**  
Christopher A. Miller, Ph.D.**

Curriculum Vitae

Updated: Aug 10, 2021

­

**Citizenship:** United States of America

**Address and** Campus Box 8501

**Telephone**  660 South Euclid Ave,

**Numbers:** St. Louis, Missouri 63110

314-286-0263

Home:

11657 Chandellay Dr

St. Louis, Missouri 63146

314-620-4262

**Present Position:**

Assistant Professor

Division of Oncology

Washington University School of Medicine

**Education:**

May 2005 B.S. Biology and Computer Science

Truman State University, Kirksville, MO

May 2011 Ph.D. Structural and Computational Biology and Molecular Biophysics Program

Baylor College of Medicine, Houston, TX

Thesis topic: Computational Cancer Genomics

**Academic Positions:**  
2011-2013 Staff Scientist - Medical Genomics

The Genome Institute

Washington University in St Louis

2013-2017 Cancer Analysis Group Leader

The Genome Institute

Washington University in St Louis

2015-2016 Instructor in Medicine

Division of Genomics and Bioinformatics

Washington University School of Medicine

2016-Present Assistant Professor in Medicine

Division of Oncology

Washington University School of Medicine

**Editorial/Review Responsibilities:**

Reviewer for *Bioinformatics*, *Cancer Cell*, *Genome Biology*, *PLoS Computational Biology*, *Nucleic Acids Research, Nature Communications, Genome Research, Blood Cancer Discovery, Scientific Data, BMC Evolutionary Biology*  
Grant reviewer for Dutch Cancer Society (KWF Kankerbestrijding)

Grant reviewer for Siteman Cancer Center Investment Fund

**Professional Societies:** American Association for Cancer Research  
 International Society for Computational Biology

**Oral Presentations (conference - title):**

2012 TCGA Symposium - Assessing Tumor Heterogeneity and Tracking Clonal Evolution Using Whole Genome or Exome Sequencing

2013 TCGA Steering Committee Meeting - Automatic inference of theraputically relevant subclones in heterogeneous tumors

2013 Precision Medicine: Personal Genomes and Pharmacogenomics – SciClone: Inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution and therapy resistance

2014 TCGA Symposium - Ultra-deep whole-genome sequencing reveals clinically relevant low-frequency subclones in an acute myeloid leukemia

2015 Genome Informatics - Assessing tumor heterogeneity and tracking clonal clearance in response to therapy

2016 Festival of Genomics - Genomic insights into tumor evolution and therapy response

2016 Genome Informatics - Characterizing genomic responses to cancer

immunotherapy

2019 Genomics in Medicine - Tumor Heterogeneity and Evolution

2020 Genomics Education Partnership (GEP) Alumni Workshop - Sequencing, Variant Calling, and Cancer Genomics

**Research Support**

1 R50 CA211782 (PI)

NIH-NCI 09/01/2017-08/31/2022

Title: Comprehensive informatic analyses of AML genomes and epigenomes

1 PO1 CA101937 (Core C Director - Sequencing and Bioinformatic Analysis)

NIH-NCI 09/19/03-03/31/2023

Title: Genomics of Acute Myeloid Leukemia (PPG)

**Teaching Title and Responsibilities:**

2005 Teaching Assistant - Advanced Topics: Quantitative Biology (BCM)

2007-2008 Teaching Assistant - Computer Aided Discovery Methods (BCM)

2008 Teaching Assistant - Computational Mathematics for Biomedical Scientists (BCM)

2015-2017 Lecturer - Investigating Eukaryotic Genomes (WUSTL)

2015-2019 Lecturer - Molecular Basis of Heredity (WUSTL)  
2017-2021 Lecturer - Computational Statistical Genetics (WUSTL)

2018 Lecturer - Research Explorations in Genomics (WUSTL)  
2019-2021 Lecturer - Human Genetics (WUSTL)

2019 Lecturer - High-Throughput Biology: From Sequence to Networks (CSHL/CBW Course)

2017- Co-organizer - WUSTL Bioinformatics Workshop - full academic year course

- developed curriculum, lectures on sequencing, informatics, somatic variant calling,

bisulfite sequencing and analysis, etc

**Trainees (date and current position):**

Mentor to undergraduate research students

Yang Li 2013 Working in industry

Callie Federer 2014 PhD, now scientist at RadiaSoft

Jonas Neichen 2017 Medical Student at Rush Medical College  
Megan Neveau 2017 Graduate Student at Iowa State University  
Zhaohe Zhao 2020 Student at WUSTL

Andrew Li 2021 Student at Missouri S&T

Training and Supervision of WUSTL computational staff, including

Dr. Gue Su Chang 2013- Cancer Analysis Group, TGI

Dr. Tiandao Li 2013- Cancer Analysis Group, TGI

Dr. Allegra Petti 2013-16 Cancer Analysis Group, TGI

Dr. Yevgeniy Gindin 2014-15 Cancer Analysis Group, TGI

Dr. Charles Lu 2013-15 Cancer Analysis Group, TGI

Sai Mukund Ramakrishnan 2019- AML PPG Core C Staff

Additional formal and informal bioinformatics training of dozens of internal and

external collaborators.)

**Bibliography:**

(\* indicates co-first authorship)

1. Cancer Genome Atlas Network. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature. 2008. doi:10.1038/nature07385

2. Hampton OA, Den Hollander P, **Miller CA**, Delgado DA, Li J, Coarfa C, Harris RA, Richards S, Scherer SE, Muzny DM, Gibbs RA, Lee AV, Milosavljevic A. A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. Genome Research. 2009. doi:10.1101/gr.080259.108

3. Coarfa C, Yu F, **Miller CA**, Chen Z, Harris RA, Milosavljevic A. Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics. 2010. doi:10.1186/1471-2105-11-572

4. **Miller CA**, Hampton O, Coarfa C, Milosavljevic A. ReadDepth: a parallel R package for detecting copy number alterations from short sequencing reads. PLoS One. 2011. doi:10.1371/journal.pone.0016327

5. **Miller CA**, Settle SH, Sulman EP, Aldape KD, Milosavljevic A. Discovering functional modules by identifying recurrent and mutually exclusive mutational patterns in tumors. BMC Medical Genomics. 2011. doi:10.1186/1755-8794-4-34

6. Hampton OA, Koriabine M, **Miller CA**, Coarfa C, Li J, Den Hollander P, Schoenherr C, Carbone L, Nefedov M, Ten Hallers BF, Lee AV, De Jong PJ, Milosavljevic A. Long-range massively parallel mate pair sequencing detects distinct mutations and similar patterns of structural mutability in two breast cancer cell lines. Cancer Genetics. 2011. doi:10.1016/j.cancergen.2011.07.009

7. Parnell LD, Lindenbaum P, Shameer K, Dall'Olio GM, Swan DC, Jensen LJ, Cockell SJ, Pedersen BS, Mangan ME, **Miller CA**, Albert I. BioStar: an online question & answer resource for the bioinformatics community. PLoS Computational Biology. 2011. doi:10.1371/journal.pcbi.1002216

8. Ding L, Ley TJ, Larson DE, **Miller CA,** Koboldt DC, Welch JS, Ritchey JK, Young MA, Lamprecht T, McLellan MD, McMichael JF, Wallis JW, Lu C, Shen D, Harris CC, Dooling DJ, Fulton RS, Fulton LL, Chen K, Schmidt H, Kalicki-Veizer J, Magrini VJ, Cook L, McGrath SD, Vickery TL, Wendl MC, Heath S, Watson MA, Link DC, Tomasson MH, Shannon WD, Payton JE, Kulkarni S, Westervelt P, Walter MJ, Graubert TA, Mardis ER, Wilson RK, DiPersio JF. Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature. 2012. doi:10.1038/nature10738

9. Ellis MJ, Ding L, Shen D, Luo J, Suman VJ, Wallis JW, Van Tine BA, Hoog J, Goiffon RJ, Goldstein TC, Ng S, Lin L, Crowder R, Snider J, Ballman K, Weber J, Chen K, Koboldt DC, Kandoth C, Schierding WS, McMichael JF, **Miller CA**, Lu C, Harris CC, McLellan MD, Wendl MC, DeSchryver K, Allred DC, Esserman L, Unzeitig G, Margenthaler J, Babiera GV, Marcom PK, Guenther JM, Leitch M, Hunt K, Olson J, Tao Y, Maher CA, Fulton LL, Fulton RS, Harrison M, Oberkfell B, Du F, Demeter R, Vickery TL, Elhammali A, Piwnica-Worms H, McDonald S, Watson M, Dooling DJ, Ota D, Chang LW, Bose R, Ley TJ, Piwnica-Worms D, Stuart JM, Wilson RK, Mardis ER. Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature. 2012. doi:10.1038/nature11143

10. Koboldt DC, Zhang Q, Larson DE, Shen D, McLellan MD, Lin L, **Miller CA**, Mardis ER, Ding L, Wilson RK. VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research. 2012. doi:10.1101/gr.129684.111

11. Young MA, Larson DE, Sun CW, George DR, Ding L, **Miller CA**, Lin L, Pawlik KM, Chen K, Fan X, Schmidt H, Kalicki-Veizer J, Cook LL, Swift GW, Demeter RT, Wendl MC, Sands MS, Mardis ER, Wilson RK, Townes TM, Ley TJ. Background mutations in parental cells account for most of the genetic heterogeneity of induced pluripotent stem cells. Cell Stem Cell. 2012. doi:10.1016/j.stem.2012.03.002

12. Welch JS\*, Ley TJ\*, Link DC\*, **Miller CA**, Larson DE, Koboldt DC, Wartman LD, Lamprecht TL, Liu F, Xia J, Kandoth C, Fulton RS, McLellan MD, Dooling DJ, Wallis JW, Chen K, Harris CC, Schmidt HK, Kalicki-Veizer JM, Lu C, Zhang Q, Lin L, O'Laughlin MD, McMichael JF, Delehaunty KD, Fulton LA, Magrini VJ, McGrath SD, Demeter RT, Vickery TL, Hundal J, Cook LL, Swift GW, Reed JP, Alldredge PA, Wylie TN, Walker JR, Watson MA, Heath SE, Shannon WD, Varghese N, Nagarajan R, Payton JE, Baty JD, Kulkarni S, Klco JM, Tomasson MH, Westervelt P, Walter MJ, Graubert TA, DiPersio JF, Ding L, Mardis ER, Wilson RK. The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell. 2012. doi:10.1016/j.cell.2012.06.023

13. The Cancer Genome Atlas Research Network. Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal Of Medicine. 2013. doi:10.1056/NEJMoa1301689

14. Walter MJ, Shen D, Shao J, Ding L, White BS, Kandoth C, **Miller CA**, Niu B, McLellan MD, Dees ND, Fulton R, Elliot K, Heath S, Grillot M, Westervelt P, Link DC, DiPersio JF, Mardis E, Ley TJ, Wilson RK, Graubert TA. Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. Leukemia. 2013. doi:10.1038/leu.2013.58

15. Gutmann DH, McLellan MD, Hussain I, Wallis JW, Fulton LL, Fulton RS, Magrini V, Demeter R, Wylie T, Kandoth C, Leonard JR, Guha A, **Miller CA**, Ding L, Mardis ER. Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research. 2013. doi:10.1101/gr.142604.112

16. Li S, Shen D, Shao J, Crowder R, Liu W, Prat A, He X, Liu S, Hoog J, Lu C, Ding L, Griffith OL, **Miller CA**, Larson D, Fulton RS, Harrison M, Mooney T, McMichael JF, Luo J, Tao Y, Goncalves R, Schlosberg C, Hiken JF, Saied L, Sanchez C, Giuntoli T, Bumb C, Cooper C, Kitchens RT, Lin A, Phommaly C, Davies SR, Zhang J, Kavuri MS, McEachern D, Dong YY, Ma C, Pluard T, Naughton M, Bose R, Suresh R, McDowell R, Michel L, Aft R, Gillanders W, DeSchryver K, Wilson RK, Wang S, Mills GB, Gonzalez-Angulo A, Edwards JR, Maher C, Perou CM, Mardis ER, Ellis MJ. Endocrine-Therapy-Resistant *ESR1* Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports. 2013. doi:10.1016/j.celrep.2013.08.022

17. Griffith M, Griffith OL, Coffman AC, Weible JV, McMichael JF, Spies NC, Koval J, Das I, Callaway MB, Eldred JM, **Miller CA**, Subramanian J, Govindan R, Kumar RD, Bose R, Ding L, Walker JR, Larson DE, Dooling DJ, Smith SM, Ley TJ, Mardis ER, Wilson RK. DGIdb: mining the druggable genome. Nature Methods. 2013. doi:10.1038/nmeth.2689

18. The Cancer Genome Atlast Network. The cancer genome atlas pan-cancer analysis project. Nature Genetics. 2013. doi:10.1038/ng.2764

19. Kandoth C, McLellan MD, Vandin F, Ye K, Niu B, Lu C, Xie M, Zhang Q, McMichael JF, Wyczalkowski MA, Leiserson MD, **Miller CA**, Welch JS, Walter MJ, Wendl MC, Ley TJ, Wilson RK, Raphael BJ, Ding L. Mutational landscape and significance across 12 major cancer types. Nature. 2013. doi:10.1038/nature12634

20. **Miller CA**, Wilson RK, Ley TJ. Response to 'Genomic Landscapes and Clonality of De Novo AML'. New England Journal Of Medicine. 2013. doi:10.1056/NEJMc1308782

21. Kanchi KL, Johnson KJ, Lu C, McLellan MD, Leiserson MD, Wendl MC, Zhang Q, Koboldt DC, Xie M, Kandoth C, McMichael JF, Wyczalkowski MA, Larson DE, Schmidt HK, **Miller CA**, Fulton RS, Spellman PT, Mardis ER, Druley TE, Graubert TA, Goodfellow PJ, Raphael BJ, Wilson RK, Ding L. Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications. 2014. doi:10.1038/ncomms4156

22. Russler-Germain DA, Spencer DH, Young MA, Lamprecht TL, **Miller CA**, Fulton R, Meyer MR, Erdmann-Gilmore P, Townsend RR, Wilson RK, Ley TJ. The R882H DNMT3A mutation associated with AML dominantly inhibits wild-type DNMT3A by blocking its ability to form active tetramers. Cancer Cell. 2014. doi:10.1016/j.ccr.2014.02.010

23. Klco JM, Spencer DH, **Miller CA**, Griffith M, Lamprecht TL, O'Laughlin M, Fronick C, Magrini V, Demeter RT, Fulton RS, Eades WC, Link DC, Graubert TA, Walter MJ, Mardis ER, Dipersio JF, Wilson RK, Ley TJ. Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell. 2014. doi:10.1016/j.ccr.2014.01.031

24. Hughes AE, Magrini V, Demeter R, **Miller CA**, Fulton R, Fulton LL, Eades WC, Elliott K, Heath S, Westervelt P, Ding L, Conrad DF, White BS, Shao J, Link DC, DiPersio JF, Mardis ER, Wilson RK, Ley TJ, Walter MJ, Graubert TA. Clonal architecture of secondary acute myeloid leukemia defined by single-cell sequencing. PLoS Genetics. 2014. doi:10.1371/journal.pgen.1004462

25. **Miller CA\***, White BS\*, Dees ND, Griffith M, Welch JS, Griffith OL, Vij R, Tomasson MH, Graubert TA, Walter MJ, Ellis MJ, Schierding W, DiPersio JF, Ley TJ, Mardis ER, Wilson RK, Ding L. Sciclone: Inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution. PLoS Computational Biology. 2014. doi:10.1371/journal.pcbi.1003665

26. Engle E, Fisher D, **Miller CA**, McLellan M, Fulton R, Moore D, Wilson R, Ley T, Oh S. Clonal evolution revealed by whole genome sequencing in a case of primary myelofibrosis transformed to secondary acute myeloid leukemia. Leukemia. 2014. 10.1038/leu.2014.289

27. Spencer DH, Young MA, Lamprecht TL, Helton NM, Fulton R, O'Laughlin M, Fronick C, Magrini V, Demeter RT, **Miller CA**, Klco JM, Wilson RK, Ley TJ. Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. Leukemia. 2015; doi: 10.1038/leu.2015.6.

28. Lu EP, McLellan M, Ding L, Fulton R, Mardis ER, Wilson RK, **Miller CA**, Westervelt P, DiPersio JF, Link DC, Walter MJ, Ley TJ, Graubert TA. Caspase 9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. Blood. 2014. doi:10.1182/blood-2014-06-582551

29. Xie M, Lu C, Wang J, McLellan MD, Johnson KJ, Wendl MC, McMichael JF, Schmidt HK, Yellapantula V, **Miller CA**, Ozenberger BA, Welch JS, Link DC, Walter MJ, Mardis ER, Dipersio JF, Chen F, Wilson RK, Ley TJ, Ding L. Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine. 2014. doi:10.1038/nm.3733

30. Ding L, Kim M, Kanchi KL, Dees ND, Lu C, Griffith M, Fenstermacher D, Sung H, **Miller CA**, Goetz B, Wendl MC, Griffith O, Cornelius LA, Linette GP, McMichael JF, Sondak VK, Fields RC, Ley TJ, Mulé JJ, Wilson RK, Weber JS. Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS One. 2014. doi:10.1371/journal.pone.0111153

31. Celik H, Mallaney C, Kothari A, Ostrander E, Eultgen E, Martens A, **Miller CA**, Hundal J, Klco J, Challen G. Enforced differentiation of Dnmt3a-null bone marrow leads to failure with c-Kit mutations driving leukemic transformation. Blood. 2014. doi:10.1182/blood-2014-08-594564

32. Wong TN\*, Ramsingh G\*, Young AL\*, **Miller CA**, Touma W, Welch JS, Lamprecht TL, Shen D, Hundal J, Fulton RS, Heath S, Baty JD, Klco JM, Ding L, Mardis ER, Westervelt P, DiPersio JF, Walter MJ, Graubert TA, Ley TJ, Druley TE, Link DC, Wilson RK. Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature. 2014. doi:10.1038/nature13968

33. Li C, Klco JM, Helton NM, George DR, Mudd JL, **Miller CA**, Lu C, Fulton R, O'Laughlin M, Fronick C, Wilson RK, Ley TJ. Genetic heterogeneity of induced pluripotent stem cells: results from 24 clones derived from a single C57BL/6 mouse.

PloS one. 2015. doi: 10.1371/journal.pone.0120585

34. Hirbe AC, Dahiya S, **Miller CA**, Li T, Fulton RS, Zhang X, McDonald S, DeSchryver K, Duncavage EJ, Walrath J, Reilly KM, Abel HJ, Pekmezci M, Perry A, Ley TJ, Gutmann DH. Whole exome sequencing reveals the order of genetic changes during malignant transformation and metastasis in a single patient with NF1-plexiform neurofibroma. Clinical Cancer Research. 2015.  doi:10.1158/1078-0432.CCR-14-3049.

35. Griffith M, Griffith OL, Smith SM, Ramu A, Callaway MB, Brummett AM, Kiwala MJ, Coffman AC, Regier AA, Oberkfell BJ, Sanderson GE, Mooney TP, Nutter NG, Belter EA, Du F, Long RL, Abbott TE, Ferguson IT, Morton DL, Burnett MM, Weible JV, Peck JB, Dukes A, McMichael JF, Lolofie JT, Derickson BR, Hundal J, Skidmore ZL, Ainscough BJ, Dees ND, Schierding WS, Kandoth C, Kim KH, Lu C, Harris CC, Maher N, Maher CA, Magrini VJ, Abbott BS, Chen K, Clark E, Das I, Fan X, Hawkins AE, Hepler TG, Wylie TN, Leonard SM, Schroeder WE, Shi X, Carmichael LK, Weil MR, Wohlstadter RW, Stiehr G, McLellan MD, Pohl CS, **Miller CA**, Koboldt DC, Walker JR, Eldred JM, Larson DE, Dooling DJ, Ding L, Mardis ER, Wilson RK. Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS computational biology. 2015. doi: 10.1371/journal.pcbi.1004274.

36. Klco JM\*, **Miller CA\***, Griffith M, Petti A, Spencer DH, Ketkar-Kulkarni S, Wartman LD, Christopher M, Lamprecht TL, Helton NM, Duncavage EJ, Payton JE, Baty J, Heath SE, Griffith OL, Shen D, Hundal J, Chang GS, Fulton R, O'Laughlin M, Fronick C, Magrini V, Demeter RT, Larson DE, Kulkarni S, Ozenberger BA, Welch JS, Walter MJ, Graubert TA, Westervelt P, Radich JP, Link DC, Mardis ER, DiPersio JF, Wilson RK, Ley TJ. Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. Jama. 2015. doi:10.1001/jama.2015.9643

37. Griffith M\*, **Miller CA**\*, Griffith OL, Krysiak K, Skidmore ZL, Ramu A, Walker JR, Dang HX, Trani L, Larson DE, Demeter RT, Wendl MC, McMichael JF, Austin RE, Magrini V, McGrath SD, Ly A, Kulkarni S, Cordes MG, Fronick CC, Fulton RS, Maher CA, Ding L, Klco JM, Mardis ER, Ley TJ, Wilson RK. Optimizing Cancer Genome Sequencing and Analysis. Cell Systems. 2015. Doi:10.1016/j.cels.2015.08.015

38. Lu C, Xie M, Wendl MC, Wang J, McLellan MD, Leiserson MD, Huang KL, Wyczalkowski MA, Jayasinghe R, Banerjee T, Ning J, Tripathi P, Zhang Q, Niu B, Ye K, Schmidt HK, Fulton RS, McMichael JF, Batra P, Kandoth C, Bharadwaj M, Koboldt DC, **Miller CA**, Kanchi KL, Eldred JM, Larson DE, Welch JS, You M, Ozenberger BA, Govindan R, Walter MJ, Ellis MJ, Mardis ER, Graubert TA, Dipersio JF, Ley TJ, Wilson RK, Goodfellow PJ, Raphael BJ, Chen F, Johnson KJ, Parvin JD, Ding L. Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications. 2015. doi:10.1038/ncomms10086.

39. Churpek JE, Pyrtel K, Kanchi KL, Shao J, Koboldt D, **Miller CA**, Shen D, Fulton R, O'Laughlin M, Fronick C, Pusic I, Uy GL, Braunstein EM, Levis M, Ross J, Elliott K, Heath S, Jiang A, Westervelt P, DiPersio JF, Link DC, Walter MJ, Welch J, Wilson R, Ley TJ, Godley LA, Graubert TA. Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood. 2015.  doi:10.1182/blood-2015-04-641100

40. Wong TN, **Miller CA**, Klco JM, Petti A, Demeter R, Helton NM, Li T, Fulton RS, Heath SE, Mardis ER, Westervelt P, DiPersio JF, Walter MJ, Welch JS, Graubert TA, Wilson RK, Ley TJ, Link DC. Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood. 2016. doi:10.1182/blood-2015-10-677021

41. Krysiak K, Christopher MJ, Skidmore ZL, Demeter RT, Magrini V, Kunisaki J, O'Laughlin M, Duncavage EJ, **Miller CA**, Ozenberger BA, Griffith M, Wartman LD, Griffith OL. A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. Blood Cancer Journal. 2016. doi:10.1038/bcj.2016.18

42. Purkait S, **Miller CA**, Kumar A, Sharma V, Pathak P, Jha P, Sharma MC, Suri V, Suri A, Sharma BS, Fulton RS, Kale SS, Dahiya S, Sarkar C. ATRX in diffuse gliomas with its mosaic/heterogeneous expression in a subset. Brain Pathol. 2016. doi: 10.1111/bpa.12364

43. Lu C, Riedell P, **Miller CA**, Hagemann IS, Westervelt P, Ozenberger BA, O'Laughlin M, Magrini V, Demeter RT, Duncavage EJ, Griffith M, Griffith OL, Wartman LD. A common founding clone with TP53 and PTEN mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. Molecular Case Studies. 2016. doi:10.1101/mcs.a000687

44. Griffith M, Griffith OL, Krysiak K, Skidmore ZL, Christopher MJ, Klco JM, Ramu A, Lamprecht TL, Wagner AH, Campbell KM, Lesurf R, Hundal J, Zhang J, Spies NC, Ainscough BJ, Larson DE, Heath SE, Fronick C, O'Laughlin S, Fulton RS, Magrini V, McGrath S, Smith SM, **Miller CA**, Maher CA, Payton JE, Walker JR, Eldred JM, Walter MJ, Link DC, Graubert TA, Westervelt P, Kulkarni S, DiPersio JF, Mardis ER, Wilson RK, Ley TJ. Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology. 2016 doi:10.1016/j.exphem.2016.04.011

45. **Miller CA**, Gindin Y, Lu C, Griffith OL, Griffith M, Shen D, Hoog J, Li T, Larson DE, Watson M, Davies SR, Hunt K, Suman VJ, Snider J, Walsh T, Colditz GA, DeSchryver K, Wilson RK, Mardis ER, Ellis MJ. Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications. 2016. doi:10.1038/ncomms12498

46. Gellert P, Segal CV, Gao Q, Lopez-Knowles E, Martin L, Dodson A, Li T, **Miller CA**, Lu C, Mardis ER, Gillman A, Morden J, Graf M, Sidhu K, Sidhu K, Evans A, Shere M, Holcombe C, McIntosh SA, Bundred N, Skene A, Maxwell W, Robertson J, Bliss JM, Smith I, Dowsett M. Impact of mutational profiles on response of primary oestrogen receptor-positive breast cancers to oestrogen deprivation. Nature Communications. 2016. doi:c10.1038/ncomms13294

47. Duncavage E, O'Brien J, Vij K, **Miller CA**, Chang G, Shao J, Jacoby M, Heath S, Janke M, Elliott K, Fulton RS, Fronick C, O'Laughlin M, Westervelt P, Ley TJ, Wilson RK, Walter MJ. Targeted sequencing informs the evaluation of normal karyotype cytopenic patients for low-grade myelodysplastic syndrome. Leukemia. 2016. doi:10.1038/leu.2016.247

48. Hundal J, **Miller CA** Griffith M, Griffith OL, Walker J, Kiwala S, Graubert A, McMichael J, Coffman A, Mardis ER. Cancer immunogenomics: computational neoantigen identification and vaccine design. Cold Spring Harbor symposia on quantitative biology. 2016. 10.1101/sqb.2016.81.030726

49. Griffith OL, Chan SR, Griffith M, Krysiak K, Skidmore ZL, Hundal J, Allen JA, Arthur CD, Runci D, Bugatti M, Miceli AP, Schmidt H, Trani L, Kanchi KL, **Miller CA**, Larson DE, Fulton RS, Vermi W, Wilson RK, Schreiber RD, Mardis ER. Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports. 2016. doi:10.1016/j.celrep.2016.08.076

50. Hundal J, **Miller CA**, Griffith M, Griffith OL, Walker J, Kiwala S, Graubert A, McMichael J, Coffman A, Mardis ER. Cancer immunogenomics: computational neoantigen identification and vaccine design. 2016. doi:10.1101/sqb.2016.81.030726

51. Johanns TM\*, **Miller CA**\*, Dorward IG, Tsien C, Chang E, Perry A, Uppaluri R, Ferguson C, Schmidt RE, Dahiya S, Ansstas G, Mardis ER, Dunn GP. Immunogenomics of Hypermutated Glioblastoma: A Patient with Germline POLE Deficiency Treated with Checkpoint Blockade Immunotherapy. Cancer Discovery. 2016. doi:10.1158/2159-8290.CD-16-0575

52. **Miller CA**, McMichael J, Dang HX, Maher CA, Ding L, Ley TJ, Mardis ER, Wilson RK. Visualizing tumor evolution with the fishplot package for R. BMC Genomics. 2016. 10.1186/s12864-016-3195-z

53. Welch JS, Petti AA, **Miller CA**, Fronick CC, O’Laughlin M, Fulton RS, Wilson RK, Baty JD, Duncavage EJ, Tandon B. TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. New England Journal Of Medicine. 2016. doi:10.1056/NEJMoa1605949

54. Johanns TM, Ward JP, **Miller CA**, Wilson C, Kobayashi DK, Bender D, Fu Y, Alexandrov A, Mardis ER, Artyomov MN, Schreiber RD, and Dunn GP. Endogenous Neoantigen-Specific CD8 T Cells Identified in Two Glioblastoma Models Using a Cancer Immunogenomics Approach. Cancer Immunology Research. 2016. doi:10.1158/2326-6066

55. Hoadley KA, Siegel MB, Kanchi KL, **Miller CA**, Ding L, Zhao W, He X, Parker JS, Wendl MC, Fulton RS, Demeter RT, Wilson RK, Carey LA, Perou CM, Mardis ER. Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine. 2016. doi:10.1371/journal.pmed.1002174

56. Duncavage EJ, Uy GL, Petti AA, **Miller CA**, Lee Y, Tandon B, Gao F, Fronick CC, O'Laughlin M, Fulton RS, Wilson RK, Jacoby MJ, Cashen AF, Wartman LD, Walter MJ, Westervelt P, Link DC, DiPersio JF, Ley TJ, and Welch JS. Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. Blood. 2017. doi:10.1182/blood-2016-10-745273

57. Zhang J, Griffith M, **Miller CA**, Griffith OL, Spencer DH, Walker J, Magrini V, McGrath SD, Ly A, Helton NM, Trissal Maria, Link DC, Dang HX, Larson DE, Kulkarni S, Cordes MG, Fronick C, Fulton RS, Klco JM, Mardis ER, Ley TJ, Wilson RK, Maher CA. Comprehensive Discovery of non-coding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology. 2017. doi: 10.1016/j.exphem.2017.07.008

58. Krysiak K, Gomez F, White BS, Matlock M, **Miller CA**, Trani L, Fronick CC, Fulton RS, Kreisel F, Cashen AF, Carson KR, Berrien-Elliott MM, Bartlett NL, Griffith M, Griffith OL, Fehniger TA. Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. Blood. 2017 doi:10.1182/blood-2016-07-729954

59. Uy GL, Duncavage EJ, Chang GS, Jacoby MA, **Miller CA**, Shao J, Heath S, Elliott K, Reinick T, Fulton RS, Fronick CC, O'Laughlin M, Ganel L, Abboud CN, Cashen AF, DiPersio JF, Wilson RK, Link DC, Welch JS, Ley TJ, Graubert TA, Westervelt P, Walter MJ. Dynamic changes in the clonal structure of MDS and AML in response to epigenetic therapy Leukemia. doi:10.1038/leu.2016.282  
  
60. The Cancer Genome Atlas Network. Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas.Cell. 2017. doi:10.1016/j.cell.2017.10.014

61. Xia J, **Miller CA**, Baty J, Ramesh A, Jotte MR, Fulton RS, Vogel TP, Cooper MA, Walkovich KJ, Makaryan V, Bolyard AA, Dinauer MC, Wilson DB, Vlachos A, Myers KC, Rothbaum RJ, Bertuch AA, Dale DC, Shimamura A, Boxer LA, Link DC. Somatic mutations and clonal hematopoiesis in congenital neutropenia. Blood. 2017. doi:10.1182/blood-2017-08-801985

62. Dang H, White B, Foltz S, **Miller CA**, Luo J, Fields R, Maher C. ClonEvol: clonal ordering and visualization in cancer sequencing. Annals Of Oncology. 2017. doi:10.1093/annonc/mdx517

63. Cole CB, Russler-Germain DA, Ketkar S, Verdoni AM, Smith AM, Bangert CV, Helton NM, Guo M, Klco JM, O’Laughlin S, Fronick C, Fulton RS, Chang GS, Petti AA, **Miller CA**, Ley TJ. Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies The Journal Of Clinical Investigation. 2017. doi:10.1172/JCI93041

64. Zhang J, Griffith M, **Miller CA**, Griffith OL, Spencer DH, Walker JR, Magrini V, McGrath SD, Ly A, Helton NM, Trissal M, Link DC, Dang HX, Larson DE, Kulkarni S, Cordes M, Fronick CC, Fulton RS, Klco JM, Mardis EM, Ley TJ, Wilson RK, Maher CA. Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology. 2017. doi:10.1016/j.exphem.2017.07.008

65. Krysiak K, Gomez F, White BS, Matlock M, **Miller CA**, Trani L, Fronick CC, Fulton RS, Kreisel F, Cashen AF, Carson KR, Berrien-Elliott MM, Bartlett NL, Griffith M, Griffith OL, Fehniger TA. Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. Blood. 2017. doi:10.1182/blood-2016-07-729954

66. Zhang X, Kim S, Hundal J, Herndon JM, Li S, Petti AA, Soysal SD, Li L, McLellan MD, Hoog J, Primeau T, Myers N, Vickery TL, Sturmoski M, Hagemann IS, **Miller CA**, Ellis MJ, Mardis ER, Hansen T, Fleming TP, Goedegebuure P, Gillanders WE. Breast cancer neoantigens can induce CD8 T cell responses and antitumor immunity.. Cancer Immunology Research. 2017. doi:10.1158/2326-6066.CIR-16-0264

67. Mahlokozera T, Vellimana AK, Li T, Mao DD, Zohny ZS, Kim DH, Tran DD, Marcus DS, Fouke SJ, Campian JL, Dunn GP, **Miller CA**, Kim AH. Biological and therapeutic implications of multisector sequencing in newly diagnosed glioblastomas. Neuro-oncology. 2017. doi: 10.1093/neuonc/nox232

68. Grigsby P, Elhammali A, Ruiz F, Markovina S, McLellan MD, **Miller CA**, Chundury A, Ta NL, Rashmi R, Pfeifer JD, Fulton RS, DeWees T, Schwarz JK. Clinical outcomes and differential effects of PI3K pathway mutation in obese versus non-obese patients with cervical cancer. Oncotarget. 2018. doi:10.18632/oncotarget.23664

69. Wong TN, **Miller CA**, Jotte MR, Bagegni N, Baty JD, Schmidt AP, Cashen AF, Duncavage EJ, Helton NM, Fiala M, et al.. Cellular stressors contribute to the expansion of hematopoietic clones of varying leukemic potential. Nature Communications. doi:10.1038/s41467-018-02858-0

70. Bansal D, Vij K, Chang GS, **Miller CA**, DiPersio JF, Vij R, Heath SE, Westervelt P, Welch JS, Fehniger TA. Lenalidomide results in a durable complete remission in acute myeloid leukemia accompanied by persistence of somatic mutations and a T-cell infiltrate in the bone marrow. Haematologica. doi:10.3324/haematol.2017.184168

71. **Miller CA**, Dahiya S, Li T, Fulton RS, Smyth MD, Dunn GP, Rubin JB, Mardis ER. Resistance-promoting effects of ependymoma treatment revealed through genomic analysis of multiple recurrences in a single patient. Molecular Case Studies. doi:10.1101/mcs.a002444

72. Cooper ML, Choi J, Staser K, Ritchey JK, Devenport JM, Eckardt K, Rettig MP, Wang B, Eissenberg LG, Ghobadi A, Gehrs LN, Prior JL, Achilefu S, **Miller CA**, Fronick CC, O’Neal J, Gao F, Weinstock DM, Gutierrez A, Fulton RS, DiPersio JF. An “off-the-shelf” fratricide-resistant CAR-T for the treatment of T cell hematologic malignancies. Leukemia. doi:10.1038/s41375-018-0065-5

73. Jacoby MA, Duncavage EJ, Chang GS, **Miller CA**, Shao J, Elliott K, Robinson J, Fulton RS, Fronick CC, O’Laughlin M, Heath SE, Pusic I, Welch JS, Link DC, DiPersio JF, Westervelt P, Ley TJ, Graubert TA, Walter MJ. Subclones dominate at MDS progression following allogeneic hematopoietic cell transplant. Jci Insight. 2018. doi:10.1172/jci.insight.98962

74. Rohan TE**\***, **Miller CA\***, Li T, Wang Y, Loudig O, Ginsberg M, Glass A, Mardis E. Somatic mutations in benign breast disease tissue and risk of subsequent invasive breast cancer. British Journal Of Cancer. doi:10.1038/s41416-018-0089-7

75. **Miller CA**, Tricarico C, Skidmore ZL, Uy GL, Lee Y, Hassan A, O’Laughlin MD, Schmidt H, Tian L, Duncavage EJ, Griffith M, Griffith OL, Welch JS, Wartman L. A case of acute myeloid leukemia with promyelocytic features characterized by expression of a novel RARG-CPSF6 fusion. Blood Advances. 2018. doi:10.1182/bloodadvances.2017014183

76. Alberti MO, Srivatsan SN, Shao J, McNulty SN, Chang GS, **Miller CA**, Dunlap JB, Yang F, Press RD, Gao Q, Ding L, Heusel JW, Duncavage EJ, Walter MJ. Discriminating a common somatic ASXL1 mutation (c. 1934dup; p. G646Wfs\* 12) from artifact in myeloid malignancies using NGS. Leukemia. 2018. doi:10.1038/s41375-018-0193-y

77. Griffith OL, Spies NC, Anurag M, Griffith M, Luo J, Tu D, Yeo B, Kunisaki J, **Miller CA**, Krysiak K, Hundal J, Ainscough J, Skidmore ZL, Campbell K, Kumar R, Fronick C, Cook L, Snider JE, Davies S, Kavuri SM, Chang EC, Magrini V, Larson DE, Fulton RS, Liu S, Leung S, Voduc D, Bose R, Dowsett M, Wilson RK, Nielsen TO, Mardis ER, Ellis MJ. The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications. 2018. doi:10.1038/s41467-018-05914-x

78. Duncavage EJ, Jacoby MA, Chang GS, **Miller CA**, Edwin N, Shao J, Elliott K, Robinson J, Abel H, Fulton RS, Fronick CC, O’Laughlin M, Heath SE, Brendel K, Saba R, Wartman LD, Christopher MJ, Pusic I, Welch JS, Uy GL, Link DC, DiPersio JF, Westervelt P, Ley TJ, Trinkaus K, Graubert TA, Walter MJ. Mutation clearance after transplantation for myelodysplastic syndrome. New England Journal Of Medicine. 2018. doi:10.1056/NEJMoa1804714

79. Christopher MJ, Petti AA, Rettig MP, **Miller CA**, Chendamarai E, Duncavage EJ, Klco JM, Helton NM, O’Laughlin M, Fronick CC, Fulton RS, Wilson RK, Wartman LD, Welch JS, Heath SE, Baty JD, Payton JE, Graubert TA, Link DC, Walter MJ, Westervelt P, Ley TJ, DiPersio JF. Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. New England Journal Of Medicine. 2018. doi:10.1056/NEJMoa1808777

80. Johanns TM, **Miller CA**, Liu CJ, Perrin RJ, DBender, Kobayashi DK, Campian JL, Chicoine MR, Dacey RG, JHuang, Fritsch EF, Gillanders WE, Artyomov MN, Mardis ER, Schreiber RD, Dunn GP. Detection of neoantigen-specific T cells following a personalized vaccine in a patient with glioblastoma. Oncoimmunology. 2019. doi: 10.1080/2162402X.2018.1561106

81. Ghobadi A\*, **Miller CA\***, Li T, O'Laughlin M, Lee YS, Ali M, Westervelt P, DiPersio JF, Wartman L. Shared cell of origin in a patient with Erdheim-Chester disease and acute myeloid leukemia. Haematologica. 2019. doi: 10.3324/haematol.2019.217794

82. Wang T, Glover B, Hadwiger G, **Miller CA**, DiMartino O, Welch JS. Smc3 is required for mouse embryonic and adult hematopoiesis. Experimental Hematology. 2019. doi:10.1016/j.exphem.2018.11.008

83. Wang T, Jacoby MA, Duncavage EJ, **Miller CA**, Heath S, Rahme R, Fenaux P, Ades L, Renneville A, Cassinat B, Takeshita A, Asou N, Miyazaki Y, Kiyoi H, Ravandi F, Westervelt P, Wartman LD, Welch JS. Exome analysis of treatment-related AML after APL suggests secondary evolution. British Journal of Haematology. 2019. doi:10.1111/bjh.15681

84. Petti AA, Williams SR, **Miller CA**, Fiddes IT, Srivatsan SN, Chen DY, Fronick CC, Fulton RS, Church DM, Ley TJ. A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. Nature Communications. 2019. doi: 10.1038/s41467-019-11591-1

85. Hundal J, Kiwala S, McMichael J, **Miller CA**, Wollam AT, Xia H, Liu CJ, Zhao S, Feng Y, Graubert AP, Wollam AZ, Neichin J, Neveau M, Walker J, Gillanders WE, 82. Mardis ER, Griffith OL, Griffith M. pVACtools: a computational toolkit to identify and visualize cancer neoantigens. Cancer Immunology Research. 2020. doi: 10.1158/2326-6066.CIR-19-0401

86. Ketkar S, Verdoni AM, Smith AM, Bangert CV, Leight ER, Chen DY, Brune MK, Helton NM, Hoock M, George DR, Fronick C, Fulton RS, Ramakrishnan SM, Chang GS, Petti AA, Spencer DH, **Miller CA**, Ley TJ. Remethylation of Dnmt3a-/- hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. Proceedings Of The National Academy Of Sciences. 2020. doi: 10.1073/pnas.1918611117

87. Liu CJ, Schaettler M, Blaha DT, Bowman-Kirigin JA, Kobayashi DK, Livingstone AJ, Bender D, **Miller CA**, Kranz DM, Johanns TM, Dunn GP. Treatment of an aggressive orthotopic murine glioblastoma model with combination checkpoint blockade and a multivalent neoantigen vaccine. Neuro-oncology. 2020. doi: 10.1093/neuonc/noaa050

88. Moon C, Tompkins W, Wang Y, Godec A, Zhang X, Pipkorn P, **Miller CA**, Dehner C, Dahiya S, Hirbe AC. Unmasking Intra-tumoral Heterogeneity and Clonal Evolution in NF1-MPNST. Genes. 2020. doi: 10.3390/genes11050499

89. Dang HX, Krasnick BA, White BS, Grossman JG, Strand MS, Zhang JZ, Cabanski CR, **Miller CA**, Fulton RS, Goedegebuure SP, Fronick CC, Griffith MZ, Larson DE, Goetz BD, Walker JR, Hawkins WG, Strasberg SM, Linehan DC, Lim KH, Lockhart AC, Mardis ER, Wilson RK, Ley TJ, Maher CA, Fields RC. The clonal evolution of metastatic colorectal cancer. Science Advances. 2020. doi: 10.1126/sciadv.aay9691

90. Oza A, Rettig MP, Powell P, O’Brien K, Clifford DB, Ritchey J, Gehrs L, Hollaway J, Major E, Fehniger TA, **Miller CA**, Soon-Shiong P, Rock A, DiPersio JF. Interleukin-15 superagonist (N-803) treatment of PML and JCV in a post--allogeneic hematopoietic stem cell transplant patient. Blood Advances. 2020. doi:10.1182/bloodadvances.2019000664

91. Li L, Zhang X, Wang X, Kim SW, Herndon JM, Becker-Hapak MK, Carreno BM, Myers NB, Sturmoski MA, McLellan MD, **Miller CA**, Johanns TM, Tan BR, Dunn GP, Fleming TP, Hansen TH, Goedegebuure SP, Gillanders WE. Optimized polyepitope neoantigen DNA vaccines elicit neoantigen-specific immune responses in preclinical models and in clinical translation. Genome Medicine. 2021. doi:10.1186/s13073-021-00872-4

92. Wadugu BA, Heard A, Srivatsan SN, Alberti MO, Ndonwi M, Grieb S, Bradley J, Shao J, Ahmed T, Shirai CL, Khanna A, Fei DL, **Miller CA**, Graubert T, Walter MJ. U2AF1 is a haplo-essential gene required for cancer cell survival. Biorxiv. 2020. doi:10.1101/2020.06.20.151035

93. Chen DY, Ferguson IM, Braun KA, Sutton LA, Helton NM, Ramakrishnan SM, Smith AM, **Miller CA**, Ley TJ. Dnmt3a deficiency in the skin causes focal, canonical DNA hypomethylation and a cellular proliferation phenotype. Proceedings Of The National Academy Of Sciences. 2021. doi:10.1073/pnas.2022760118

94. Inkman MJ, Jayachandran K, Ellis TM, Ruiz F, McLellan MD, **Miller CA**, Wu Y, Ojesina AI, Schwarz JK, Zhang J. HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports. 2020. doi:10.1038/s41598-020-71300-7

95. Wells DK, van BMM, Dang KK, Hubbard-Lucey VM, Sheehan KC, Campbell KM, Lamb A, Ward JP, Sidney J, Blazquez AB, *et al*. Key parameters of tumor epitope immunogenicity revealed through a consortium approach improve neoantigen prediction. Cell. 2020. doi:10.1016/j.cell.2020.09.015

96. Xia H, McMichael JF, Supabphol S, Richters MM, Basu A, Ramirez CA, Puig-Saus C, Cotto KC, Hundal J, Kiwala S, Goedegebuure SP, Johanns TM, Dunn GP, Fehniger TA, Ribas A, **Miller CA**, Gillanders WE, Griffith OL, Griffith M. Accurate neoantigen prediction depends on mutation position relative to patient allele-specific MHC anchor location. Biorxiv. 2020. doi:10.1101/2020.12.08.416271

97. Li Y, **Miller CA**, Shea LK, Jiang X, Guzman MA, Chandler RJ, Ramakrishnan SM, Smith SN, Venditti CP, Vogler CA, Ory DS, Ley TJ, Sands MS. Enhanced efficacy and increased long-term toxicity of CNS-directed, AAV-based combination therapy for Krabbe disease. Molecular Therapy. 2021. doi:10.1016/j.ymthe.2020.12.031

98. Duncavage EJ, Schroeder MC, O’Laughlin M, Wilson R, MacMillan S, Bohannon A, Kruchowski S, Garza J, Du F, Hughes AE, Kruchowski S, Garza J, Du F, Hughes AEO, Robinson J, Hughes E, Heath SE, Baty JD, Neidich J, Christopher MJ, Jacoby MA, Uy GL, Fulton RS, **Miller CA,** Payton JE, Link DC, Walter MJ, Westervelt P, DiPersio JF, Ley TJ, Spencer DH Genome sequencing as an alternative to cytogenetic analysis in myeloid cancers. New England Journal Of Medicine. 2021. doi:10.1056/NEJMoa2024534

99. Wilson ER, Helton N, Heath SE, Fulton RS, **Miller CA**, Payton JE, Welch JS, Walter M, Westervelt P, DiPersio JF, Link DC, Ley TJ, Spencer DH. Genome-wide analysis of focal DNA hypermethylation in IDH-mutant AML samples. Biorxiv. 2021. doi:10.1101/2021.03.03.433799

100. Dehner C, Moon CI, Zhang X, Zhou Z, Miller CA, Xu H, Wan X, Yang K, Mashl J, Gosline SJ, Wang W, Zhang X, Godec A, Jones PA, Dahiya S, Bhatia H, Primeau T, Li S, Pollard K, Rodriguez FJ, Ding L, Pratilas CA, Shern JF, Hirbe AC Chromosome 8 gain is associated with high-grade transformation in MPNST

et al.. Jci Insight. 2021. doi:10.1172/jci.insight.146351

101. **Miller CA**, Walker JR, Jensen TL, Hooper WF, Fulton RS, Painter JS, Sekeres MA, Ley TJ, Spencer DH, Goll JB, Walter MJ. Failure to detect mutations in U2AF1 due to changes in the GRCh38 reference sequence. Biorxiv. 2021. doi:10.1101/2021.05.07.442430

102. Katerndahl CD, Rogers OR, Day RB, Cai MA, Rooney TP, Helton NM, Hoock M, Ramakrishnan SM, Srivatsan SN, Wartman LD, **Miller CA**, Ley TJ. Tumor suppressor function of Gata2 in Acute Promyelocytic Leukemia. Blood. 2021. doi:10.1182/blood.2021011758

103. Smith AM, LaValle TA, Shinawi M, Ramakrishnan SM, Abel HJ, Hill CA, Kirkland NM, Rettig MP, Helton NM, Heath SE, Ferraro F, Chen DY, Adak S, Semenkovich CF, Christian DL, Martin JL, Gabel HW, **Miller CA**, Ley TJ. Functional and epigenetic phenotypes of humans and mice with DNMT3A Overgrowth Syndrome. Nature Communications. 2021. doi:10.1038/s41467-021-24800-7

104. Tian L, Chavez M, Chang GS, Helton NM, Katerndahl CD, **Miller CA**, Wartman L. Kdm6a Deficiency Restricted to Mouse Hematopoietic Cells Causes an Age-and Sex-dependent Myelodysplastic Syndrome-Like Phenotype. Biorxiv. 2021. doi:10.1101/2021.08.04.455117

105. Khanna A, Larson DE, Srivatsan SN, Mosior M, Abbott TE, Kiwala S, Ley TJ, Duncavage EJ, Walter MJ, Walker JR, Griffith OL, Griffith M, **Miller CA**. Bam-readcount-rapid generation of basepair-resolution sequence metrics. Arxiv. 2021. doi:arXiv:2107.12817

106. Ruiz FJ, Inkman M, Rashmi R, Muhammad N, Gabriel N, Miller CA, McLellan MD, Goldstein M, Markovina S, Grigsby PW, Zhang J, Schwarz JK. Jci Insight. 2021. doi:10.1172/jci.insight.138734 HPV transcript expression affects cervical cancer response to chemoradiation