Ryan Mills

Associate Professor
University of Michigan Medical School, Computational Medicine and Bioinformatics, 100 Washtenaw Ave, Room 2055B, Ann Arbor, MI, 48019, United States
734-647-9628 - remills@umich.edu

Education and Training

Education

08/1996-05/2000	AB, Wabash College, Crawfordsville, United States
08/2000-08/2003	MS, Georgia Institute of Technology, Atlanta, United States
09/2003-05/2006	PhD, Georgia Institute of Technology, Atlanta, United States

Postdoctoral Training

01/2006-10/2008	Postdoctoral Fellow, Genetics/Genomics, Emory University, Biochemistry, Atlanta, GA, Dr. Scott Devine

Work Experience

Academic Appointment

01/2012-09/2018	Assistant Professor, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI
01/2012-09/2018	Assistant Professor, Human Genetics, University of Michigan, Ann Arbor, MI
09/2018-Present	Associate Professor, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, (Tenured)
09/2018-Present	Associate Professor, Human Genetics, University of Michigan, Ann Arbor, MI

Administrative Appointment

01/2009-12/2011	Team Leader, Bioinformatics and Medical Diagnostics Team, Molecular Genetic Research Unit, Brigham and Women's Hospital, Boston, MA
04/2022-Present	Program Director of DCMB Computing Infrastructure, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI

Research Position

11/2008-12/2011	Research Associate, Pathology, Brigham & Women's Hospital, Harvard Medical School, Boston, MA

Research Interests

- The primary purpose of sequencing genomes is to identify the underlying genetic variation between individuals and to explore what role those changes have on human phenotypes. Our research laboratory develops and implements methods to precisely identify and resolve different types of genomic variation. Our goal is to integrate this information with other forms of biologically and medically relevant data to improve our overall understanding of human health and disease.

Grants

Current Grants

Improving Bioinformatics Methods for Analysis of Virus-Associated Cancers:
Co-I (Principal Investigator:Chad Brenner)
Innovation in Cancer Informatics (ICI)
08/2022 - 08/2024
$224,000

N/A:*Repetitive elements in human health and disease:*
MPI
Ryan Mills(MPI)
Taubman Institute Innovation Program (TIIP)
07/2022 - 06/2024
$659,764

U01HG011952:*Predicting the Impact of Genomic Variation on Cellular States:*
Co-I (Principal Investigator:Alan Boyle)
National Institutes of Health
08/2021 - 05/2026
$3,179,945

F31DE030000:*Analysis of the E7-Mediated Mechanism of MHC Class I Repression in HNSCC:*
Co-I (Principal Investigator:Chad Brenner)
National Institutes of Health
07/2020 - 06/2023
$114,167

U24HG007497:*Identifying and Characterizing the Full Spectrum of Haplotype-resolved Structural Variation in Human Genome:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
08/2019 - 05/2023
$597,831

R35GM128836:*Mechanisms of translational control:*
Co-I (Principal Investigator:Kristin Koutmou)
National Institutes of Health
08/2018 - 07/2023
$1,847,095

Past Grants

R21HG011493:*New technologies for accurate capture and sequencing of repeat-associated regions:*
PI
National Institutes of Health
12/2020 - 11/2022
$643,024

F31HG010569:*Discovering Novel Structural Genomic Rearrangements Using Deep Neural Networks:*
PI
National Institutes of Health
04/2019 - 03/2022
$112,983

U41HG007497:*An Integrative Analysis of Structural Variation for the 1000 Genomes Project:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
09/2017 - 08/2018
$84,451

R01AI118886:*Fidelity, robustness, and diversity in RNA virus evolution and pathogenesis:*
Co-I (Principal Investigator:Adam Lauring)
National Institutes of Health
01/2016 - 12/2021
$2,023,562

U01MH106892:*2/3 Schizophrenia Genetics and Brain Somatic Mosaicism:*
Co-I (Principal Investigator:John Moran)
National Institutes of Health
05/2015 - 01/2022
$4,706,350

F31NS090883:*Upstream open reading frames in neuronal function: a singular and genome-wide approach:*
Co-I (Principal Investigator:Peter Todd)
National Institutes of Health
03/2015 - 02/2018
$102,399

U41HG007497:*An Integrative Analysis of Structural Variation for the 1000 Genomes Project:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
09/2013 - 08/2018
$355,492

R01HG007068:*Discovery and Analysis of Structural Variation in Whole Genome Sequences:*
PI
National Institutes of Health
09/2013 - 07/2018
$1,509,405

R01GM103961:*Comprehensive Characterization of Canine Genomic Structural Diversity:*
Co-I (Principal Investigator:Jeffrey Kidd)
National Institutes of Health
09/2013 - 04/2017
$985,991

F32HG004207:*Improving INDEL Identification in Genomic Sequences:*
Funded by
National Human Genome Research Institute
09/2006 - 10/2008
$99,022

Honors and Awards

National

2006 - 2008	Ruth L. Kirschstein National Research Service Award (NRSA) Individual Postdoctoral Fellowship, Emory University

2012	Sixth Annual Young Investigators, GenomeWeb
2015	Highlighted in "Copy Number Analysis Starts to Add Up, Genetic Engineering & Biotechnology News
2015	Profiled, Journal of Young Investigators
2018	Profiled, Georgia Tech, College of Sciences

Institutional

2014	Endowment for the Basic Sciences Teaching Award, Medical School
2020	Accelerator Award from the Endowment of Basic Sciences, Medical School
2021	Leadership Academy, Medical School, Office of Faculty Affairs & Faculty Development

Study Sections, Editorial Boards, Journal & Abstract Review

Study Sections

National

2014	NIH Study Section - Interpreting Variation in Human Non-Coding Genomic Regions Using Computational Approaches and Experimental Assessment, NIH, (Ad Hoc)
2015	NIH Study Section – Interpreting Variation in Human Non-Coding Genomic Regions Using Computational Approaches and Experimental Assessment, NIH, (Ad Hoc)
2015	NIH Study Section – Genomics, Computational Biology and Technology, NIH, (Ad Hoc)
2016	NIH Study Section – Maximizing Investigators' Research Award for New and Early Stage Investigators, NIH, (Ad Hoc)
2018	NIH Special Emphasis Panel - Rare Genetic Disorders as a Window into the Genetic Architecture of Mental Disorders (Co-Chair), NIH, (Ad Hoc)
2019	NIH Study Section – Genomics, Computational Biology and Technology (February), NIH, (Ad Hoc)
2019	NIH Study Section – Genomics, Computational Biology and Technology (October), NIH, (Ad Hoc)
2022	NIH Study Section - Bioengineering, Biodata, and Biomodeling Technologies, NIH, (Ad Hoc)
2022	Special Emphasis Panel - Expert-Driven Small Projects to Strengthen Gabriella Miller Kids First Discovery, NIH, (Ad Hoc)

Institutional

2018	University of Michigan Precision Health Investigators Awards - Reviewer, Medical School, (Ad Hoc)
2022	PRR Trainee Committee - Application Review, University of Michigan, (Ad Hoc)

Editorial Boards / Journal & Abstract Reviews

Editorial Boards

2015 - present	Editorial Board Member, Scientific Reports
2017 - present	Editorial Board Member, PeerJ

Journal Review

2012 - present	Bioinformatics (Ad Hoc)

2012 - present	BMC Bioinformatics (Ad Hoc)
2012 - present	Genome Biology (Ad Hoc)
2012 - present	Genome Research (Ad Hoc)
2012 - present	American Journal of Human Genetics (Ad Hoc)
2012 - present	Nature Genetics (Ad Hoc)
2013 - present	Nature Communications (Ad Hoc)
2013 - present	Nature Protocols (Ad Hoc)
2014 - present	Human Genetics (Ad Hoc)
2015 - present	PLoS Computational Biology (Ad Hoc)
2016 - present	Methods (Ad Hoc)
2018 - present	European Journal of Human Genetics (Ad Hoc)
2020 - present	Genetics (Ad Hoc)
2021 - present	Nature (Ad Hoc)

Teaching

Mentorship

Faculty Member

01/2020-Present	Weichen Zhou, University of Michigan, Computational Medicine and Bioinformatics, Research Investigator

Postdoctoral Fellow

01/2012-01/2016	Gargi Dayama, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow
01/2015-01/2020	Weichen Zhou, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow
01/2019-01/2020	Yifan Wang, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow

Graduate Student

01/2013-01/2017	Xuefang Zhao, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2013-01/2018	Sang Chun, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2014-01/2014	Fan Zhang, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2014-01/2018	Akima George, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2014-01/2019	Yifan Wang, University of Michigan, Human Genetics, PhD Degree
01/2015-01/2022	Marcus Sherman, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2016-01/2017	Nan Lin, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2016-01/2022	Alexandra Weber, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2017-Present	Chen Sun, University of Michigan, Computational Medicine and Bioinformatics, PhD Student

01/2017-01/2017	Catherine Barnier, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2017-05/2018	Zhenning Zhang, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2019-Present	Steve Ho, University of Michigan, Human Genetics, PhD Student
01/2021-01/2021	Kai Li, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2022-Present	Shaomiao Xia, University of Michigan, Computational Medicine and Bioinformatics, MS Student
01/2022-Present	Jinhao Wang, University of Michigan, Biostatistics, MS Student
01/2022-01/2022	Maya Bose, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
08/2022-10/2022	Brandt Bessell, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student

Undergraduate Student

01/2018-01/2019	Byungjun Kim, Cornell University, Summer Research
01/2019-01/2019	Samantha Rondeau, University of Michigan, Research Experience
01/2020-01/2021	Priya Ghandi, University of Michigan, Research Experience
01/2021-01/2022	Yanming Gan, University of Michigan, Research Experience
01/2022-01/2022	Thomas Chang, University of Michigan, Summer Research
08/2022-Present	Sophia Marcotte, University of Michigan, Research Experience

Teaching Activity

National

06/2014-06/2019	Lecturer, Mathematical and Theoretical Biology Institute, Arizona State University

Institutional

01/2012-Present	Doctoral Preliminary Exams (n=37), University of Michigan
09/2012-09/2012	Lecturer, HG 632 – Experimental Genetics Systems, University of Michigan
09/2012-12/2018	Coursemaster/Lecturer, BIOL 527 – Introduction to Bioinformatics, University of Michigan
01/2014-01/2014	Lecturer, UM NIEHS P30 Center and UM BRCF Bioinformatics Core Workshop – Introduction to Genome Variation, University of Michigan
09/2014-09/2014	Lecturer, Coursera (online) – Introduction to Bioinformatics, University of Michigan
01/2015-05/2019	Lecturer, BIOINF 525 - Foundations in Bioinformatics and Systems Biology, University of Michigan
08/2015-08/2019	Coursemaster/Lecturer, BIOINF/HUMGEN/BIOSTATS 606 – Introduction to Biocomputing, University of Michigan
03/2016-Present	HUMGEN 803 – Current Methods, University of Michigan, Human Genetics, Lecturer
03/2016-Present	Lecturer, HUMGEN 551 – Computational Genomics, University of Michigan
01/2019-Present	Coursemaster/Lecturer, BIOINF 529 - Bioinformatics Concepts and Algorithms, University of Michigan
01/2021-Present	Session Leader, PIBS 503 - Responsible Conduct in Research, University of Michigan

Dissertation Committees

05/2013-04/2017	Xuefang Zhao, Understanding the complexity of human structural genomic variation through multiple whole genome sequencing platforms, University of Michigan, Computational Medicine and Bioinformatics, Chair
05/2013-11/2017	Sang Chun, Development and Application of Next-Generation Sequencing Methods to Profile Cellular Translational Dynamics, University of Michigan, Computational Medicine and Bioinformatics, Chair
09/2013-09/2016	Brendan Veeneman, Development and application of methods to discover cancer-associated transcript variants, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
05/2014-05/2019	Yifan Wang, Detection of Rare Events in Complex Sequencing Data, University of Michigan, Human Genetics, Chair
07/2014-03/2016	Kärt Tomberg, Identification of Thrombosis Modifier Genes Using ENU Mutagenesis in the Mouse, University of Michigan, Human Genetics, Committee Member
08/2014-04/2016	Killeen Kirkconnell, Capturing transcriptional dynamics using nascent RNA sequencing, University of Michigan, Human Genetics, Committee Member
09/2014-03/2018	Caitlin Rodriguez, The role of upstream open reading frames in regulating neuronal protein synthesis, University of Michigan, Neuroscience, Committee Member
09/2014-09/2017	Diane Flasch, LINE-1 Integration Preferences in Human Somatic Cells, University of Michigan, Human Genetics, Committee Member
04/2015-04/2017	Andy Kong, Computational strategies for proteogenomic analyses, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
10/2015-09/2017	Daniel H. Hovelson, Precision oncology opportunities and disease insights from next-generation sequencing profiling of routine clinical biospecimens, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
01/2016-07/2022	Marcus Sherman, Cultivation of enhanced bioinformatic-specific pedagogical manipulatives, interventions, and professional development, University of Michigan, Computational Medicine and Bioinformatics, Chair
06/2016-04/2019	Fan Zhang, , Leveraging Genetic Variants for Rapid, Robust, and Scalable Analysis of Massive Sequence Datasets, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
08/2016-09/2020	Sierra Nishizaki, Decoding the Non-coding Genome: Novel Technologies for the Characterization of Non-coding Elements and Variation, University of Michigan, Human Genetics, Committee Member
09/2016-05/2022	Alexandra Weber, Integrating Diverse Technologies for Genomic Variant Discovery, University of Michigan, Computational Medicine and Bioinformatics, Chair
10/2016-05/2021	Nguyen Vo, The Genetic Heterogeneity and Drug Resistance Mechanisms in Relapse Refractory Multiple Myeloma, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
10/2016-04/2018	Adrian Tan, Statistical and Computational Methods for the Unified Analysis of Short Genetic Variants, University of Michigan, Biostatistics, Committee Member
04/2017-03/2021	Shengcheng Dong, Computational methods to identify regulatory variants in the non-coding regions of the human genome, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
05/2017-Present	Hillary Miller, University of Michigan, Cellular and Molecular Biology, Committee Member

01/2018-Present	Chris Castro, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2018-06/2019	Scott Ronquist, Methods for Analyzing the 4D Nucleome, with Application to Cellular Reprogramming, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2018-Present	Chen Sun, University of Michigan, Computational Medicine and Bioinformatics, Chair
04/2018-01/2022	Ningxin Ouyang, Deciphering Transcriptional Regulatory Circuits: Transcription Factor Binding and Regulatory Variants Identification, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
12/2018-05/2021	Siyu Liu, Epigenetic effects in head and neck cancer and di-2-ethylhexyl phthalate (DEHP) exposure, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
01/2019-Present	Steve Ho, University of Michigan, Human Genetics, Chair
01/2019-Present	Wenjin Gu, University of Michigan, Computational Medicine and Bioinformatics, Chair
01/2019-07/2020	James Delorme, Linking intracellular events to network reorganization in sleep-dependent memory consolidation, University of Michigan, Neuroscience, Committee Member
05/2019-Present	Kevin Hu, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
08/2019-Present	Elizabeth Gensterblum-Miller, University of Michigan, Cellular and Molecular Biology, Committee Member
03/2020-07/2022	Daniel Geislzer, Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
11/2020-Present	Camille Mumm, University of Michigan, Human Genetics, Committee Member
09/2021-Present	Samantha Grudzien, University of Michigan, Neuroscience, Committee Member
02/2022-Present	D. Ford Hannum, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2022-Present	Shiting Li, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
04/2022-Present	Anthony Nguyen, University of Michigan, Human Genetics, Committee Member
05/2022-Present	Itzaira Mercado-Hernandez, University of Michigan, Human Genetics, Committee Member
06/2022-Present	Noshad Hosseini, University of Michigan, Computational Medicine and Bioinformatics, Committee Member

Memberships in Professional Societies

2009 - Present	American Society of Human Genetics
2011 - Present	International Society for Computational Biology

Committee/Service

National

2011	Program Committee, First RECOMB Satellite Workshop on Massively Parallel Sequencing, Member
2015 - present	Program Committee, Great Lakes Bioinformatics Conference, Member

2015	Program Committee, Fifth RECOMB Satellite Workshop on Massively Parallel Sequencing, Member
2016	Abstract Committee, American Society of Human Genetics, Other, Abstract Reviewer
2018 - present	Program Committee, Intl. Conference on Algorithms for Computational Biology, Member
2018	Abstract Committee, American Society of Human Genetics, Other, Abstract Reviewer
2019 - present	National Association of Wabash Men, Wabash College, Board of Directors

Departmental

2012	Master's Program Admissions Committee, DCM&B, Member
2013 - 2020	Master's Admission Committee, Human Genetics, Member
2014 - 2016	Seminar Series Committee, DCM&B, Co-Chair
2014 - 2017	Picnic Committee, Human Genetics, Chair
2014 - 2021	PhD Admissions Committee, DCM&B, Member
2016 - present	Chair's Advisory Committee, DCM&B, Member
2016 - 2019	Website Committee, DCM&B, Chair
2019 - present	Space Committee, DCM&B, Member
2021 - present	Faculty Search Committee, DCM&B, Member
2021 - present	IT Committee, DCM&B, Chair
2022 - present	PhD Admissions Committee, DCM&B, Co-Chair
2022	Retreat Committee, DCM&B, Chair

Institutional

2015 - 2016	Faculty Leading Change, U-M ADVANCE Program, Other, Participant
2017 - present	Basic Research IT (BRIT) Committee, Medical School, Co-Chair
2018 - 2020	HITS Learning Services Governance Committee, Medical School, Member
2019 - 2020	PIBS Curriculum Committee, Medical School, Member
2020 - 2022	Advisory Committee on Appointments, Promotions, and Tenure (ACAPT), Medical School, Member
2020 - 2022	Pedagogy of Interdisciplinary Science Education (POISE) Training Program, University of Michigan, Advisory Board
2022 - present	Advisory Committee on Appointments, Promotions, and Tenure (ACAPT), Medical School, Chair
2022	Grievance Hearing Board, University of Michigan, Member

Scholarly Activities

Presentations

Extramural Invited Presentation

Speaker

1. Improving gene annotation of cytomegalovirus genomes by statistical and comparative genomics as verified by a proteomics-based analysis of isolated MCMV virions, 9th International Cytomegalovirus Workshop, 05/2003, Maastricht, Netherlands

2. Designing Custom CGH Arrays: Considerations for CNV Discovery and Genotyping, Agilent Technologies Workshop, American Society of Human Genetics, 10/2009, Honolulu, HI

3. Capturing Structural Variation from Whole Genome Population-Scale Sequencing: Perspectives from the 1000 Genomes Project, Cambridge Healthtech Institute, X-GEN Congress and Expo, 03/2011, San Diego, CA

4. Challenges in Mapping Copy Number Variation from Population-scale Genome Sequence Data, Open Science Grid, 2011 All Hands Meeting, 03/2011, Boston, MA

5. Structural Variation in the 1000 Genomes Project, Genomic Disorders 2012, Wellcome Trust Sanger Institute, 03/2012, Hinxton, UK

6. Discovery and functional impact of structural variation across 1000 genomes, Cambridge Healthtech Institute, NGx: Applying Next Generation Sequencing, 08/2012, Providence, RI

7. Discovery and Analysis of Structural Genomic Variation in Human Populations, School of Biology Seminar, Wabash College, 10/2012, Crawfordsville, IN

8. 1000 Genomes Project Data Tutorial, International Congress of Human Genetics, 11/2012, Montreal, Canada

9. 1000 Genomes Project Data Tutorial, American Society of Human Genetics Annual Meeting, 11/2012, San Francisco, CA

10. Mapping structural variation by population-scale genome sequencing, Radiation Effects Research Foundation, 03/2013, Hiroshima, Japan

11. Exploring Complex Structural Genomic Variation using Next-Gen Sequencing, BioConference Live, Genetics and Genomics, 08/2014, Online (Live Virtual Presentation)

12. Genomic landscape of polymorphic nuclear mitochondrial insertions in humans and other primates, American Society of Human Genetics Annual Meeting, 10/2014, San Diego, CA

13. Exploring the Hidden Genome: Deciphering Cryptic and Complex Structural Variation, Ewha Womans University, 07/2016, Seoul, South Korea

14. Excavating the Deep Genome: Deciphering Structural Variation in Complex and Repetitive Regions, Oakland University, 04/2019, Rochester, MI

15. Identification and Characterization of Cryptic Structural Variation in Human Genomes, Association for Molecular Pathology Annual Meeting & Expo, 11/2019, Baltimore, MD

16. Identification and Characterization of Cryptic Genomic Repetitive Elements, Stanford University, 05/2020, Stanford, CA (Live Virtual Presentation)

17. Identification and Characterization of Structural Variation in Human Genomes, Future Biotech Winter Retreat, 11/2020, Novosibirsk, Russia

18. New Technologies for Identifying and Characterizing Genomic Repetitive Elements, Department of Biomedical Informatics Colloquium, University of Pittsburgh, 02/2021, Pittsburgh, PA (Live Virtual Presentation)

19. New Technologies for Identifying and Characterizing Genomic Repetitive Elements, SV Working Group, Broad Institute, 02/2022, Boston, MA (Live Virtual Presentation)

Moderator

1. Platform Moderator, American Society of Human Genetics Annual Meeting, 11/2012, San Francisco, CA

2. Invited Session Moderator, American Society of Human Genetics Annual Meeting, 10/2014, San Diego, CA

Panel

1. Panel Discussion: Copy Number Variants, 3rd Annual PQG Conference, Harvard School of Public Health, 11/2009, Boston, MA

Intramural Invited Presentation

Speaker

1. Analysis of Structural Variationin the 1000 Genomes Project Pilot:New Methods, New Insights (co-speaker), Medical and Population Genetics Seminar, Broad Institute, 09/2010, Boston, MA

2. Natural Structural Variation in the Human Genome, Interdisciplinary Group Seminar (IGS), Rackham Graduate School, University of Michigan, 04/2012, Ann Arbor, MI

3. Navigating Genomic Complexity: Discovery and Analysis of Structural Variation, NCIBI Tools and Technology Series, University of Michigan, 05/2012, Ann Arbor, MI

Publications/Scholarship

Peer-Reviewed

Journal Article

1. Borodovsky M, **Mills R**, Besemer J, Lomsadze A: Prokaryotic gene prediction using GeneMark and GeneMark.hmm., *Curr Protoc Bioinformatics*.Chapter 4: Unit4.5, 05/2003. United States, PM18428700

2. Borodovsky M, Lomsadze A, Ivanov N, **Mills R**: Eukaryotic gene prediction using GeneMark.hmm., *Curr Protoc Bioinformatics*.Chapter 4: Unit4.6, 05/2003. United States, PM18428701

3. Perelygina L, Zhu L, Zurkuhlen H, **Mills R**, Borodovsky M, Hilliard JK: Complete sequence and comparative analysis of the genome of herpes B virus (Cercopithecine herpesvirus 1) from a rhesus monkey, *Journal of Virology*.77(11): 6167-6177, 06/2003. PM12743273

4. **Mills R**, Rozanov M, Lomsadze A, Tatusova T, Borodovsky M: Improving gene annotation of complete viral genomes., *Nucleic Acids Res*.31(23): 7041-7055, 12/2003. England, PM14627837

5. Kattenhorn LM, **Mills R**, Wagner M, Lomsadze A, Makeev V, Borodovsky M, Ploegh HL, Kessler BM: Identification of proteins associated with murine cytomegalovirus virions., *J Virol*.78(20): 11187-11197, 10/2004. United States, PM15452238

6. **Mills RE**, Bennett EA, Iskow RC, Luttig CT, Tsui C, Pittard WS, Devine SE: Recently mobilized transposons in the human and chimpanzee genomes., *Am J Hum Genet*.78(4): 671-679, 04/2006. United States, PM16532396

7. **Mills RE**, Luttig CT, Larkins CE, Beauchamp A, Tsui C, Pittard WS, Devine SE: An initial map of insertion and deletion (INDEL) variation in the human genome., *Genome Res*.16(9): 1182-1190, 09/2006. United States, PM16902084

8. Lange A, **Mills RE**, Lange CJ, Stewart M, Devine SE, Corbett AH: Classical Nuclear Localization Signals: Definition, Function, and Interaction with Importin α, *Journal of Biological Chemistry*.282(8): 5101-5105, 02/2007. PM17170104

9. **Mills RE**, Bennett EA, Iskow RC, Devine SE: Which transposable elements are active in the human genome?, *Trends Genet*.23(4): 183-191, 04/2007. England, PM17331616

10. Lange A, **Mills RE**, Devine SE, Corbett AH: A PY-NLS nuclear targeting signal is required for nuclear localization and function of the Saccharomyces cerevisiae mRNA-binding protein Hrp1., *J Biol Chem*.283 (19): 12926-12934, 05/2008. United States, PM18343812

11. Bennett EA, Keller H, **Mills RE**, Schmidt S, Moran JV, Weichenrieder O, Devine SE: Active Alu retrotransposons in the human genome., *Genome Res*.18(12): 1875-1883, 12/2008. United States, PM18836035

12. Kim J-I, Ju YS, Park H, Kim S, Lee S, Yi J-H, Mudge J, Miller NA, Hong D, Bell CJ, Kim H-S, Chung I-S, Lee W-C, Lee J-S, Seo S-H, Yun J-Y, Woo HN, Lee H, Suh D, Lee S, Kim H-J, Yavartanoo M, Kwak M, Zheng Y, Lee MK, Park H, Kim JY, Gokcumen O, **Mills RE**, Zaranek AW, Thakuria J, Wu X, Kim RW, Huntley JJ, Luo S, Schroth GP, Wu TD, Kim H, Yang K-S, Park W-Y, Kim H, Church GM, Lee C, Kingsmore SF, Seo J-S: A highly annotated whole-genome sequence of a Korean individual., *Nature*.460(7258): 1011-1015, 08/2009. England, PM19587683

13. Lange A, McLane LM, **Mills RE**, Devine SE, Corbett AH: Expanding the definition of the classical bipartite nuclear localization signal., *Traffic*.11(3): 311-323, 03/2010. England, PM20028483

14. Park H, Kim J-I, Ju YS, Gokcumen O, **Mills RE**, Kim S, Lee S, Suh D, Hong D, Kang HP, Yoo YJ, Shin J-Y, Kim H-J, Yavartanoo M, Chang YW, Ha J-S, Chong W, Hwang G-R, Darvishi K, Kim H, Yang SJ, Yang K-S, Kim H, Hurles ME, Scherer SW, Carter NP, Tyler-Smith C, Lee C, Seo J-S: Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing., *Nat Genet*.42(5): 400-405, 05/2010. United States, PM20364138

15. Iskow RC, McCabe MT, **Mills RE**, Torene S, Pittard WS, Neuwald AF, Van Meir EG, Vertino PM, Devine SE: Natural mutagenesis of human genomes by endogenous retrotransposons., *Cell*.141(7): 1253-1261, 06/2010. United States, PM20603005

16. Mullaney JM, **Mills RE**, Pittard WS, Devine SE: Small insertions and deletions (INDELs) in human genomes., *Hum Mol Genet*.19(R2): R131-R136, 10/2010. England, PM20858594

17. 1000 Genomes Project Consortium, Abecasis GR, Altshuler D, Auton A, Brooks LD, Durbin RM, Gibbs RA, Hurles ME, McVean GA: A map of human genome variation from population-scale sequencing., *Nature*.467(7319): 1061-1073, 10/2010. England, PM20981092

18. Sudmant PH, Kitzman JO, Antonacci F, Alkan C, Malig M, Tsalenko A, Sampas N, Bruhn L, Shendure J, 1000 Genomes Project, Eichler EE: Diversity of human copy number variation and multicopy genes., *Science*.330(6004): 641-646, 10/2010. United States, PM21030649

19. Gokcumen O, Babb PL, Iskow RC, Zhu Q, Shi X, **Mills RE**, Ionita-Laza I, Vallender EJ, Clark AG, Johnson WE, Lee C: Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection., *Genome Biol*.12(5): R52, 01/2011. England, PM21627829

20. **Mills RE**, Pittard WS, Mullaney JM, Farooq U, Creasy TH, Mahurkar AA, Kemeza DM, Strassler DS, Ponting CP, Webber C, Devine SE: Natural genetic variation caused by small insertions and deletions in the human genome., *Genome Res*.21(6): 830-839, 06/2011. United States, PM21460062

21. Pinto D, Darvishi K, Shi X, Rajan D, Rigler D, Fitzgerald T, Lionel AC, Thiruvahindrapuram B, MacDonald JR, Mills R, Prasad A, Noonan K, Gribble S, Prigmore E, Donahoe PK, Smith RS, Park JH, Hurles ME, Carter NP, Lee C, Scherer SW, Feuk L: Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants, *Nature Biotechnology*.29(6): 512-520, 06/2011. PM21552272

22. Conrad DF, Keebler JE M, DePristo MA, Lindsay SJ, Zhang Y, Casals F, Idaghdour Y, Hartl CL, Torroja C, Garimella KV, Zilversmit M, Cartwright R, Rouleau GA, Daly M, Stone EA, Hurles ME, Awadalla P, 1000 Genomes Project: Variation in genome-wide mutation rates within and between human families., *Nat Genet*.43(7): 712-714, 06/2011. United States, PM21666693

23. Gravel S, Henn BM, Gutenkunst RN, Indap AR, Marth GT, Clark AG, Yu F, Gibbs RA, 1000 Genomes Project, Bustamante CD: Demographic history and rare allele sharing among human populations., *Proc Natl Acad Sci U S A*.108(29): 11983-11988, 07/2011. United States, PM21730125

24. Marth GT, Yu F, Indap AR, Garimella K, Gravel S, Leong WF, Tyler-Smith C, Bainbridge M, Blackwell T, Zheng-Bradley X, Chen Y, Challis D, Clarke L, Ball EV, Cibulskis K, Cooper DN, Fulton B, Hartl C, Koboldt D, Muzny D, Smith R, Sougnez C, Stewart C, Ward A, Yu J, Xue Y, Altshuler D, Bustamante CD, Clark AG, Daly M, DePristo M, Flicek P, Gabriel S, Mardis E, Palotie A, Gibbs R, 1000 Genomes Project: The functional spectrum of low-frequency coding variation., *Genome Biol*.12(9): R84, 09/2011. England, PM21917140

25. Xue Y, Chen Y, Ayub Q, Huang N, Ball EV, Mort M, Phillips AD, Shaw K, Stenson PD, Cooper DN, Tyler-Smith C, 1000 GP C: Deleterious- and disease-allele prevalence in healthy individuals: insights from current predictions, mutation databases, and population-scale resequencing., *American journal of human genetics*.91(6)01/2012. PM23217326

26. Chen X, Shi X, Xu X, Wang Z, **Mills R**, Lee C, Xu J: A two-graph guided multi-task Lasso approach for eQTL mapping, *Proceedings of the 15th International Conference of Artificial Intelligence and Statistics (AISTATS)*.22: 208-217, 01/2012

27. Brown KH, Dobrinski KP, Lee AS, Gokcumen O, **Mills RE**, Shi X, Chong WW S, Chen JY H, Yoo P, David S, Peterson SM, Raj T, Choy KW, Stranger BE, Williamson RE, Zon LI, Freeman JL, Lee C: Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis., *Proc Natl Acad Sci U S A*.109(2): 529-534, 01/2012. United States, PM22203992

28. MacArthur DG, Balasubramanian S, Frankish A, Huang N, Morris J, Walter K, Jostins L, Habegger L, Pickrell JK, Montgomery SB, Albers CA, Zhang ZD, Conrad DF, Lunter G, Zheng H, Ayub Q, DePristo MA, Banks E, Hu M, Handsaker RE, Rosenfeld JA, Fromer M, Jin M, Mu XJ, Khurana E, Ye K, Kay M, Saunders GI, Suner M-M, Hunt T, Barnes IH A, Amid C, Carvalho-Silva DR, Bignell AH, Snow C, Yngvadottir B, Bumpstead S, Cooper DN, Xue Y, Romero IG, 1000 Genomes Project Consortium, Wang J, Li Y, Gibbs RA, McCarroll SA, Dermitzakis ET, Pritchard JK, Barrett JC, Harrow J, Hurles ME, Gerstein MB, Tyler-Smith C: A systematic survey of loss-of-function variants in human protein-coding genes., *Science*.335 (6070): 823-828, 02/2012. United States, PM22344438

29. Chiang C, Jacobsen JC, Ernst C, Hanscom C, Heilbut A, Blumenthal I, **Mills RE**, Kirby A, Lindgren AM, Rudiger SR, McLaughlan CJ, Bawden CS, Reid SJ, Faull RL M, Snell RG, Hall IM, Shen Y, Ohsumi TK, Borowsky ML, Daly MJ, Lee C, Morton CC, MacDonald ME, Gusella JF, Talkowski ME: Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration., *Nat Genet*.44(4): 390-S1, 03/2012. United States, PM22388000

30. Clarke L, Zheng-Bradley X, Smith R, Kulesha E, Xiao C, Toneva I, Vaughan B, Preuss D, Leinonen R, Shumway M, Sherry S, Flicek P, 1000 Genomes Project Consortium: The 1000 Genomes Project: data management and community access., *Nat Methods*.9(5): 459-462, 04/2012. United States, PM22543379

31. Iskow RC, Gokcumen O, Abyzov A, Malukiewicz J, Zhu Q, Sukumar AT, Pai AA, **Mills RE**, Habegger L, Cusanovich DA, Rubel MA, Perry GH, Gerstein M, Stone AC, Gilad Y, Lee C: Regulatory element copy number differences shape primate expression profiles., *Proc Natl Acad Sci U S A*.109(31): 12656-12661, 07/2012. United States, PM22797897

32. 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA: An integrated map of genetic variation from 1,092 human genomes., *Nature*.491(7422): 56-65, 11/2012. England, PM23128226

33. Montgomery SB, Goode DL, Kvikstad E, Albers CA, Zhang ZD, Mu XJ, Ananda G, Howie B, Karczewski KJ, Smith KS, Anaya V, Richardson R, Davis J, 1000 GP C, MacArthur DG, Sidow A, Duret L, Gerstein M, Makova KD, Marchini J, McVean G, Lunter G: The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes., *Genome research*.23(5)01/2013. PM23478400

34. Rogers AJ, Chu J-H, Darvishi K, Ionita-Laza I, Lehmann H, **Mills R**, Lee C, Raby BA: Copy number variation prevalence in known asthma genes and their impact on asthma susceptibility., *Clin Exp Allergy*.43 (4): 455-462, 04/2013. England, PM23517041

35. Chu J-H, Rogers A, Ionita-Laza I, Darvishi K, **Mills RE**, Lee C, Raby BA: Copy number variation genotyping using family information., *BMC Bioinformatics*.14: 157, 05/2013. England, PM23656838

36. Todd PK, Oh SY, Krans A, He F, Sellier C, Frazer M, Renoux AJ, Chen K-C, Scaglione KM, Basrur V, Elenitoba-Johnson K, Vonsattel JP, Louis ED, Sutton MA, Taylor JP, **Mills RE**, Charlet-Berguerand N, Paulson HL: CGG Repeat-Associated Translation Mediates Neurodegeneration in Fragile X Tremor Ataxia Syndrome, *Neuron*.79(2): 402-402, 07/2013

37. Gokcumen O, Tischler V, Tica J, Zhu Q, Iskow RC, Lee E, Fritz MH-Y, Langdon A, Stütz AM, Pavlidis P, Benes V, **Mills RE**, Park PJ, Lee C, Korbel JO: Primate genome architecture influences structural variation mechanisms and functional consequences., *Proc Natl Acad Sci U S A*.110(39): 15764-15769, 09/2013. United States, PM24014587

38. Khurana E, Fu Y, Colonna V, Mu XJ, Kang HM, Lappalainen T, Sboner A, Lochovsky L, Chen J, Harmanci A, Das J, Abyzov A, Balasubramanian S, Beal K, Chakravarty D, Challis D, Chen Y, Clarke D, Clarke L, Cunningham F, Evani US, Flicek P, Fragoza R, Garrison E, Gibbs R, Gümüş ZH, Herrero J, Kitabayashi N, Kong Y, Lage K, Liluashvili V, Lipkin SM, MacArthur DG, Marth G, Muzny D, Pers TH, Ritchie GR S, Rosenfeld JA, Sisu C, Wei X, Wilson M, Xue Y, Yu F, 1000 Genomes Project Consortium, Dermitzakis ET, Yu H, Rubin MA, Tyler-Smith C, Gerstein M: Integrative annotation of variants from 1092 humans: application to cancer genomics., *Science*.342(6154): 1235587, 10/2013. United States, PM24092746

39. Abyzov A, Iskow R, Gokcumen O, Radke DW, Balasubramanian S, Pei B, Habegger L, 1000 Genomes Project Consortium, Lee C, Gerstein M: Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division., *Genome Res*.23(12): 2042-2052, 12/2013. United States, PM24026178

40. Park H, Kim D, Kim CH, Mills RE, Chang MY, Iskow RC, Ko S, Moon JI, Choi HW, Yoo PS M, Do JT, Han MJ, Lee EG, Jung JK, Zhang C, Lanza R, Kim KS: Increased genomic integrity of an improved protein-based mouse induced pluripotent stem cell method compared with current viral-induced strategies, *Stem Cells Translational Medicine*.3(5): 599-609, 01/2014. PM24763686

41. Silva AG, Krepischi AC V, Torrezan GT, Capelli LP, Carraro DM, D'Angelo CS, Koiffmann CP, Zatz M, Naslavsky MS, Masotti C, Otto PA, Achatz MI W, **Mills RE**, Lee C, Pearson PL, Rosenberg C: Does germ-line deletion of the PIP gene constitute a widespread risk for cancer?, *European Journal of Human Genetics*.22(3): 307-309, 03/2014. PM23778870

42. Delaneau O, Marchini J, 1000 Genomes Project Consortium, 1000 Genomes Project Consortium: Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel., *Nat Commun*.5: 3934, 06/2014. England, PM25653097

43. Colonna V, Ayub Q, Chen Y, Pagani L, Luisi P, Pybus M, Garrison E, Xue Y, Tyler-Smith C, 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA: Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences., *Genome Biol*.15(6): R88, 06/2014. England, PM24980144

44. Brand H, Pillalamarri V, Collins RL, Eggert S, O'Dushlaine C, Braaten EB, Stone MR, Chambert K, Doty ND, Hanscom C, Rosenfeld JA, Ditmars H, Blais J, **Mills R**, Lee C, Gusella JF, McCarroll S, Smoller JW, Talkowski ME, Doyle AE: Cryptic and complex chromosomal aberrations in early-onset neuropsychiatric disorders., *Am J Hum Genet*.95(4): 454-461, 10/2014. United States, PM25279985

45. Dayama G, Emery SB, Kidd JM, **Mills RE**: The genomic landscape of polymorphic human nuclear mitochondrial insertions., *Nucleic Acids Res*.42(20): 12640-12649, 11/2014. England, PM25348406

46. Jorge DM D M, **Mills RE**, Lauring AS: CodonShuffle: a tool for generating and analyzing synonymously mutated sequences., *Virus Evol*.1(1): vev012, 01/2015. England, PM27774284

47. Sudmant PH, Rausch T, Gardner EJ, Handsaker RE, Abyzov A, Huddleston J, Zhang Y, Ye K, Jun G, Fritz MH-Y, Konkel MK, Malhotra A, Stütz AM, Shi X, Casale FP, Chen J, Hormozdiari F, Dayama G, Chen K, Malig M, Chaisson MJ P, Walter K, Meiers S, Kashin S, Garrison E, Auton A, Lam HY K, Mu XJ, Alkan C, Antaki D, Bae T, Cerveira E, Chines P, Chong Z, Clarke L, Dal E, Ding L, Emery S, Fan X, Gujral M, Kahveci F, Kidd JM, Kong Y, Lameijer E-W, McCarthy S, Flicek P, Gibbs RA, Marth G, Mason CE, Menelaou A, Muzny DM, Nelson BJ, Noor A, Parrish NF, Pendleton M, Quitadamo A, Raeder B, Schadt EE, Romanovitch M, Schlattl A, Sebra R, Shabalin AA, Untergasser A, Walker JA, Wang M, Yu F, Zhang C, Zhang J, Zheng-Bradley X, Zhou W, Zichner T, Sebat J, Batzer MA, McCarroll SA, 1000 Genomes Project Consortium, **Mills RE**, Gerstein MB, Bashir A, Stegle O, Devine SE, Lee C, Eichler EE, Korbel JO: An integrated map of structural variation in 2,504 human genomes., *Nature*.526(7571): 75-81, 10/2015. England, PM26432246

48. Auton A**, Abecasis GR**, Altshuler DM, Durbin RM, Abecasis GR**, Bentley DR, Chakravarti A, Clark AG, Donnelly P, Eichler EE, Flicek P, Gabriel SB, Gibbs RA, Green ED, Hurles ME, Knoppers BM, Korbel JO, Lander ES, Lee C, Lehrach H, Mardis ER, Marth GT, McVean GA, Nickerson DA, Schmidt JP, Sherry ST, Wang J, Wilson RK, Chakravarti A, Knoppers BM, Abecasis GR**, Barnes KC, Beiswanger C, Burchard EG, Bustamante CD, Cai H, Cao H, Durbin RM, Gerry NP, Gharani N, Gibbs RA, Gignoux CR, Gravel S, Henn B, Jones D, Jorde L, Kaye JS, Keinan A, Kent A, Kerasidou A, Li Y, Mathias R, McVean GA, Moreno-Estrada A, Ossorio PN, Parker M, Resch AM, Rotimi CN, Royal CD, Sandoval K, Su Y, Sudbrak R, Tian Z, Tishkoff S, Toji LH, Tyler-Smith C, Via M, Wang Y, Yang H, Yang L, Zhu J, Brooks LD, Felsenfeld AL, McEwen JE, Vaydylevich Y, Green ED, Duncanson A, Dunn M, Schloss JA, Wang J, Yang H, Auton A**, Brooks LD, Durbin RM, Garrison EP, Min Kang H, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR**: A global reference for human genetic variation, *Nature*.526(7571): 68-74, 10/2015. PM26432245

49. Zhao X, Emery SB, Myers B, Kidd JM, **Mills RE**: Resolving complex structural genomic rearrangements using a randomized approach., *Genome Biol*.17(1): 126, 06/2016. England, PM27287201

50. Chun SY, Rodriguez CM, Todd PK, **Mills RE**: SPECtre: a spectral coherence--based classifier of actively translated transcripts from ribosome profiling sequence data., *BMC Bioinformatics*.17(1): 482, 11/2016. England, PM27884106

51. Fang Q, George AS, Brinkmeier ML, Mortensen AH, Gergics P, Cheung LY M, Daly AZ, Ajmal A, Pérez Millán MI, Ozel AB, Kitzman JO, **Mills RE**, Li JZ, Camper SA: Genetics of Combined Pituitary Hormone Deficiency: Roadmap into the Genome Era., *Endocr Rev*.37(6): 636-675, 12/2016. United States, PM27828722

52. McConnell MJ, Moran JV, Abyzov A, Akbarian S, Bae T, Cortes-Ciriano I, Erwin JA, Fasching L, Flasch DA, Freed D, Ganz J, Jaffe AE, Kwan KY, Kwon M, Lodato MA, **Mills RE**, Paquola AC M, Rodin RE, Rosenbluh C, Sestan N, Sherman MA, Shin JH, Song S, Straub RE, Thorpe J, Weinberger DR, Urban AE, Zhou B, Gage FH, Lehner T, Senthil G, Walsh CA, Chess A, Courchesne E, Gleeson JG, Kidd JM, Park PJ, Pevsner J, Vaccarino FM, Brain SM N: Intersection of diverse neuronal genomes and neuropsychiatric disease. The Brain Somatic Mosaicism Network., 01/2017. PM28450582

53. Zhao X, Weber AM, **Mills RE**: A recurrence-based approach for validating structural variation using long-read sequencing technology., *Gigascience*.6(8): 1-9, 08/2017. United States, PM28873962

54. Hovelson DH, Liu C, Wang Y, Kang Q, Henderson J, Gursky A, Ramnath N, Krauss JC, Talpaz M, Kandarpa M, Chugh R, Tuck M, Herman K, Grasso CS, Quist MJ, Feng FY, Haakenson C, Langmore J, Kamberov E, Tesmer T, Husain H, Lonigro RJ, Robinson D, Smith DC, Alva AS, Hussain MH, Chinnaiyan AM, Tewari M, **Mills RE**, Morgan Tomlins SA: Rapid, Ultra Low Coverage Copy Number Profiling of Cell-Free DNA as a Precision Oncology Screening Strategy, *Oncotarget*.09/2017. PM29163793

55. Gardner EJ, Lam VK, Harris DN, Chuang NT, Scott EC, Pittard WS, **Mills RE**, 1000 Genomes Project Consortium, Devine SE: The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology., *Genome Res*.27(11): 1916-1929, 11/2017. United States, PM28855259

56. Becker T, Lee W-P, Leone J, Zhu Q, Zhang C, Liu S, Sargent J, Shanker K, Mil-Homens A, Cerveira E, Ryan M, Cha J, Navarro FC P, Galeev T, Gerstein M, **Mills RE**, Shin D-G, Lee C, Malhotra A: FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods., *Genome Biol*.19(1): 38, 03/2018. England, PM29559002

57. D Sherman M, E Mills R: BAMnostic: an OS-agnostic toolkit for genomic sequence analysis, *The Journal of Open Source Software*.3(28): 826-826, 08/2018

58. Ferrer-Torres D, Nancarrow DJ, Steinberg H, Wang Z, Kuick R, Weh KM, Mills RE, Ray D, Ray P, Lin J, Chang AC, Reddy RM, Orringer MB, Canto MI, Shaheen NJ, Kresty LA, Chak A, Wang TD, Rubenstein JH, Beer DG: Constitutively Higher Level of GSTT2 in Esophageal Tissues From African Americans Protects Cells Against DNA Damage, *Gastroenterology*.156(5): 1404-1415, 04/2019. PM30578782

59. Chaisson MJ P, Sanders AD, Zhao X, Malhotra A, Porubsky D, Rausch T, Gardner EJ, Rodriguez OL, Guo L, Collins RL, Fan X, Wen J, Handsaker RE, Fairley S, Kronenberg ZN, Kong X, Hormozdiari F, Lee D, Wenger AM, Hastie AR, Antaki D, Anantharaman T, Audano PA, Brand H, Cantsilieris S, Cao H, Cerveira E, Chen C, Chen X, Chin C-S, Chong Z, Chuang NT, Lambert CC, Church DM, Clarke L, Farrell A, Flores J, Galeev T, Gorkin DU, Gujral M, Guryev V, Heaton WH, Korlach J, Kumar S, Kwon JY, Lam ET, Lee JE, Lee J, Lee W-P, Lee SP, Li S, Marks P, Viaud-Martinez K, Meiers S, Munson KM, Navarro FC P, Nelson BJ, Nodzak C, Noor A, Kyriazopoulou-Panagiotopoulou S, Pang AW C, Qiu Y, Rosanio G, Ryan M, Stütz A, Spierings DC J, Ward A, Welch AE, Xiao M, Xu W, Zhang C, Zhu Q, Zheng-Bradley X, Lowy E, Yakneen S, McCarroll S, Jun G, Ding L, Koh CL, Ren B, Flicek P, Chen K, Gerstein MB, Kwok P-Y, Lansdorp PM, Marth GT, Sebat J, Shi X, Bashir A, Ye K, Devine SE, Talkowski ME, **Mills RE**, Marschall T, Korbel JO, Eichler EE, Lee C: Multi-platform discovery of haplotype-resolved structural variation in human genomes., *Nat Commun*.10(1): 1784, 04/2019. England, PM30992455

60. Rodriguez CM, Chun SY, Mills RE**, Todd PK**: Translation of upstream open reading frames in a model of neuronal differentiation, *BMC Genomics*.20(1)05/2019. PM31109297

61. Sun C, Li H, **Mills RE**, Guan Y: Prognostic model for multiple myeloma progression integrating gene expression and clinical features., *Gigascience*.8(12)12/2019. United States, PM31886876

62. Shanta O, Noor A, Human Genome Structural Variation Consortium (HGSV, Sebat J: The effects of common structural variants on 3D chromatin structure., *BMC Genomics*.21(1): 95, 01/2020. England, PM32000688

63. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Kidd JM, Moran JV, **Mills RE**: Identification and characterization of occult human-specific LINE-1 insertions using long-read sequencing technology., *Nucleic Acids Res*.48(3): 1146-1163, 02/2020. England, PM31853540

64. Ho SS, Urban AE, **Mills RE**: Structural variation in the sequencing era., *Nat Rev Genet*.21(3): 171-189, 03/2020. England, PM31729472

65. Shi X, Radhakrishnan S, Wen J, Chen JY, Chen J, Lam BA, **Mills RE**, Stranger BE, Lee C, Setlur SR: Association of CNVs with methylation variation., *NPJ Genom Med*.5(1): 41, 09/2020. England, PM34556651

66. Zook JM, Hansen NF, Olson ND, Chapman L, Mullikin JC, Xiao C, Sherry S, Koren S, Phillippy AM, Boutros PC, Sahraeian SM E, Huang V, Rouette A, Alexander N, Mason CE, Hajirasouliha I, Ricketts C, Lee J, Tearle R, Fiddes IT, Barrio AM, Wala J, Carroll A, Ghaffari N, Rodriguez OL, Bashir A, Jackman S, Farrell JJ, Wenger AM, Alkan C, Soylev A, Schatz MC, Garg S, Church G, Marschall T, Chen K, Fan X, English AC, Rosenfeld JA, Zhou W, **Mills RE**, Sage JM, Davis JR, Kaiser MD, Oliver JS, Catalano AP, Chaisson MJ P, Spies N, Sedlazeck FJ, Salit M: A robust benchmark for detection of germline large deletions and insertions., *Nat Biotechnol*.38(11): 1347-1355, 11/2020. United States, PM32541955

67. Dayama G, Zhou W, Prado-Martinez J, Marques-Bonet T, **Mills RE**: Characterization of nuclear mitochondrial insertions in the whole genomes of primates., *NAR Genom Bioinform*.2(4): lqaa089, 12/2020. England, PM33575633

68. Oleksyk TK**, Wolfsberger WW, Weber AM, Shchubelka K, Oleksyk OT, Levchuk O, Patrus A, Lazar N, Castro-Marquez SO, Hasynets Y, Boldyzhar P, Neymet M, Urbanovych A, Stakhovska V, Malyar K, Chervyakova S, Podoroha O, Kovalchuk N, Rodriguez-Flores JL, Zhou W, Medley S, Battistuzzi F, Liu R, Hou Y, Chen S, Yang H, Yeager M, Dean M, Mills RE**, Smolanka V: Genome diversity in Ukraine, *GigaScience*.10(1)01/2021. PM33438729

69. Rodin RE, Dou Y, Kwon M, Sherman MA, D'Gama AM, Doan RN, Rento LM, Girskis KM, Bohrson CL, Kim SN, Nadig A, Luquette LJ, Gulhan DC, Brain SM N, Park PJ, Walsh CA: The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing., 01/2021. PM33432195

70. Pinatti LM, Wenjin GM S, Wang Y, Hossiny AE, Bhangale AD, Brummel CV, Carey TE, **Mills RE****, Brenner C**: SearcHPV: a novel approach to identify and assemble human papillomavirus-host genomic integration events in cancer, *Cancer*.01/2021. PM34160069

71. Zhu X, Zhou B, Pattni R, Gleason K, Tan C, Kalinowski A, Sloan S, Fiston-Lavier A-S, Mariani J, Petrov D, Barres BA, Duncan L, Abyzov A, Vogel H, Brain Somatic Mosaicism Network, Moran JV, Vaccarino FM, Tamminga CA, Levinson DF, Urban AE: Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia., *Nat Neurosci*.24(2): 186-196, 02/2021. United States, PM33432196

72. Wang Y, Bae T, Thorpe J, Sherman MA, Jones AG, Cho S, Daily K, Dou Y, Ganz J, Galor A, Lobon I, Pattni R, Rosenbluh C, Tomasi S, Tomasini L, Yang X, Zhou B, Akbarian S, Ball LL, Bizzotto S, Emery SB, Doan R, Fasching L, Jang Y, Juan D, Lizano E, Luquette LJ, Moldovan JB, Narurkar R, Oetjens MT, Rodin RE, Sekar S, Shin JH, Soriano E, Straub RE, Zhou W, Chess A, Gleeson JG, Marquès-Bonet T, Park PJ, Peters MA, Pevsner J, Walsh CA, Weinberger DR, Vaccarino FM, Moran JV, Urban AE, Kidd JM, **Mills RE**, Abyzov A: Comprehensive identification of somatic nucleotide variants in human brain tissue, 03/2021

73. Ebert P, Audano PA, Zhu Q, Rodriguez-Martin B, Porubsky D, Bonder MJ, Sulovari A, Ebler J, Zhou W, Serra Mari R, Yilmaz F, Zhao X, Hsieh P, Lee J, Kumar S, Lin J, Rausch T, Chen Y, Ren J, Santamarina M, Höps W, Ashraf H, Chuang NT, Yang X, Munson KM, Lewis AP, Fairley S, Tallon LJ, Clarke WE, Basile AO, Byrska-Bishop M, Corvelo A, Evani US, Lu T-Y, Chaisson MJ P, Chen J, Li C, Brand H, Wenger AM, Ghareghani M, Harvey WT, Raeder B, Hasenfeld P, Regier AA, Abel HJ, Hall IM, Flicek P, Stegle O, Gerstein MB, Tubio JM C, Mu Z, Li YI, Shi X, Hastie AR, Ye K, Chong Z, Sanders AD, Zody MC, Talkowski ME, **Mills RE**, Devine SE, Lee C, Korbel JO, Marschall T, Eichler EE: Haplotype-resolved diverse human genomes and integrated analysis of structural variation., *Science*.372(6537)04/2021. United States, PM33632895

74. Zhao X, Collins RL, Lee W-P, Weber AM, Jun Y, Zhu Q, Weisburd B, Huang Y, Audano PA, Wang H, Walker M, Lowther C, Fu J, Human Genome Structural Variation Consortium, Gerstein MB, Devine SE, Marschall T, Korbel JO, Eichler EE, Chaisson MJ P, Lee C, **Mills RE**, Brand H, Talkowski ME: Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies., *Am J Hum Genet*.108(5): 919-928, 05/2021. United States, PM33789087

75. Bao Y, Wadden J, Erb-Downward JR, Ranjan P, Zhou W, McDonald TL, **Mills RE**, Boyle AP, Dickson RP, Blaauw D, Welch JD: SquiggleNet: real-time, direct classification of nanopore signals., *Genome Biol*.22 (1): 298, 10/2021. England, PM34706748

76. McDonald TL, Zhou W, Castro CP, Mumm C, Switzenberg JA, **Mills RE****, Boyle AP**: Cas9 targeted enrichment of mobile elements using nanopore sequencing, *Nature Communications*.12(1)12/2021. PM34117247

77. Breuss MW, Yang X, Schlachetzki JC M, Antaki D, Lana AJ, Xu X, Chung C, Chai G, Stanley V, Song Q, Newmeyer TF, Nguyen A, O'Brien S, Hoeksema MA, Cao B, Nott A, McEvoy-Venneri J, Pasillas MP, Barton ST, Copeland BR, Nahas S, Van DK L, Ding Y, NIMH BS M N, Glass CK, Gleeson JG: Somatic mosaicism reveals clonal distributions of neocortical development., 01/2022. PM35444276

78. Cao Y, Haring CT, Brummel C, Bhambhani C, Aryal M, Lee C, Heft Neal M, Bhangale A, Gu W, Casper K, Malloy K, Sun Y, Shuman A, Prince ME, Spector ME, Chinn S, Shah J, Schonewolf C, McHugh JB, **Mills RE**, Tewari M, Worden FP, Swiecicki PL, Mierzwa M, Brenner JC: Early HPV ctDNA Kinetics and Imaging Biomarkers Predict Therapeutic Response in p16+ Oropharyngeal Squamous Cell Carcinoma., *Clin Cancer Res*.28(2): 350-359, 01/2022. United States, PM34702772

79. Lin J, Yang X, Kosters W, Xu T, Jia Y, Wang S, Zhu Q, Ryan M, Guo L, Zhang C, Human Genome Structural Variation Consortium, Lee C, Devine SE, Eichler EE, Ye K: Mako: A Graph-based Pattern Growth Approach to Detect Complex Structural Variants., *Genomics Proteomics Bioinformatics*.20(1): 205-218, 02/2022. China, PM34224879

80. Byrska-Bishop M, Evani US, Zhao X, Basile AO, Abel HJ, Regier AA, Corvelo A, Clarke WE, Musunuri R, Nagulapalli K, Fairley S, Runnels A, Winterkorn L, Lowy E, Human Genome Structural Variation Consortium, Paul Flicek, Germer S, Brand H, Hall IM, Talkowski ME, Narzisi G, Zody MC: High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios., *Cell*.185(18): 3426-3440.e19, 09/2022. United States, PM36055201

81. Gu W, Bhangale A, Heft Neal ME, Smith JD, Brummel C, McHugh JB, Spector ME, **Mills RE**, Brenner JC: Analysis of Human Papilloma Virus Content and Integration in Mucoepidermoid Carcinoma., *Viruses*.14 (11)10/2022. Switzerland, PM36366450

Non-Peer Reviewed

Published Erratum

1. Zook JM, Hansen NF, Olson ND, Chapman L, Mullikin JC, Xiao C, Sherry S, Koren S, Phillippy AM, Boutros PC, Sahraeian SM E, Huang V, Rouette A, Alexander N, Mason CE, Hajirasouliha I, Ricketts C, Lee J, Tearle R, Fiddes IT, Barrio AM, Wala J, Carroll A, Ghaffari N, Rodriguez OL, Bashir A, Jackman S, Farrell JJ, Wenger AM, Alkan C, Soylev A, Schatz MC, Garg S, Church G, Marschall T, Chen K, Fan X, English AC, Rosenfeld JA, Zhou W, **Mills RE**, Sage JM, Davis JR, Kaiser MD, Oliver JS, Catalano AP, Chaisson MJ P, Spies N, Sedlazeck FJ, Salit M: Author Correction: A robust benchmark for detection of germline large deletions and insertions., *Nat Biotechnol*.38(11): 1357, 11/2020. United States, PM32699374

2. Rodin RE, Dou Y, Kwon M, Sherman MA, D'Gama AM, Doan RN, Rento LM, Girskis KM, Bohrson CL, Kim SN, Nadig A, Luquette LJ, Gulhan DC, Brain Somatic Mosaicism Network, Park PJ, Walsh CA: Author Correction: The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing., *Nat Neurosci*.24(4): 611, 04/2021. United States, PM33753946