Population Genomics Meeting, University of California, Davis, CA
 2014 Stanford Biosciences Student Association Poster Session, Stanford, CA
 2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [1/2]
 2014 Society for Molecular Biology & Evolution, San Juan, Puerto Rico [2/2]
 2014 Ctr. for Computational, Evolutionary, and Human Genomics Symposium, Palo Alto, CA
 2013 Bay Area Population Genomics Meeting, Stanford, CA
 2013 Annual Meeting of the Society for Integrative & Comparative Biology, San Francisco, CA
 2012 Arthropod Genomics Symposium, Kansas City, MO
 2012 Joint Congress on Evolutionary Biology, Ottawa, Canada

Research mentoring

Research mentoring since starting faculty position:

POSTDOCTORATE (3 current, 1 graduated)

2024–Present Margaret Starostik, Postdoctoral Fellow, Johns Hopkins University
 2023–Present Arjun Biddanda, Postdoctoral Fellow, Johns Hopkins University
 2024–2026 Lalor Foundation Fellowship, Total award: \$110,000
 2022–Present Michael Tassia, Postdoctoral Fellow, Johns Hopkins University
 2024–2026 NIH Training Program in Hematology (T32)

2024–2026	American Society of Hematology Fellowship, Total award: \$100,000
2020–2022	Daniel Ariad, Postdoctoral Fellow, Johns Hopkins University Current position: Senior Data Scientist, PrognomiQ, Inc., San Mateo, CA
GRADUATE THESIS (3 current, 5 graduated)	
2025–Present	Joshua Bauman, PhD Student in CMDB, Johns Hopkins University
2024–Present	Betty Huang, PhD Student in CMDB, Johns Hopkins University
2021–Present	Andrew Bortvin, PhD Candidate in CMDB, Johns Hopkins University
2025–2026	JHU Dissertation Prize Fellowship
2024–2025	JHU Dean’s Teaching Fellowship, Total award: \$21,212
2020–2025	Sara Carioscia, PhD Candidate in CMDB, Johns Hopkins University
2025	Stephen and Carolyn Oppenheimer Thesis Award, CMDB
2025	Harold M. Weintraub Award Nominee, CMDB
2021–2026	NSF Graduate Research Fellowship, DGE1746891, Total award: \$138,000
2021–2022	JHU Ctr. for Teaching Excellence and Innovation Technology Fellowship, Total award: \$5500; Award to S. Carioscia: \$2000 Current position: Data Scientist, Valo Health
2020–2024	Dylan Taylor, PhD Candidate in CMDB, Johns Hopkins University
2025	Stephen and Carolyn Oppenheimer Thesis Award, CMDB
2024	Harold M. Weintraub Award Nominee, CMDB
2023–2024	NIH/NHGRI NRSA Predoctoral Fellowship, F31HG012900, Total award: \$95,388
2021–2022	JHU Ctr. for Teaching Excellence and Innovation Technology Fellowship, Total award: \$5500; Award to D. Taylor: \$2000 Current position: Human Geneticist, Arena BioWorks
2019–2024	Stephanie Yan, PhD Candidate in CMDB, Johns Hopkins University
2024	Stephen and Carolyn Oppenheimer Thesis Award, CMDB
2022–2024	NIH/NHGRI NRSA Predoctoral Fellowship, F31HG012495, Total award: \$94,446
2021–2023	JHU Ctr. for Teaching Excellence and Innovation Technology Fellowship, Total award: \$5500; Award to S. Yan: \$2000 Current position: Scientist, Genomics, Plc.
2020–2023	Kathryn Isaac (Weaver), PhD Candidate in CMDB, Johns Hopkins University
2023	Stephen and Carolyn Oppenheimer Thesis Award, CMDB
2022–2023	JHU Dean’s Teaching Fellowship, Total award: \$19,664
2021–2023	JHU Ctr. for Teaching Excellence and Innovation Technology Fellowship, Total award: \$5500; Award to K. Isaac: \$2000 Current position: Postdoc, Fred Hutchinson Cancer Center, Seattle, WA
2018–2020	Arta Seyedian, Masters of Science Student in Bioinformatics, Johns Hopkins University Current position: Bioinformatician, Center for Single Cell Biology, Children’s Hospital of Philadelphia, Philadelphia, PA
GRADUATE QUALIFYING PROJECT (2 graduated)	
2024–2025	Arun Das, PhD Candidate in Computer Science (Qualifying Project), Johns Hopkins University
2021	Taher Mun, PhD Candidate in Computer Science (Qualifying Project), Johns Hopkins University

Current position: Senior Bioinformatics Scientist, Illumina, Inc.

GRADUATE ROTATION (36)

2018–Present	Rotation students in CMDB, Johns Hopkins University: Graydon Moorhead (2025), Carsten Hoeke (2025), Rose Runyan (2025), Brooke Weingard (2025), Olivia Choi (2025), Colina Qiao (2025), Tabor Roderiques (2025), Francesca Battelli (2024), Xingyu Chen (2024), Izabella Mastroianni (2024), Joshua Bauman (2024), Maya Mastronardo (2024), Jake Galvin (2024), Betty Huang (2024), Catherine Rogers (2023), David Bass (2023), Catherine Brown (2023), Emily Shen (2023), Tye Chicha (2023), Jack Dorman (2023), Calvin Runnels (2023), Matthew Isada (2022), Joshua Schultz (2022), Bradley Olinger (2022), Rylee Genner (2021), Sadhana Chidambaran (2021), Catherine Henderson (2021), Robyn Styx (2021), Radhika Jangi (2021), Andrew Bortvin (2020), Simon Zhang (2020), Sara Debic (2020), Natalie Murphy (2019), Sara Carioscia (2019), Dylan Taylor (2019), Stephanie Yan (2018), Margaret Starostik (2018), Katie Farney (2018)
2023–Present	Rotation students in Human Genetics, Johns Hopkins University: J. Noah Workman (2023)

UNDERGRADUATE (2 current, 10 former/graduated)

2024–Present	Sukriti Gupta, Bachelor of Science Student in Biology and Applied Mathematics, Johns Hopkins University
2023–Present	Angela Yang, Bachelor of Science Student in Biology and Computer Science, Johns Hopkins University
2024–2026	Provost's Undergraduate Research Award, Total award: \$6000
2024	Ameena Beg, Bachelor of Science Student in Biology, Johns Hopkins University
2022–2024	Hao Pan, Bachelor of Science Student in Biology and Applied Mathematics, Johns Hopkins University
2022–2023	Anika Misra, Bachelor of Science Student in Biology and Computer Science, Johns Hopkins University
2023	Emma Smith, Research Experience for Undergraduates (REU) Student from The College of Wooster, Johns Hopkins University
2020–2023	Divya Nair, Bachelor of Science Student in Biology, Johns Hopkins University
2022	Katherine Gilbert, Research Experience for Undergraduates (REU) Student from Wesleyan University, Johns Hopkins University
2018–2020	Joel Espinoza, Bachelor of Science Student in Biology, Johns Hopkins University
2019–2020	Peter Huang, Bachelor of Science Student in Biology, Johns Hopkins University
2019–2020	Nicholas Parente, Bachelor of Science Student in Applied Mathematics & Statistics and Computer Science, Johns Hopkins University
2018	Vincent Huang, Bachelor of Science Student in Biology, Johns Hopkins University

HIGH SCHOOL (3)

2022–2023	Cosima Billotte Bermudez, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD
2020–2021	Miles Fancher, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD

2020–2021 Aram Zaprosyan, Ingenuity Project, Baltimore Polytechnic Institute, Baltimore, MD

Research mentoring prior to starting faculty position:

2014–2015 Jack McGregor, Undergraduate Senior Honors Thesis (Co-Advised), Stanford University

Teaching

Teaching experience since starting faculty position:

COURSES AS INSTRUCTOR OF RECORD (~40 hours/year)

2020–Present Quantitative Biology Lab (AS.020.617, Fall; graduate; 20-30 students; ~12 hours/year; co-instructors: Frederick Tan, Michael Sauria), Johns Hopkins University

2020–Present Quantitative Biology Bootcamp (AS.020.607, Fall; graduate; 20-30 students; ~12 hours/year; co-instructors: Frederick Tan, Michael Sauria), Johns Hopkins University

*2020–Present Human Genome Variation Computational Lab (AS.020.321, Spring; undergraduate; 10-20 students; ~13 hours/year), Johns Hopkins University; *KSAS teaching leave in 2022

*2020–Present Human Genome Variation (AS.020.319, Spring; undergraduate; 30-40 students; ~3 hours/year; co-instructor: Kyle Cunningham), Johns Hopkins University; *KSAS teaching leave in 2022

GUEST LECTURES (~7 hours/year)

2025 Advanced Topics in Human Genetics (ME.710.700, Spring; graduate; 12 students; 3 hours), Johns Hopkins University

2021–2025 Genetics (AS.020.303, Spring; undergraduate; 300-400 students; 1.5 hours), Johns Hopkins University

2021–2025 Biology of Disease (AS.020.314, Fall; undergraduate; 100-200 students; 2.5 hours), Johns Hopkins University

2019, 2022 Human Genome Variation (AS.020.319, Spring; undergraduate; 30-40 students; 3 hours), Johns Hopkins University

2018–2019 Guest Instructor, Quantitative Biology Bootcamp (AS.020.607, Fall; graduate; 20-30 students; 3 hours), Johns Hopkins University

WORKSHOPS

2019 Participant, Best Practices in University Teaching Workshop, Johns Hopkins University

Teaching experience prior to starting faculty position:

2017–2018 Science Teaching Experience for Postdocs (STEP) Program, University of Washington

2017 Participant, Undergraduate Faculty Genetics Education Workshop, American Society of Human Genetics

2014	Teaching Assistant Mentor, Department of Biology, Stanford University
2013 & 2011	Teaching Assistant: Ecology, Evolution, and Plant Biology, Stanford University
2013 & 2012	Biocore Explorations Course Instructor, Department of Biology, Stanford University
2012	Teaching Assistant: Conservation Biology, Stanford University
2010	Undergraduate Workshop Leader: Evolution and Biodiversity, University of Miami
2009–2010	Peer Tutor, Camner Academic Resource Center, University of Miami

Academic, community, & university service

Service activities since starting faculty position:

DOCTORAL THESIS COMMITTEES (19)

2025–Present	Jake Galvin, CMDB, Johns Hopkins University
2025–Present	Lance O'Connor, CMDB, Johns Hopkins University
2025–Present	Maya Mastronardo, CMDB, Johns Hopkins University
2025–Present	Samuel Fridell, CMDB, Johns Hopkins University
2024–Present	Megan Miller, Earth and Planetary Sciences, Johns Hopkins University
2024–Present	Theresa Mai, CMDB, Johns Hopkins University
2024–Present	Catherine Brown, CMDB, Johns Hopkins University
2024–Present	Darren Boydston, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
2023–Present	Calvin Runnels, CMDB, Johns Hopkins University
2022–Present	Catherine Henderson, CMDB, Johns Hopkins University
2022–Present	Radhika Jangi, CMDB, Johns Hopkins University
2021–Present	Dylan Sucich, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
2023–2025	Rylee Genner, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
2023–2025	Nicolas Moya, CMDB, Johns Hopkins University
2023–2024	Bradley Olinger, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
2021–2024	Danielle Nicklas, Pathobiology, Johns Hopkins University
2020–2024	Margaret Starostik, CMDB, Johns Hopkins University
2020–2023	Jeremiah Miller, CMDB, Johns Hopkins University
2020–2021	T. Rhyker Ranallo-Benavidez, Biomedical Engineering, Johns Hopkins University

GRADUATE BOARD ORAL EXAMINATION COMMITTEES (19)

2025	April Kim, Computer Science, Johns Hopkins University
2025	Kavya Vaddadi, Computer Science, Johns Hopkins University
2025	Stephen Hwang, Cross-Disciplinary Biology (XDBio), Johns Hopkins University
2025	Jamie Moore, Biomedical Engineering, Johns Hopkins University
2024	Zitong He, Computer Science, Johns Hopkins University
2024	Bohan Ni, Computer Science, Johns Hopkins University
2023	Jessica Bonnie, Computer Science, Johns Hopkins University
2023	Bailey Spiegelberg, Human Genetics, Johns Hopkins University

2023 Luke Morina, Biomedical Engineering, Johns Hopkins University
 2022 Matthew Isada, CMDB, Johns Hopkins University
 2022 Arun Das, Computer Science, Johns Hopkins University
 2022 Christian Wesselborg, CMDB, Johns Hopkins University
 2022 Samantha Zarate, Computer Science, Johns Hopkins University
 2021 Radhika Jangi, CMDB, Johns Hopkins University
 2021 Sadhana Chidambaran, CMDB, Johns Hopkins University
 2021 Xiangning Chen, CMDB, Johns Hopkins University
 2021 Katie Farney, CMDB, NIH Graduate Partnership Program, Johns Hopkins University
 2021 Catherine Henderson, CMDB, Johns Hopkins University
 2021 Nae-Chyun Chen, Computer Science, Johns Hopkins University

UNIVERSITY AND DEPARTMENTAL SERVICE

2025–Present Undergraduate Mentoring Committee, Department of Biology, Johns Hopkins University
 2023–Present Ruh Chih Huang Colloquium Series Organizer, Department of Biology, Johns Hopkins University
 2022–Present CMDB Admissions Committee, Johns Hopkins University
 2021–Present Biology Futures Committee, Department of Biology, Johns Hopkins University
 2022–Present Graduate Curriculum Committee, Department of Biology, Johns Hopkins University
 2020–Present Undergraduate Curriculum Committee, Department of Biology, Johns Hopkins University
 2019–Present CMDB Awards Committee, Johns Hopkins University
 2023–2024 Search Committee for Open Rank and Open Research Topic Position, Department of Biology, Johns Hopkins University
 2021–2023 Diversity Advocate and Member, Search Committee for Computational Genomics, Department of Biology, Johns Hopkins University
 2022 Faculty Focus Group Panelist, External Review of Research Compliance Program, Johns Hopkins University

ACADEMIC AND PROFESSIONAL ORGANIZATIONS

2024–Present Awards Committee, American Society of Human Genetics
 2021–2024 Co-Chair, Origins of Human Aneuploidy Research Consortium

CONFERENCES

2021–Present Organizing Committee, Origins of Human Aneuploidy Meeting, Online
 2024 Session Co-Chair, Complex Traits and Genomic Medicine, Biology of Genomes, Cold Spring Harbor Laboratory, NY
 2019 Pre-Conference Workshop Chair, Annual Conference of the Foundation for Reproductive Medicine, New York, NY
 2019 Session Moderator, Reproductive Fitness - The Genetics of Infertility, 69th Annual Meeting of the American Society of Human Genetics, Houston, TX

JOURNAL PEER REVIEW

2024–Present	Editorial Board Member, <i>Journal of Assisted Reproduction & Genetics</i>
2013–Present	Ad Hoc Reviewer, <i>American Journal of Human Genetics</i> , <i>American Journal of Obstetrics & Gynecology</i> , <i>BioData Mining</i> , <i>Bioinformatics</i> , <i>BMC Biology</i> , <i>Cell Genomics</i> , <i>Cell Proliferation</i> , <i>Current Urology</i> , <i>Development</i> , <i>eLife</i> , <i>G3</i> , <i>Genes</i> , <i>Genetics</i> , <i>Genome Biology</i> , <i>Genome Biology and Evolution</i> , <i>Genome Research</i> , <i>Human Reproduction</i> , <i>Journal of Assisted Reproduction & Genetics</i> , <i>Journal of Biogeography</i> , <i>Journal of Heredity</i> , <i>Journal of Ovarian Research</i> , <i>Molecular Biology and Evolution</i> , <i>Molecular Ecology</i> , <i>Nature</i> , <i>Nature Communications</i> , <i>Nature Ecology & Evolution</i> , <i>Nature Medicine</i> , <i>Nature Structural & Molecular Biology</i> , <i>PLoS Biology</i> , <i>PLoS Genetics</i> , <i>PLoS One</i> , <i>Prenatal Diagnosis</i> , <i>Proceedings of the National Academy of Sciences U.S.A.</i> , <i>Proceedings of the Royal Society B</i> , <i>Reproduction</i> , <i>Science</i> , <i>Science Advances</i>

GRANT AND CONFERENCE REVIEW

2025	Ad Hoc Reviewer, Research Foundation Flanders (FWO) Fundamental Research Projects
2025	Ad Hoc Reviewer, Woodrow Wilson Fellowship, Office of Undergraduate Research, Scholarly, and Creative Activity, Johns Hopkins University
2025	Ad Hoc Reviewer, Research Foundation Flanders (FWO) Excellence Prize
2024	Ad Hoc Panelist, Maximizing Investigators' Research Award A Study Section (MRAA), Center for Scientific Review, National Institutes of Health
2023–2025	Ad Hoc Reviewer, Provost's Undergraduate Research Award, Johns Hopkins University
2022–2024	Ad Hoc Reviewer, Annual Meeting of the European Society of Human Reproduction and Embryology
2023	Ad Hoc Reviewer, Discovery Awards, Johns Hopkins University
2022, 2024	Outside Reviewer, Israel Science Foundation
2022	College of Expert Reviewers, European Science Foundation
2022	Ad Hoc Reviewer, Kleberg Foundation Scholars Program Internal Competition, Office of Foundation Relations, Johns Hopkins University
2022	Outside Reviewer, Medical Research Council, United Kingdom Research and Innovation
2022	Ad Hoc Reviewer, NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL) Cloud Credits Continued Program (AC3)
2021	Outside Reviewer, Independent Research Fund Denmark, Danish Agency for Higher Education and Science
2018–2019, 2021	Outside Reviewer, Biological Anthropology Program, National Science Foundation

EDUCATION, VOLUNTEERING, & OUTREACH

2020, 2024	Representative of JHU CMDB, NIH Graduate & Professional School Fair, Bethesda, MD
2024	Speaker, Faculty Salon Career Mentorship Series, Department of Biology, Johns Hopkins University
2024	Keynote Speaker, Northeast District 2 Annual Convention, TriBeta Biological Honors Society, Johns Hopkins University

2022–2024	Virtual Training Program Mentor, Society for Molecular Biology and Evolution
2023	Judge, Postdoctoral Conference Poster Session (Online), Johns Hopkins University
2023	Co-author, Cloud-based modules for interactive exploration of human genomic variation, https://mccoy-lab.github.io/hgv_modules/
2018, 2021–2025	Mock F31 Panelist, Communicating Science (020.619, Spring), Johns Hopkins University
2023	South Asian Students at Hopkins Faculty Panelist, Johns Hopkins University
2022	Ingenuity Speaker Series, Baltimore Polytechnic Institute, Baltimore, MD
2020	Visiting Fellow in Biology Assessment, AP Higher Education, The College Board
2019	Undergraduate Mentor, Society for Molecular Biology & Evolution, Manchester, England
2018–2019	Senior Project Mentor, School Without Walls, Washington, DC
2018	Bioethics Panelist, Biology Club, Univ. of Maryland, Baltimore County, Catonsville, MD

Service activities prior to starting faculty position:

2018 & 2017	Education Outreach Volunteer, University Prep Middle School, Seattle, WA
2018	Judge, NWABR Middle School Essay Contest, Seattle, WA
2017	Session Moderator, Detection and Interpretation of Structural Variation, 67th Annual Meeting of the American Society of Human Genetics, Orlando, FL
2017	Invited Speaker, Emerald City Rotary, Seattle, WA
2016	Volunteer, University of Washington Paws-On Science, Pacific Science Center, Seattle, WA
2016	Invited Speaker, Open Mic Science, Treehouse Cafe, Bainbridge Island, WA
2014	AP Biology E-mentor, Arroyo High School, San Lorenzo, CA
2012–2013	Copy Editor, <i>Six Degrees: The Stanford Journal of Human Rights</i>
2012	Judge, Synopsys Silicon Valley Science and Technology Championship, San Jose, CA
2012	PhD Interview Visit Committee, Department of Biology, Stanford University
2011	New PhD Student Orientation Committee, Department of Biology, Stanford University

Selected media

Selected media coverage since starting faculty position:

2025	Rentz, A. Human genome sequencing powers personalized, precision medicine. Johns Hopkins University Hub .
2024	Anderson, A. Gene expression, underlying genetic variation profiled in diverse human populations. GenomeWeb .
2024	Candanosa, R. M. New study addresses long-standing diversity bias in human genetics. Johns Hopkins University Hub .
2024	Jiménez, G. Many pregnancy losses are caused by errors in cell division. Scientific American .
2023	Zhu, V. Study on chromosomal abnormalities sheds light on in early embryo development in human reproduction and IVF. The Johns Hopkins News-Letter .
2023	Marshall, M. Why the human genome was never completed. BBC .

- 2023 Rogers, M. A. Researchers assemble the first complete sequence of a human Y chromosome. [NHGRI Press Release](#).
- 2023 Candanosa, R. M. Male sex chromosome, missing piece in human genome, finally decoded. [Johns Hopkins University Hub](#).
- 2022 Kolata, G. Link between long telomeres and long life is a tall tale, study finds. [The New York Times](#).
- 2022 Contie, V. Long telomeres may heighten cancer risks. [NIH Research Matters](#).
- 2022 Park, A. The human genome is finally fully sequenced. [TIME](#).
- 2022 Browne, E. Genome defined as human genetic blueprint fully sequenced for first time. [Newsweek](#).
- 2022 Yeung, E. Hopkins team plays a role in sequencing complete human genome. [The Johns Hopkins News-Letter](#).
- 2022 Rieland, R. Johns Hopkins scientists contribute to the first complete sequence of human genome. [Johns Hopkins University Hub](#).
- 2021 Zimmer, C. Scientists finish the human genome at last. [The New York Times](#).
- 2020 Aneuploidy common in early-stage human embryos, single-cell RNA-seq study reveals. [GenomeWeb](#).
- 2020 Donovan, D. Abnormal cells in embryos might not prevent IVF success. [Johns Hopkins University Hub](#).

Selected media coverage prior to starting faculty position:

- 2018 Boissoneault, L. A new genetic study suggests modern Flores island pygmies and ancient hobbits are unrelated. [Smithsonian Magazine](#).
- 2018 Davidson, A. Small height evolved twice on 'Hobbit' island of Flores. [BBC](#).
- 2018 Zimmer, C. Bodies keep shrinking on this island, and scientists aren't sure why. [The New York Times](#).
- 2017 What Neanderthal DNA is doing to your genome (video). [SciShow](#).
- 2017 Panko, B. How ancient Neanderthal DNA still influences our genes today. [Smithsonian Magazine](#).
- 2015 Schindler, K. A scrambled mess. [The Scientist](#).