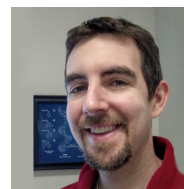


Christopher A. Miller, Ph.D.

Curriculum Vitae

Updated: November 1st, 2018



Citizenship: United States of America

Address and Telephone Numbers: Campus Box 8501
4444 Forest Park Ave,
St. Louis, Missouri 63108
314-286-0263

Home:
11657 Chandellay Dr
St. Louis, Missouri 63146
314-620-4262

Present Position:

Assistant Professor
Division of Oncology
McDonnell Genome Institute
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:

Ad-hoc reviewer for *Bioinformatics*, *Cancer Cell*, *Genome Biology*, *PLoS Computational Biology*, *Nucleic Acids Research*, *Nature Communications*, *Genome Research*.

Grant reviewer for Dutch Cancer Society (KWF Kankerbestrijding)

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 therapeutically 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

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)

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 (2005)
2007-2008	Teaching Assistant - Computer Aided Discovery Methods
2008	Teaching Assistant - Computational Mathematics for Biomedical Scientists
2015-2017	Lecturer - Investigating Eukaryotic Genomes
2015-2019	Lecturer - Molecular Basis of Heredity
2017-2018	Lecturer - Computational Statistical Genetics
2018	Lecturer - Research Explorations in Genomics
2018-	Co-organizer – MGI Bioinformatics Workshops

Trainees (date and current position):

Mentor to undergraduate research students

Yang Li	2013	Working in industry
Callie Federer	2014	Graduate Student in Bioinformatics at University of Colorado – Denver
Jonas Neichen	2017	Student at WUSTL
Megan Neveau	2017	Student at Truman State University

Training and Supervision of Genome Institute 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

Training of external collaborators:

Dr. Corrine Segal	2013	ICR, London UK
Dr. Alice Gao,	2013	ICR, London UK

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 Atlas 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. Kline 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**, Klcó 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, Klcó 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, Klcó 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. 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

47. 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

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. 2016. doi:10.1101/sqb.2016.81.030726

49. Johanns TM*, **Miller CA***, Dorward IG, Tsien C, Chang E, Perry A, Uppaluri R, Ferguson C, Schmidt RE, Dahiya S, Anstas 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

50. **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

51. 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

52. 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

53. 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

54. 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

55. 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, Klcio 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

56. 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

57. 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

58. 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

59. 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

60. 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

61. 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

62. 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

63. 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

64. 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

65. 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

66. 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

67. 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

68. 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

69. Griffith OL, Spies NC, Anurag M, Griffith M, Luo J, Tu D, Yeo B, Kunisaki J, **Miller CA**, Krysiak K, Hundal J, Ainscough B, Skidmore Z, 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 RW, Nielsen TO, Mardis ER, Ellis MJ. The prognostic effects of somatic mutations in ER-positive breast cancer. *Biorxiv*. doi:10.1101/235846

70. **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

71. 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

72. 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

73. 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

74. **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

75. 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

76. 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

77. 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

78. 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

79. 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

80. 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

81. 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

82. 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. Biorxiv. 2019. doi:10.1101/501817

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