Sean Davis

Curriculum Vita

9531 Rommel Drive
Columbia, MD 21046
✉ *sdavis2@mail.nih.gov*
http://seandavi.github.io/
Google Scholar–i10-index: 75; h-index: 45; 16,227 citations

Education and Professional Experience

2009–Present **Staff Scientist**, *Center for Cancer Research, National Cancer Institute.*

2007–2008 **Research Fellow**, *National Cancer Institute.*

2005–2007 **Research Fellow**, *National Human Genome Research Institute.*

2002–2005 **Clinical Fellow**, *Combined Johns Hopkins and National Cancer Institute Pediatric Hematology/Oncology Fellowship.*

1999–2002 **Pediatric Resident**, *Children's Hospital and Regional Medical Center, University of Washington.*

1993–1999 **MD**, *University of Pittsburgh School of Medicine.*

1995–1997 **PhD**, *University of Pittsburgh Graduate School of Public Health.*
Department of Human Genetics

1989-1993 **B.S.E.**, *Princeton University*, *With Honors.*
Mechanical and Aerospace Engineering

Professional Involvement and Service

March, 2018 *Co-organizer*, Kidney Cancer Hackathon, in collaboration with `https://sv.ai` and Google, San Francisco, CA

December, 2017 *NIH Intramural Representative*, NIH Data Commons working group

December, 2017 *Co-organizer*, NIH Hour of Code, Data Science Special Interest Group, NIH, Bethesda, MD

November, 2017 *NIH Representative to US Department of Agriculture*, Blueprint for USDA Efforts in Agricultural Animal Genomics, Beltsville, MD

August, 2017 *NIH Intramural Representative*, NIH Data Commons Review Committee

February, 2017 *Organizer*, NIH/NIST Medical Devices Cybersecurity Workshop, Bethesda, MD

January, 2017-present Cancer Moonshot Blue Ribbon Panel Implementation Working Group, National Cancer Data Ecosystem

January, 2017 *Organizer*, Globus Data Platform Hackathon and Workshop, NIH, Bethesda, MD

January, 2017	*NCI Representative*, NHLBI TopMed Data Commons Planning Workshop
December, 2016-present	*Founding Member*, NIH Data Science Special Interest Group
July, 2016-July, 2017	*NCI Representative*, NIH Data Commons Reference Dataset Working Group
July, 2016	*Co-organizer*, Frontiers of Predictive Oncology and Computing Symposium, Washington, DC
June, 2016	*Organizer*, Bioconductor 2016 Annual Meeting and Developer Conference. Stanford, CA.
April-November, 2016	Presidential Subcommittee on AI and Machine Learning, Cancer Moonshot Initiative
December, 2015	*NCI representative and panel member*, FDA Informatics and Precision Medicine Workshop
January, 2016	*Co-organizer*, NCBI Genomics and Bioinformatics Hackathon
November, 2015-present	NCI Cancer Cloud Pilot, Leading Intramural Research Program evaluation and implementation
July, 2015	*Organizer*, Bioconductor 2015 Annual Meeting and Developer Conference. Seattle, WA.
June, 2015	*Course organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
May, 2015-present	CCR Representative to CBIIT Strategic Planning Committee
2015	NCI Intramural Research Program Representative, NCI Cancer Cloud Initiative
2015	NCI Desktop Linux Working Group
2015-Present	Member of Genomic Alliance for Genomic Health (GA4GH), Tools and Workflows Working Group
2014-Present	Software Carpentry Instructor
2014-Present	NIH and NCI Genomic Data Sharing Policy Implementation working groups
July, 2014	*Organizer*, Bioconductor 2014 Annual Meeting and Developer Conference. Boston, MA.
June, 2014	*Course organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
May 12-13, 2014	*Intramural NIH representative*, BD2K Software Development Conference
January, 2014	*Organizer and Instructor*, Bioinformatics Summer Course, Riberão Preto Medical School, University of São Paulo, Brazil
2014	NCI Center for Cancer Genomics Genomic Data Commons Review Committee

July, 2013	*Organizer*, Bioconductor 2013 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
June, 2013	*Course organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
February, 2013	*NIH Representative*, Big Data Conference, Agricultural Research Service, USDA, Beltsville, MD
2008-Present	*Bioconductor Core Development Team*, share responsibility (with 5 others) for the ongoing leadership of the Bioconductor Project
2012-Present	*Founding Member*, NIH High Performance and Scientific Computing Working Group
2012-2016	High Throughput Molecular Data Working Group, National Cancer Institute
2010-Present	*Steering Committee*, NCI Center of Excellence in Integrative Cancer Biology and Genomics
2009-Present	Sequencing Facility Steering and Review Committee, Center for Cancer Research, NCI
July, 2012	*Organizer*, Bioconductor 2012 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
2011	NCI PacBio User Committee
July, 2011	*Organizer*, Bioconductor 2011 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
2010-2012	Scientific Liaison, Center for Cancer Research Bioinformatics Core
2009-2010	*Chair*, Center for Cancer Research Bioinformatics Planning and Implementation Committee
September, 2010	*NIH Representative*, NIFA, USDA, Genomics and Bioinformatics Workshop, Washington, DC
2009	*Team Leader*, Advanced Biomedical Computing Center Review Committee
April, 2008	*Organizer*, European Bioconductor Developer Conference, Lausanne, Switzerland

Invited Presentations, Teaching, and Short Courses

Note: Limited to last 8 years.

January, 2018	*A Data Ecosystem for Biomedical Big Data*, Grand Rounds, Wake Forest School of Medicine, Winston-Salem, NC
November, 2017	*Thoughts on Components of an Agricultural Data Ecosystem*, Blueprint for USDA Efforts in Agricultural Animal Genomics, Beltsville, MD
July, 2017	*What can I do with my data?*, National Institute of Nursing Research, BigData Bootcamp, Bethesda, MD
July, 2017	*Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY

June, 2017 *Cloud-scale genomics with the Cancer Genomics Cloud Pilots* and *Machine Learning in Biomedicine*, Purdue University, West Lafayette, IN

January, 2017 *A cloud-based data ecosystem for cancer research*, Dana Farber Cancer Institute, Boston, MA

January, 2017 *Open APIs with R and Bioconductor*, Harvard/Boston R/Bioconductor Meetup, Boston, MA

October, 2016 *Big data science careers in Government*, University of California, Riverside, CA

October, 2016 *Democratizing access to Big Cancer Data*, Midatlantic Bioinformatics Conference, University of Pennsylvania, Philadelphia, PA

July, 2016 *Bioconductor: Where Biology and Software Meet*, National Institute of Nursing Research, Bethesda, MD

July, 2016 *The Central Role of Data in Biomedical Research*, Purdue University, West Lafayette, IN

June, 2016 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY

April, 2016 Software Carpentry, National Institute on Aging, Baltimore, MD

March, 2016 Using the NCI Cancer Genomics Cloud, a Hands-on Tutorial, NIH

February, 2016 Introduction to RNA-Seq Data Analysis, NCI

January, 2016 Introduction to Bioconductor: Code and Practice, DataCommunityDC, Washington DC

October, 2015 *Course organizer and faculty*: Harvard School of Engineering and Applied Science: CS290 Extreme Computing

September, 2015 BioIT: A Symbiotic Relationship Between Biological Research and IT Infrastructure, Converged IT Summit, San Francisco, CA

June, 2015 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY

May, 2015 Beyond the Promise of Precision Medicine, Health 2.0 Meetup, Bethesda, MD

April, 2015 Relational Databases and R: a Powerful Combination for Science, NCI, DCEG

February, 2015 Introduction to RNA-Seq Data Analysis, NCI

January, 2015 Introduction to R and Bioconductor, NCI

December, 2014 Introduction to R for Data Manipulation and Visualization, NIH

June, 2014 *Course Organizer*,Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY

February, 2014 One-day course on RNA-seq data analysis and visualization, CIT, NIH

February, 2014	Reproducible research using the Snakemake workflow toolkit on Biowulf, CIT, NIH
January, 2014	*Course Organizer*, Bioinformatics Summer Course, Riberão Preto Medical School, University of São Paulo, Brazil
July 19, 2013	Accessing Public Genomics Data Using R and Bioconductor, Bioconductor Conference, Fred Hutchinson Cancer Research Center, Seattle, WA
June, 2013	*Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
February 6, 2013	Planning for High Performance and Scientific Computing at the NIH, Agricultural Research Service, USDA, Beltsville, MD
November 6, 2012	Introduction to Next Generation Sequencing Technologies, Bioinformatics Training and Education Program, CCR, NCI
July 24, 2012	Accessing Public Genomics Data Using R and Bioconductor, Bioconductor Conference, Fred Hutchinson Cancer Research Center, Seattle, WA
June, 2012	*Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY. Topics taught: public data access and data integration lab
2005-2012, except 2008	AACR Molecular Biology in Clinical Oncology (one-week course), Aspen & Snowmass, CO
March 28, 2012	Featured Speaker, Bioinformatics for Medical Genetics Symposium, American College of Medical Genetics, Charlotte, NC
February 27-28, 2012	Advanced R and Bioconductor Workshop on High-Throughput Genetic Analysis, Fred Hutchinson Cancer Research Center, Seattle, WA
January 13, 2012	Introduction to Next-Generation Sequencing: Mapping and Counting, Center of Excellence in Integrative Cancer Biology and Genomics Seminar Series, NCI
November 18, 2011	High-resolution Views of the Cancer Genome Using Next-Generation Sequencing Approaches, Lombardi Cancer Center, Georgetown University
July, 2011	*Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory. Topics taught: exome sequencing, methylation arrays, comparative genomic hybridization, public data access, and data integration lab
March, 2011	Introduction to Next-Generation Sequence Data Analysis, Center for Information Technology
January 28, 2011	Complete Genomics Data Tutorial, Center for Cancer Research, NCI
October 22, 2010	BioConductor: Tools for the Comprehension of Genomic Data, Translational Genomics Conference, Center of Excellence in Integrative Cancer Biology and Genomics annual meeting
October 22, 2010	Bioinformatics at the Center for Cancer Research, An Update, Center of Excellence in Integrative Cancer Biology and Genomics annual meeting
September 9, 2010	Potential Applications of Genomics in Agriculturally Important Species, NIFA, U.S. Department of Agriculture

Spring, 2010	Microarray Data Analysis Using R and Bioconductor, Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University
February 23, 2010	Genomic Technologies for Viewing the Cancer Genome, Georgetown University
July, 2010	*Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
November 18, 2009	Structural Variant Discovery in Short Read Sequencing using R and Bioconductor, Fred Hutchinson Cancer Research Center, Seattle, WA
November 18-20, 2009	Instructor, High throughput sequence analysis tools and approaches with Bioconductor, Fred Hutchinson Cancer Research Center, Seattle, WA
March 17, 2009	High-resolution Views of the Cancer Genome: Tools for examining the genome in a high-throughput way, Case Western Reserve University, Cleveland, OH
February 12, 2009	Genomics for the Pediatrician: An Overview of Genomics Technologies, Pediatric Grand Rounds, Oklahoma University Health Sciences Center, Oklahoma City, OK

Awards and Honors

2016 & 2017	National Cancer Institute Technology Transfer Award
2016	United States Department of Health and Human Services Director's Award
2015	National Institutes of Health Director's Award
2012	Staff Scientist/Staff Clinician Travel Award, Center for Cancer Research, NCI
2002-2007	NIH General Loan Repayment Program
2002	Family-Centered Care Award, University of Washington
1995	W.M. Keck Fellowship for Advanced Scientific Computing
1989	National Merit Scholar
1989	National Honor Society Scholarship
1988	Pennsylvania Governor's School for Science
1988	Young Humanitarian of the Year, Pennsylvania Association for Gifted Education

Editorial Responsibilities

2015-Present	Editor, F1000Research Bioconductor Channel
2010-Present	Associate Editor, BMC Bioinformatics
2009	Book reviewer, CRC Press, 2009

Peer Reviewer

- Bioinformatics
- BMC Bioinformatics
- Breast Cancer Research
- Cancer Research
- Clinical Cancer Research
- Database
- Endocrine-Related Cancer
- EURASIP Journal on Bioinformatics and Systems Biology
- Genetic Epidemiology
- Genomics
- Genome Research
- Gigascience
- Molecular Carcinogenesis
- Molecular Cancer Research
- Nature Methods
- Nucleic Acids Research
- Pigment Cell & Melanoma Research
- PLoS Computational Biology
- PLoS One
- Transactions on Computational Biology and Bioinformatics

References

[1] Y. Liu-Chittenden, M. Jain, K. Gaskins, S. Wang, M. J. Merino, S. Kotian, S. Kumar Gara, S. Davis, L. Zhang, and E. Kebebew. "RARRES2 functions as a tumor suppressor by promoting β-catenin phosphorylation/degradation and inhibiting p38 phosphorylation in adrenocortical carcinoma". In: *Oncogene* (Jan. 2017).

[2] Martin Morgan and Sean R. Davis. *GenomicDataCommons: a Bioconductor Interface to the NCI Genomic Data Commons*. 2017. DOI: 10.1101/117200. URL: http://doi.org/10.1101/117200.

[3] Marcel Ramos, Lucas Schiffer, Angela Re, Rimsha Azhar, Azfar Basunia, Carmen Rodriguez Cabrera, Tiffany Chan, Philip Chapman, Sean Davis, David Gomez-Cabrero, Aedin C. Culhane, Benjamin Haibe-Kains, Kasper Hansen, Hanish Kodali, Marie Stephie Louis, Arvind Singh Mer, Markus Riester, Martin Morgan, Vincent Carey, and Levi Waldron. *Software For The Integration Of Multi-Omics Experiments In Bioconductor*. 2017. DOI: 10.1101/144774. URL: http://doi.org/10.1101/144774.

[4] Vivek Shukla, Mahadev Rao, Hongen Zhang, Jeanette Beers, Darawalee Wangsa, Danny Wangsa, Floryne O Buishand, Yonghong Wang, Zhiya Yu, Holly S Stevenson, et al. "ASXL3 is a Novel Pluripotency Factor in Human Respiratory Epithelial Cells and a Potential Therapeutic Target in Small Cell Lung Cancer". In: *Cancer Research* 77.22 (2017), pp. 6267–6281.

[5] Hsinyi Tsang, KanakaDurga Addepalli, and Sean R. Davis. "Resources for Interpreting Variants in Precision Genomic Oncology Applications". In: *Frontiers in Oncology* 7 (2017), p. 214. ISSN: 2234-943X. DOI: 10.3389/fonc.2017.00214. URL: http://journal.frontiersin.org/article/10.3389/fonc.2017.00214.

[6] Feng Zhu, Jami Willette-Brown, Na-Young Song, Dakshayani Lomada, Yongmei Song, Liyan Xue, Zane Gray, Zitong Zhao, Sean R. Davis, Zhonghe Sun, Peilin Zhang, Xiaolin Wu, Qimin Zhan, Ellen R. Richie, and Yinling Hu. "Autoreactive T Cells and Chronic Fungal Infection Drive Esophageal Carcinogenesis". In: *Cell Host Microbe* 21.4 (2017), 478–493.e7. ISSN: 1931-3128. DOI: https://doi.org/10.1016/j.chom.2017.03.006. URL: http://www.sciencedirect.com/science/article/pii/S1931312817301166.

[7] M. Comas-Garcia, S. R. Davis, and A. Rein. "On the Selective Packaging of Genomic RNA by HIV-1". In: *Viruses* 8.9 (2016). [PubMed Central:PMC5035960] [DOI:10.3390/v8090246] [PubMed:27626441].

[8] Sean Davis and Ewy Mathe, eds. *Statistical Genomics*. Springer, 2016.

[9] F. T. Hakim, S. Memon, P. Jin, M. M. Imanguli, H. Wang, N. Rehman, X. Y. Yan, J. Rose, J. W. Mays, S. Dhamala, V. Kapoor, W. Telford, J. Dickinson, S. Davis, D. Halverson, H. B. Naik, K. Baird, D. Fowler, D. Stroncek, E. W. Cowen, S. Z. Pavletic, and R. E. Gress. "Upregulation of IFN-Inducible and Damage-Response Pathways in Chronic Graft-versus-Host Disease". In: *J. Immunol.* 197.9 (Nov. 2016), pp. 3490–3503.

[10] L. Kannan, M. Ramos, A. Re, N. El-Hachem, Z. Safikhani, D. M. Gendoo, S. Davis, D. Gomez-Cabrero, R. Castelo, K. D. Hansen, V. J. Carey, M. Morgan, A. C. Culhane, B. Haibe-Kains, and L. Waldron. "Public data and open source tools for multi-assay genomic investigation of disease". In: *Brief. Bioinformatics* 17.4 (July 2016). [PubMed Central:PMC4945830] [DOI:10.1093/bib/bbv080] [PubMed:26463000], pp. 603–615.

[11] J. Li, S. L. Woods, S. Healey, J. Beesley, X. Chen, J. S. Lee, H. Sivakumaran, N. Wayte, K. Nones, J. J. Waterfall, J. Pearson, A. M. Patch, J. Senz, M. A. Ferreira, P. Kaurah, R. Mackenzie, A. Heravi-Moussavi, S. Hansford, T. R. Lannagan, A. B. Spurdle, P. T. Simpson, L. da Silva, S. R. Lakhani, A. D. Clouston, M. Bettington, F. Grimpen, R. A. Busuttil, N. Di Costanzo, A. Boussioutas, M. Jeanjean, G. Chong, A. Fabre, S. Olschwang, G. J. Faulkner, E. Bellos, L. Coin, K. Rioux, O. F. Bathe, X. Wen, H. C. Martin, D. W. Neklason, S. R. Davis, R. L. Walker, K. A. Calzone, I. Avital, T. Heller, C. Koh, M. Pineda, U. Rudloff, M. Quezado, P. N. Pichurin, P. J. Hulick, S. M. Weissman, A. Newlin, W. S. Rubinstein, J. E. Sampson, K. Hamman, D. Goldgar, N. Poplawski, K. Phillips, L. Schofield, J. Armstrong, C. Kiraly-Borri, G. K. Suthers, D. G. Huntsman, W. D. Foulkes, F. Carneiro, N. M. Lindor, S. L. Edwards, J. D. French, N. Waddell, P. S. Meltzer, D. L. Worthley, K. A. Schrader, and G. Chenevix-Trench. "Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant". In: *Am. J. Hum. Genet.* 98.5 (May 2016). [PubMed Central:PMC4863475] [DOI:10.1016/j.ajhg.2016.03.001] [PubMed:27087319], pp. 830–842.

[12] R. Sorber, Y. Teper, A. Abisoye-Ogunniyan, J. J. Waterfall, S. Davis, J. K. Killian, M. Pineda, S. Ray, M. R. McCord, H. Pflicke, S. S. Burkett, P. S. Meltzer, and U. Rudloff. "Whole Genome Sequencing of Newly Established Pancreatic Cancer Lines Identifies Novel Somatic Mutation (c.2587G>A) in Axon Guidance Receptor Plexin A1 as Enhancer of Proliferation and Invasion". In: *PLoS ONE* 11.3 (2016). [PubMed Central:PMC4786220] [DOI:10.1371/journal.pone.0149833] [PubMed:26962861], e0149833.

[13] H. Zhang, P. S. Meltzer, and S. R. Davis. "caOmicsV: an R package for visualizing multidimensional cancer genomic data". In: *BMC Bioinformatics* 17 (2016). [PubMed Central:PMC4804509] [DOI:10.1186/s12859-016-0989-6] [PubMed:27005934], p. 141.

[14] M. Boufraqech, N. Nilubol, L. Zhang, S. K. Gara, S. M. Sadowski, A. Mehta, M. He, S. Davis, J. Dreiling, J. A. Copland, R. C. Smallridge, M. M. Quezado, and E. Kebebew. "miR30a inhibits LOX expression and anaplastic thyroid cancer progression". In: *Cancer Res.* 75.2 (Jan. 2015). [DOI:10.1158/0008-5472.CAN-14-2304] [PubMed:25488748], pp. 367–377.

[15] J. D. Figueroa, H. Yang, M. Garcia-Closas, S. Davis, P. Meltzer, J. Lissowska, H. N. Horne, M. E. Sherman, and M. Lee. "Integrated analysis of DNA methylation, immunohistochemistry and mRNA expression, data identifies a methylation expression index (MEI) robustly associated with survival of ER-positive breast cancer patients". In: *Breast Cancer Res. Treat.* 150.2 (Apr. 2015). [PubMed Central:PMC4989123] [DOI:10.1007/s10549-015-3314-6] [PubMed:25773928], pp. 457–466.

[16] W. Huber, V. J. Carey, R. Gentleman, S. Anders, M. Carlson, B. S. Carvalho, H. C. Bravo, S. Davis, L. Gatto, T. Girke, R. Gottardo, F. Hahne, K. D. Hansen, R. A. Irizarry, M. Lawrence, M. I. Love, J. MacDonald, V. Obenchain, A. K. Ole, H. Pages, A. Reyes, P. Shannon, G. K. Smyth, D. Tenenbaum, L. Waldron, and M. Morgan. "Orchestrating high-throughput genomic analysis with Bioconductor". In: *Nat. Methods* 12.2 (Feb. 2015). [PubMed Central:PMC4509590] [DOI:10.1038/nmeth.3252] [PubMed:25633503], pp. 115–121.

[17] W. Huber, V. Carey, S. Davis, K. D. Hansen, and M. Morgan. "The Bioconductor channel in F1000Research". In: *F1000Res* 4 (2015). [DOI:10.12688/f1000research.6758.2] [PubMed:26998224], p. 217.

[18] A. Mehta, L. Zhang, M. Boufraqech, Y. Liu-Chittenden, Y. Zhang, D. Patel, S. Davis, A. Rosenberg, K. Ylaya, R. Aufforth, Z. Li, M. Shen, and E. Kebebew. "Inhibition of Survivin with YM155 Induces Durable Tumor Response in Anaplastic Thyroid Cancer". In: *Clin. Cancer Res.* 21.18 (Sept. 2015). [PubMed Central:PMC4573822] [DOI:10.1158/1078-0432.CCR-14-3251] [PubMed:25944801], pp. 4123–4132.

[19] L. Mirabello, R. Koster, B. S. Moriarity, L. G. Spector, P. S. Meltzer, J. Gary, M. J. Machiela, N. Pankratz, O. A. Panagiotou, D. Largaespada, Z. Wang, J. M. Gastier-Foster, R. Gorlick, C. Khanna, S. R. de Toledo, A. S. Petrilli, A. Patino-Garcia, L. Sierrasesumaga, F. Lecanda, I. L. Andrulis, J. S. Wunder, N. Gokgoz, M. Serra, C. Hattinger, P. Picci, K. Scotlandi, A. M. Flanagan, R. Tirabosco, M. F. Amary, D. Halai, M. L. Ballinger, D. M. Thomas, S. Davis, D. A. Barkauskas, N. Marina, L. Helman, G. M. Otto, K. L. Becklin, N. K. Wolf, M. T. Weg, M. Tucker, S. Wacholder, J. F. Fraumeni, N. E. Caporaso, J. F. Boland, B. D. Hicks, A. Vogt, L. Burdett, M. Yeager, R. N. Hoover, S. J. Chanock, and S. A. Savage. "A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma". In: *Cancer Discov* 5.9 (Sept. 2015). [PubMed Central:PMC4560660] [DOI:10.1158/2159-8290.CD-15-0125] [PubMed:26084801], pp. 920–931.

[20] O. Shakhova, P. Cheng, P. J. Mishra, D. Zingg, S. M. Schaefer, J. Debbache, J. Hausel, C. Matter, T. Guo, S. Davis, P. Meltzer, D. Mihic-Probst, H. Moch, M. Wegner, G. Merlino, M. P. Levesque, R. Dummer, R. Santoro, P. Cinelli, and L. Sommer. "Antagonistic cross-regulation between Sox9 and Sox10 controls an anti-tumorigenic program in melanoma". In: *PLoS Genet.* 11.1 (Jan. 2015). [PubMed Central:PMC4309598] [DOI:10.1371/journal.pgen.1004877] [PubMed:25629959], e1004877.

[21] G. Vahedi, Y. Kanno, Y. Furumoto, K. Jiang, S. C. Parker, M. R. Erdos, S. R. Davis, R. Roychoudhuri, N. P. Restifo, M. Gadina, Z. Tang, Y. Ruan, F. S. Collins, V. Sartorelli, and J. J. O'Shea. "Super-enhancers delineate disease-associated regulatory nodes in T cells". In: *Nature* 520.7548 (Apr. 2015). [PubMed Central:PMC4409450] [DOI:10.1038/nature14154] [PubMed:25686607], pp. 558–562.

[22] X. R. Yang, J. K. Killian, S. Hammond, L. S. Burke, H. Bennett, Y. Wang, S. R. Davis, L. C. Strong, J. Neglia, M. Stovall, R. E. Weathers, L. L. Robison, S. Bhatia, K. Mabuchi, P. D. Inskip, and P. Meltzer. "Characterization of genomic alterations in radiation-associated breast cancer among childhood cancer survivors, using comparative genomic hybridization (CGH) arrays". In: *PLoS ONE* 10.3 (2015). [PubMed Central:PMC4357472] [DOI:10.1371/journal.pone.0116078] [PubMed:25764003], e0116078.

[23] L. Zhang, Y. Zhang, A. Mehta, M. Boufraqech, S. Davis, J. Wang, Z. Tian, Z. Yu, M. B. Boxer, J. A. Kiefer, J. A. Copland, R. C. Smallridge, Z. Li, M. Shen, and E. Kebebew. "Dual inhibition of HDAC and EGFR signaling with CUDC-101 induces potent suppression of tumor growth and metastasis in anaplastic thyroid cancer". In: *Oncotarget* 6.11 (Apr. 2015). [PubMed Central:PMC4496203] [DOI:10.18632/oncotarget.3268] [PubMed:25940539], pp. 9073–9085.

[24] L. Zhang, Y. Zhang, A. Mehta, M. Boufraqech, S. Davis, J. Wang, Z. Tian, Z. Yu, M. B. Boxer, J. A. Kiefer, J. A. Copland, R. C. Smallridge, Z. Li, M. Shen, and E. Kebebew. "Dual inhibition of HDAC and EGFR signaling with CUDC-101 induces potent suppression of tumor growth and metastasis in anaplastic thyroid cancer". In: *Oncotarget* (Apr. 2015). [DOI:10.18632/oncotarget.3268] [PubMed:25929339].

[25] J. Abraham, Y. Nunez-Alvarez, S. Hettmer, E. Carrio, H. I. Chen, K. Nishijo, E. T. Huang, S. I. Prajapati, R. L. Walker, S. Davis, J. Rebeles, H. Wiebush, A. T. McCleish, S. T. Hampton, C. R. Bjornson, A. S. Brack, A. J. Wagers, T. A. Rando, M. R. Capecchi, F. C. Marini, B. R. Ehler, L. A. Zarzabal, M. W. Goros, J. E. Michalek, P. S. Meltzer, D. M. Langenau, R. D. LeGallo, A. Mansoor, Y. Chen, M. Suelves, B. P. Rubin, and C. Keller. "Lineage of origin in rhabdomyosarcoma informs pharmacological response". In: *Genes Dev.* 28.14 (July 2014). [PubMed Central:PMC4102765] [DOI:10.1101/gad.238733.114] [PubMed:25030697], pp. 1578–1591.

[26] R. J. Ellis, Y. Wang, H. S. Stevenson, M. Boufraqech, D. Patel, N. Nilubol, S. Davis, D. C. Edelman, M. J. Merino, M. He, L. Zhang, P. S. Meltzer, and E. Kebebew. "Genome-wide methylation patterns in papillary thyroid cancer are distinct based on histological subtype and tumor genotype". In: *J. Clin. Endocrinol. Metab.* 99.2 (Feb. 2014). [PubMed Central:PMC3913809] [DOI:10.1210/jc.2013-2749] [PubMed:24423287], E329–337.

[27] Z. Kang, Y. Yu, Y. J. Zhu, S. Davis, R. Walker, P. S. Meltzer, L. J. Helman, and L. Cao. "Downregulation of IGFBP2 is associated with resistance to IGF1R therapy in rhabdomyosarcoma". In: *Oncogene* 33.50 (Dec. 2014). [DOI:10.1038/onc.2013.509] [PubMed:24292683], pp. 5697–5705.

[28] W. C. Reinhold, S. Varma, F. Sousa, M. Sunshine, O. D. Abaan, S. R. Davis, S. W. Reinhold, K. W. Kohn, J. Morris, P. S. Meltzer, J. H. Doroshow, and Y. Pommier. "NCI-60 whole exome sequencing and pharmacological CellMiner analyses". In: *PLoS ONE* 9.7 (2014). [PubMed Central:PMC4102467] [DOI:10.1371/journal.pone.0101670] [PubMed:25032700], e101670.

[29] J. J. Waterfall, E. Arons, R. L. Walker, M. Pineda, L. Roth, J. K. Killian, O. D. Abaan, S. R. Davis, R. J. Kreitman, and P. S. Meltzer. "High prevalence of MAP2K1 mutations in variant and IGHV4-34-expressing hairy-cell leukemias". In: *Nat. Genet.* 46.1 (Jan. 2014). [PubMed Central:PMC3905739] [DOI:10.1038/ng.2828] [PubMed:24241536], pp. 8–10.

[30] O. D. Abaan, E. C. Polley, S. R. Davis, Y. J. Zhu, S. Bilke, R. L. Walker, M. Pineda, Y. Gindin, Y. Jiang, W. C. Reinhold, S. L. Holbeck, R. M. Simon, J. H. Doroshow, Y. Pommier, and P. S. Meltzer. "The exomes of the NCI-60 panel: a genomic resource for cancer biology and systems pharmacology". In: *Cancer Res.* 73.14 (July 2013). [PubMed Central:PMC4893961] [DOI:10.1158/0008-5472.CAN-12-3342] [PubMed:23856246], pp. 4372–4382.

[31] T. Barrett, S. E. Wilhite, P. Ledoux, C. Evangelista, I. F. Kim, M. Tomashevsky, K. A. Marshall, K. H. Phillippy, P. M. Sherman, M. Holko, A. Yefanov, H. Lee, N. Zhang, C. L. Robertson, N. Serova, S. Davis, and A. Soboleva. "NCBI GEO: archive for functional genomics data sets–update". In: *Nucleic Acids Res.* 41.Database issue (Jan. 2013). [PubMed Central:PMC3531084] [DOI:10.1093/nar/gks1193] [PubMed:23193258], pp. D991–995.

[32] S. Bilke, R. Schwentner, F. Yang, M. Kauer, G. Jug, R. L. Walker, S. Davis, Y. J. Zhu, M. Pineda, P. S. Meltzer, and H. Kovar. "Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer". In: *Genome Res.* 23.11 (Nov. 2013). [PubMed Central:PMC3814880] [DOI:10.1101/gr.151340.112] [PubMed:23940108], pp. 1797–1809.

[33] J. J. Gartner, S. C. Parker, T. D. Prickett, K. Dutton-Regester, M. L. Stitzel, J. C. Lin, S. Davis, V. L. Simhadri, S. Jha, N. Katagiri, V. Gotea, J. K. Teer, X. Wei, M. A. Morken, U. K. Bhanot, G. Chen, L. L. Elnitski, M. A. Davies, J. E. Gershenwald, H. Carter, R. Karchin, W. Robinson, S. Robinson, S. A. Rosenberg, F. S. Collins, G. Parmigiani, A. A. Komar, C. Kimchi-Sarfaty, N. K. Hayward, E. H. Margulies, Y. Samuels, J. Becker, B. Benjamin, R. Blakesley, G. Bouffard, S. Brooks, H. Coleman, M. Dekhtyar, M. Gregory, X. Guan, J. Gupta, J. Han, A. Hargrove, S. L. Ho, T. Johnson, R. Legaspi, S. Lovett, Q. Maduro, C. Masiello, B. Maskeri, J. McDowell, C. Montemayor, J. Mullikin, M. Park, N. Riebow, K. Schandler, B. Schmidt, C. Sison, M. Stantripop, J. Thomas, P. Thomas, M. Vemulapalli, and A. Young. "Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma". In: *Proc. Natl. Acad. Sci. U.S.A.* 110.33 (Aug. 2013). [PubMed Central:PMC3746936] [DOI:10.1073/pnas.1304227110] [PubMed:23901115], pp. 13481–13486.

[34] D. Hirsch, R. Kemmerling, S. Davis, J. Camps, P. S. Meltzer, T. Ried, and T. Gaiser. "Chromothripsis and focal copy number alterations determine poor outcome in malignant melanoma". In: *Cancer Res.* 73.5 (Mar. 2013). [PubMed Central:PMC4535704] [DOI:10.1158/0008-5472.CAN-12-0928] [PubMed:23271725], pp. 1454–1460.

[35] K. Kikuchi, E. Taniguchi, H. I. Chen, M. N. Svalina, J. Abraham, E. T. Huang, K. Nishijo, S. Davis, C. Louden, L. A. Zarzabal, O. Recht, A. Bajwa, N. Berlow, M. Suelves, S. L. Perkins, P. S. Meltzer, A. Mansoor, J. E. Michalek, Y. Chen, B. P. Rubin, and C. Keller. "Rb1 loss modifies but does not initiate alveolar rhabdomyosarcoma". In: *Skelet Muscle* 3.1 (2013). [PubMed Central:PMC4177545] [DOI:10.1186/2044-5040-3-27] [PubMed:24274149], p. 27.

[36] I. Petrini, A. Rajan, T. Pham, D. Voeller, S. Davis, J. Gao, Y. Wang, and G. Giaccone. "Whole genome and transcriptome sequencing of a B3 thymoma". In: *PLoS ONE* 8.4 (2013). [PubMed Central:PMC3618227] [DOI:10.1371/journal.pone.0060572] [PubMed:23577124], e60572.

[37] C. Praetorius, C. Grill, S. N. Stacey, A. M. Metcalf, D. U. Gorkin, K. C. Robinson, E. Van Otterloo, R. S. Kim, K. Bergsteinsdottir, M. H. Ogmundsdottir, E. Magnusdottir, P. J. Mishra, S. R. Davis, T. Guo, M. R. Zaidi, A. S. Helgason, M. I. Sigurdsson, P. S. Meltzer, G. Merlino, V. Petit, L. Larue, S. K. Loftus, D. R. Adams, U. Sobhiafshar, N. C. Emre, W. J. Pavan, R. Cornell, A. G. Smith, A. S. McCallion, D. E. Fisher, K. Stefansson, R. A. Sturm, and E. Steingrimsson. "A polymorphism in IRF4 affects human pigmentation through a tyrosinase-dependent MITF/TFAP2A pathway". In: *Cell* 155.5 (Nov. 2013). [PubMed Central:PMC3873608] [DOI:10.1016/j.cell.2013.10.022] [PubMed:24267888], pp. 1022–1033.

[38] L. R. Webster, P. J. Provan, D. J. Graham, K. Byth, R. L. Walker, S. Davis, E. L. Salisbury, A. L. Morey, R. L. Ward, N. J. Hawkins, C. L. Clarke, P. S. Meltzer, and R. L. Balleine. "Prohibitin expression is associated with high grade breast cancer but is not a driver of amplification at 17q21.33". In: *Pathology* 45.7 (Dec. 2013). [DOI:10.1097/PAT.0000000000000004] [PubMed:24247619], pp. 629–636.

[39] C. L. Yauk, J. Lucas Argueso, S. S. Auerbach, P. Awadalla, S. R. Davis, D. M. Demarini, G. R. Douglas, Y. E. Dubrova, R. K. Elespuru, T. W. Glover, B. F. Hales, M. E. Hurles, C. B. Klein, J. R. Lupski, D. K. Manchester, F. Marchetti, A. Montpetit, J. J. Mulvihill, B. Robaire, W. A. Robbins, G. A. Rouleau, D. T. Shaughnessy, C. M. Somers, J. G. Taylor, J. Trasler, M. D. Waters, T. E. Wilson, K. L. Witt, and J. B. Bishop. "Harnessing genomics to identify environmental determinants of heritable disease". In: *Mutat. Res.* 752.1 (2013). [PubMed Central:PMC3556182] [DOI:10.1016/j.mrrev.2012.08.002] [PubMed:22935230], pp. 6–9.

[40] H. Zhang, P. Meltzer, and S. Davis. "RCircos: an R package for Circos 2D track plots". In: *BMC Bioinformatics* 14 (2013). [PubMed Central:PMC3765848] [DOI:10.1186/1471-2105-14-244] [PubMed:23937229], p. 244.

[41] Y. Zhu, R. M. Stephens, P. S. Meltzer, and S. R. Davis. "SRAdb: query and use public next-generation sequencing data from within R". In: *BMC Bioinformatics* 14 (2013). [PubMed Central:PMC3560148] [DOI:10.1186/1471-2105-14-19] [PubMed:23323543], p. 19.

[42] J. Debbache, M. R. Zaidi, S. Davis, T. Guo, K. Bismuth, X. Wang, S. Skuntz, D. Maric, J. Pickel, P. Meltzer, G. Merlino, and H. Arnheiter. "In vivo role of alternative splicing and serine phosphorylation of the microphthalmia-associated transcription factor". In: *Genetics* 191.1 (May 2012). [PubMed Central:PMC3338255] [DOI:10.1534/genetics.111.135996] [PubMed:22367038], pp. 133–144.

[43] J. J. Gartner, S. Davis, X. Wei, J. C. Lin, N. S. Trivedi, J. K. Teer, P. S. Meltzer, S. A. Rosenberg, and Y. Samuels. "Comparative exome sequencing of metastatic lesions provides insights into the mutational progression of melanoma". In: *BMC Genomics* 13 (2012). [PubMed Central:PMC3500261] [DOI:10.1186/1471-2164-13-505] [PubMed:23006843], p. 505.

[44] J. K. Killian, R. L. Walker, S. Bilke, Y. Chen, S. Davis, R. Cornelison, W. I. Smith, and P. S. Meltzer. "Genome-wide methylation profiling in archival formalin-fixed paraffin-embedded tissue samples". In: *Methods Mol. Biol.* 823 (2012). [DOI:10.1007/978-1-60327-216-2$_8$] [PubMed:22081342], pp. 107–118.

[45] N. Kouprina, N. C. Lee, A. Pavlicek, A. Samoshkin, J. H. Kim, H. S. Lee, S. Varma, W. C. Reinhold, J. Otstot, G. Solomon, S. Davis, P. S. Meltzer, J. Schleutker, and V. Larionov. "Exclusion of the 750-kb genetically unstable region at Xq27 as a candidate locus for prostate malignancy in HPCX1-linked families". In: *Genes Chromosomes Cancer* 51.10 (Oct. 2012). [PubMed Central:PMC3412920] [DOI:10.1002/gcc.21977] [PubMed:22733720], pp. 933–948.

[46] P. J. O'Shea, D. W. Kim, J. G. Logan, S. Davis, R. L. Walker, P. S. Meltzer, S. Y. Cheng, and G. R. Williams. "Advanced bone formation in mice with a dominant-negative mutation in the thyroid hormone receptor Îš gene due to activation of Wnt/Îš-catenin protein signaling". In: *J. Biol. Chem.* 287.21 (May 2012). [PubMed Central:PMC3366792] [DOI:10.1074/jbc.M111.311464] [PubMed:22442145], pp. 17812–17822.

[47] G. Zoppoli, S. Solier, W. C. Reinhold, H. Liu, J. W. Connelly, A. Monks, R. H. Shoemaker, O. D. Abaan, S. R. Davis, P. S. Meltzer, J. H. Doroshow, and Y. Pommier. "CHEK2 genomic and proteomic analyses reveal genetic inactivation or endogenous activation across the 60 cell lines of the US National Cancer Institute". In: *Oncogene* 31.4 (Jan. 2012). [DOI:10.1038/onc.2011.283] [PubMed:21765476], pp. 403–418.

[48] P. J. Grohar, G. M. Woldemichael, L. B. Griffin, A. Mendoza, Q. R. Chen, C. Yeung, D. G. Currier, S. Davis, C. Khanna, J. Khan, J. B. McMahon, and L. J. Helman. "Identification of an inhibitor of the EWS-FLI1 oncogenic transcription factor by high-throughput screening". In: *J. Natl. Cancer Inst.* 103.12 (June 2011). [PubMed Central:PMC3119649] [DOI:10.1093/jnci/djr156] [PubMed:21653923], pp. 962–978.

[49] J. K. Killian, S. Bilke, S. Davis, R. L. Walker, E. Jaeger, M. S. Killian, J. J. Waterfall, M. Bibikova, J. B. Fan, W. I. Smith, and P. S. Meltzer. "A methyl-deviator epigenotype of estrogen receptor-positive breast carcinoma is associated with malignant biology". In: *Am. J. Pathol.* 179.1 (July 2011). [PubMed Central:PMC3123808] [DOI:10.1016/j.ajpath.2011.03.022] [PubMed:21641572], pp. 55–65.

[50] M. M. Martin, M. Ryan, R. Kim, A. L. Zakas, H. Fu, C. M. Lin, W. C. Reinhold, S. R. Davis, S. Bilke, H. Liu, J. H. Doroshow, M. A. Reimers, M. S. Valenzuela, Y. Pommier, P. S. Meltzer, and M. I. Aladjem. "Genome-wide depletion of replication initiation events in highly transcribed regions". In: *Genome Res.* 21.11 (Nov. 2011). [PubMed Central:PMC3205567] [DOI:10.1101/gr.124644.111] [PubMed:21813623], pp. 1822–1832.

[51] B. P. Rubin, K. Nishijo, H. I. Chen, X. Yi, D. P. Schuetze, R. Pal, S. I. Prajapati, J. Abraham, B. R. Arenkiel, Q. R. Chen, S. Davis, A. T. McCleish, M. R. Capecchi, J. E. Michalek, L. A. Zarzabal, J. Khan, Z. Yu, D. M. Parham, F. G. Barr, P. S. Meltzer, Y. Chen, and C. Keller. "Evidence for an unanticipated relationship between undifferentiated pleomorphic sarcoma and embryonal rhabdomyosarcoma". In: *Cancer Cell* 19.2 (Feb. 2011). [PubMed Central:PMC3040414] [DOI:10.1016/j.ccr.2010.12.023] [PubMed:21316601], pp. 177–191.

[52] M. S. Valenzuela, Y. Chen, S. Davis, F. Yang, R. L. Walker, S. Bilke, J. Lueders, M. M. Martin, M. I. Aladjem, P. P. Massion, and P. S. Meltzer. "Preferential localization of human origins of DNA replication at the 5'-ends of expressed genes and at evolutionarily conserved DNA sequences". In: *PLoS ONE* 6.5 (2011). [PubMed Central:PMC3094316] [DOI:10.1371/journal.pone.0017308] [PubMed:21602917], e17308.

[53] X. Wei, V. Walia, J. C. Lin, J. K. Teer, T. D. Prickett, J. Gartner, S. Davis, K. Stemke-Hale, M. A. Davies, J. E. Gershenwald, W. Robinson, S. Robinson, S. A. Rosenberg, and Y. Samuels. "Exome sequencing identifies GRIN2A as frequently mutated in melanoma". In: *Nat. Genet.* 43.5 (May 2011). [PubMed Central:PMC3161250] [DOI:10.1038/ng.810] [PubMed:21499247], pp. 442–446.

[54] M. R. Zaidi, S. Davis, F. P. Noonan, C. Graff-Cherry, T. S. Hawley, R. L. Walker, L. Feigenbaum, E. Fuchs, L. Lyakh, H. A. Young, T. J. Hornyak, H. Arnheiter, G. Trinchieri, P. S. Meltzer, E. C. De Fabo, and G. Merlino. "Interferon-γ*linksultravioletradiationtomelanomagenesis* In: *Nature* 469.7331 (Jan. 2011). [PubMed Central:PMC3140101] [DOI:10.1038/nature09666] [PubMed:21248750], pp. 548–553.

[55] K. L. Bolton, M. Garcia-Closas, R. M. Pfeiffer, M. A. Duggan, W. J. Howat, S. M. Hewitt, X. R. Yang, R. Cornelison, S. L. Anzick, P. Meltzer, S. Davis, P. Lenz, J. D. Figueroa, P. D. Pharoah, and M. E. Sherman. "Assessment of automated image analysis of breast cancer tissue microarrays for epidemiologic studies". In: *Cancer Epidemiol. Biomarkers Prev.* 19.4 (Apr. 2010). [PubMed Central:PMC2852578] [DOI:10.1158/1055-9965.EPI-09-1023] [PubMed:20332278], pp. 992–999.

[56] A. Camilleri, M. R. Johnston, M. Brennan, S. Davis, and D. G. Caldicott. "Chemical analysis of four capsules containing the controlled substance analogues 4-methylmethcathinone, 2-fluoromethamphetamine, alpha-phthalimidopropiophenone and N-ethylcathinone". In: *Forensic Sci. Int.* 197.1-3 (Apr. 2010). [DOI:10.1016/j.forsciint.2009.12.048] [PubMed:20074881], pp. 59–66.

[57] J. K. Killian, R. L. Walker, M. Suuriniemi, L. Jones, S. Scurci, P. Singh, R. Cornelison, S. Harmon, N. Boisvert, J. Zhu, Y. Wang, S. Bilke, S. Davis, G. Giaccone, W. I. Smith, and P. S. Meltzer. "Archival fine-needle aspiration cytopathology (FNAC) samples: untapped resource for clinical molecular profiling". In: *J Mol Diagn* 12.6 (Nov. 2010). [PubMed Central:PMC2963906] [DOI:10.2353/jmoldx.2010.090238] [PubMed:20959611], pp. 739–745.

[58] F. Liu, J. K. Killian, M. Yang, R. L. Walker, J. A. Hong, M. Zhang, S. Davis, Y. Zhang, M. Hussain, S. Xi, M. Rao, P. A. Meltzer, and D. S. Schrump. "Epigenomic alterations and gene expression profiles in respiratory epithelia exposed to cigarette smoke condensate". In: *Oncogene* 29.25 (June 2010). [DOI:10.1038/onc.2010.129] [PubMed:20440268], pp. 3650–3664.

[59] S. Morisot, A. S. Wayne, O. Bohana-Kashtan, I. M. Kaplan, C. D. Gocke, R. Hildreth, M. Stetler-Stevenson, R. L. Walker, S. Davis, P. S. Meltzer, S. J. Wheelan, P. Brown, R. J. Jones, L. D. Shultz, and C. I. Civin. "High frequencies of leukemia stem cells in poor-outcome childhood precursor-B acute lymphoblastic leukemias". In: *Leukemia* 24.11 (Nov. 2010). [PubMed Central:PMC3035974] [DOI:10.1038/leu.2010.184] [PubMed:20739953], pp. 1859–1866.

[60] S. John, T. A. Johnson, M. H. Sung, S. C. Biddie, S. Trump, C. A. Koch-Paiz, S. R. Davis, R. Walker, P. S. Meltzer, and G. L. Hager. "Kinetic complexity of the global response to glucocorticoid receptor action". In: *Endocrinology* 150.4 (Apr. 2009). [PubMed Central:PMC2659280] [DOI:10.1210/en.2008-0863] [PubMed:19131569], pp. 1766–1774.

[61] M. Kauer, J. Ban, R. Kofler, B. Walker, S. Davis, P. Meltzer, and H. Kovar. "A molecular function map of Ewing's sarcoma". In: *PLoS ONE* 4.4 (2009). [PubMed Central:PMC2671847] [DOI:10.1371/journal.pone.0005415] [PubMed:19404404], e5415.

[62] J. K. Killian, S. Bilke, S. Davis, R. L. Walker, M. S. Killian, E. B. Jaeger, Y. Chen, J. Hipp, S. Pittaluga, M. Raffeld, R. Cornelison, W. I. Smith, M. Bibikova, J. B. Fan, M. R. Emmert-Buck, E. S. Jaffe, and P. S. Meltzer. "Large-scale profiling of archival lymph nodes reveals pervasive remodeling of the follicular lymphoma methylome". In: *Cancer Res.* 69.3 (Feb. 2009). [DOI:10.1158/0008-5472.CAN-08-2984] [PubMed:19155300], pp. 758–764.

[63] L. H. Palavalli, T. D. Prickett, J. R. Wunderlich, X. Wei, A. S. Burrell, P. Porter-Gill, S. Davis, C. Wang, J. C. Cronin, N. S. Agrawal, J. C. Lin, W. Westbroek, S. Hoogstraten-Miller, A. A. Molinolo, P. Fetsch, A. C. Filie, M. P. O'Connell, C. E. Banister, J. D. Howard, P. Buckhaults, A. T. Weeraratna, L. C. Brody, S. A. Rosenberg, and Y. Samuels. "Analysis of the matrix metalloproteinase family reveals that MMP8 is often mutated in melanoma". In: *Nat. Genet.* 41.5 (May 2009). [PubMed Central:PMC2748394] [DOI:10.1038/ng.340] [PubMed:19330028], pp. 518–520.

[64] D. Palmieri, D. Fitzgerald, S. M. Shreeve, E. Hua, J. L. Bronder, R. J. Weil, S. Davis, A. M. Stark, M. J. Merino, R. Kurek, H. M. Mehdorn, G. Davis, S. M. Steinberg, P. S. Meltzer, K. Aldape, and P. S. Steeg. "Analyses of resected human brain metastases of breast cancer reveal the association between up-regulation of hexokinase 2 and poor prognosis". In: *Mol. Cancer Res.* 7.9 (Sept. 2009). [PubMed Central:PMC2746883] [DOI:10.1158/1541-7786.MCR-09-0234] [PubMed:19723875], pp. 1438–1445.

[65] D. Palmieri, P. R. Lockman, F. C. Thomas, E. Hua, J. Herring, E. Hargrave, M. Johnson, N. Flores, Y. Qian, E. Vega-Valle, K. S. Taskar, V. Rudraraju, R. K. Mittapalli, J. A. Gaasch, K. A. Bohn, H. R. Thorsheim, D. J. Liewehr, S. Davis, J. F. Reilly, R. Walker, J. L. Bronder, L. Feigenbaum, S. M. Steinberg, K. Camphausen, P. S. Meltzer, V. M. Richon, Q. R. Smith, and P. S. Steeg. "Vorinostat inhibits brain metastatic colonization in a model of triple-negative breast cancer and induces DNA double-strand breaks". In: *Clin. Cancer Res.* 15.19 (Oct. 2009). [DOI:10.1158/1078-0432.CCR-09-1039] [PubMed:19789319], pp. 6148–6157.

[66] M. Paoloni, S. Davis, S. Lana, S. Withrow, L. Sangiorgi, P. Picci, S. Hewitt, T. Triche, P. Meltzer, and C. Khanna. "Canine tumor cross-species genomics uncovers targets linked to osteosarcoma progression". In: *BMC Genomics* 10 (2009). [PubMed Central:PMC2803201] [DOI:10.1186/1471-2164-10-625] [PubMed:20028558], p. 625.

[67] M. Rahman, S. R. Davis, J. G. Pumphrey, J. Bao, M. M. Nau, P. S. Meltzer, and S. Lipkowitz. "TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype". In: *Breast Cancer Res. Treat.* 113.2 (Jan. 2009). [PubMed Central:PMC2615075] [DOI:10.1007/s10549-008-9924-5] [PubMed:18266105], pp. 217–230.

[68] R. L. Balleine, L. R. Webster, S. Davis, E. L. Salisbury, J. P. Palazzo, G. F. Schwartz, D. B. Cornfield, R. L. Walker, K. Byth, C. L. Clarke, and P. S. Meltzer. "Molecular grading of ductal carcinoma in situ of the breast". In: *Clin. Cancer Res.* 14.24 (Dec. 2008). [DOI:10.1158/1078-0432.CCR-08-0939] [PubMed:19088042], pp. 8244–8252.

[69] A. Bhoumik, B. Fichtman, C. Derossi, W. Breitwieser, H. M. Kluger, S. Davis, A. Subtil, P. Meltzer, S. Krajewski, N. Jones, and Z. Ronai. "Suppressor role of activating transcription factor 2 (ATF2) in skin cancer". In: *Proc. Natl. Acad. Sci. U.S.A.* 105.5 (Feb. 2008). [PubMed Central:PMC2234203] [DOI:10.1073/pnas.0706057105] [PubMed:18227516], pp. 1674–1679.

[70] A. P. Boyle, S. Davis, H. P. Shulha, P. Meltzer, E. H. Margulies, Z. Weng, T. S. Furey, and G. E. Crawford. "High-resolution mapping and characterization of open chromatin across the genome". In: *Cell* 132.2 (Jan. 2008). [PubMed Central:PMC2669738] [DOI:10.1016/j.cell.2007.12.014] [PubMed:18243105], pp. 311–322.

[71] S. John, P. J. Sabo, T. A. Johnson, M. H. Sung, S. C. Biddie, S. L. Lightman, T. C. Voss, S. R. Davis, P. S. Meltzer, J. A. Stamatoyannopoulos, and G. L. Hager. "Interaction of the glucocorticoid receptor with the chromatin landscape". In: *Mol. Cell* 29.5 (Mar. 2008). [DOI:10.1016/j.molcel.2008.02.010] [PubMed:18342607], pp. 611–624.

[72] T. Walsh, J. M. McClellan, S. E. McCarthy, A. M. Addington, S. B. Pierce, G. M. Cooper, A. S. Nord, M. Kusenda, D. Malhotra, A. Bhandari, S. M. Stray, C. F. Rippey, P. Roccanova, V. Makarov, B. Lakshmi, R. L. Findling, L. Sikich, T. Stromberg, B. Merriman, N. Gogtay, P. Butler, K. Eckstrand, L. Noory, P. Gochman, R. Long, Z. Chen, S. Davis, C. Baker, E. E. Eichler, P. S. Meltzer, S. F. Nelson, A. B. Singleton, M. K. Lee, J. L. Rapoport, M. C. King, and J. Sebat. "Rare structural variants disrupt multiple genes in neurodevelopmental pathways in schizophrenia". In: *Science* 320.5875 (Apr. 2008). [DOI:10.1126/science.1155174] [PubMed:18369103], pp. 539–543.

[73] Y. Zhu, S. Davis, R. Stephens, P. S. Meltzer, and Y. Chen. "GEOmetadb: powerful alternative search engine for the Gene Expression Omnibus". In: *Bioinformatics* 24.23 (Dec. 2008). [PubMed Central:PMC2639278] [DOI:10.1093/bioinformatics/btn520] [PubMed:18842599], pp. 2798–2800.

[74] E. Birney et al. "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project". In: *Nature* 447.7146 (June 2007). [PubMed Central:PMC2212820] [DOI:10.1038/nature05874] [PubMed:17571346], pp. 799–816.

[75] S. R. Davis and P. S. Meltzer. "Modeling synovial sarcoma: timing is everything". In: *Cancer Cell* 11.4 (Apr. 2007). [DOI:10.1016/j.ccr.2007.03.016] [PubMed:17418406], pp. 305–307.

[76] S. Davis and P. S. Meltzer. "GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor". In: *Bioinformatics* 23.14 (July 2007). [DOI:10.1093/bioinformatics/btm254] [PubMed:17496320], pp. 1846–1847.

[77] J. J. Johnston, R. L. Walker, S. Davis, F. Facio, J. T. Turner, D. P. Bick, D. L. Daentl, J. W. Ellison, P. S. Meltzer, and L. G. Biesecker. "Zoom-in comparative genomic hybridisation arrays for the characterisation of variable breakpoint contiguous gene syndromes". In: *J. Med. Genet.* 44.1 (Jan. 2007). [PubMed Central:PMC2597909] [DOI:10.1136/jmg.2006.042473] [PubMed:17098889], e59.

[78] J. Kamradt, V. Jung, K. Wahrheit, L. Tolosi, J. Rahnenfuehrer, M. Schilling, R. Walker, S. Davis, M. Stoeckle, P. Meltzer, and B. Wullich. "Detection of novel amplicons in prostate cancer by comprehensive genomic profiling of prostate cancer cell lines using oligonucleotide-based arrayCGH". In: *PLoS ONE* 2.8 (2007). [PubMed Central:PMC1940319] [DOI:10.1371/journal.pone.0000769] [PubMed:17712417], e769.

[79] K. T. Kim, K. Baird, S. Davis, O. Piloto, M. Levis, L. Li, P. Chen, P. Meltzer, and D. Small. "Constitutive Fms-like tyrosine kinase 3 activation results in specific changes in gene expression in myeloid leukaemic cells". In: *Br. J. Haematol.* 138.5 (Sept. 2007). [DOI:10.1111/j.1365-2141.2007.06696.x] [PubMed:17686054], pp. 603–615.

[80] N. B. Sutter, C. D. Bustamante, K. Chase, M. M. Gray, K. Zhao, L. Zhu, B. Padhukasahasram, E. Karlins, S. Davis, P. G. Jones, P. Quignon, G. S. Johnson, H. G. Parker, N. Fretwell, D. S. Mosher, D. F. Lawler, E. Satyaraj, M. Nordborg, K. G. Lark, R. K. Wayne, and E. A. Ostrander. "A single IGF1 allele is a major determinant of small size in dogs". In: *Science* 316.5821 (Apr. 2007). [PubMed Central:PMC2789551] [DOI:10.1126/science.1137045] [PubMed:17412960], pp. 112–115.

[81] G. E. Crawford, S. Davis, P. C. Scacheri, G. Renaud, M. J. Halawi, M. R. Erdos, R. Green, P. S. Meltzer, T. G. Wolfsberg, and F. S. Collins. "DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays". In: *Nat. Methods* 3.7 (July 2006). [PubMed Central:PMC2698431] [DOI:10.1038/nmeth888] [PubMed:16791207], pp. 503–509.

[82] G. E. Crawford, I. E. Holt, J. Whittle, B. D. Webb, D. Tai, S. Davis, E. H. Margulies, Y. Chen, J. A. Bernat, D. Ginsburg, D. Zhou, S. Luo, T. J. Vasicek, M. J. Daly, T. G. Wolfsberg, and F. S. Collins. "Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS)". In: *Genome Res.* 16.1 (Jan. 2006). [PubMed Central:PMC1356136] [DOI:10.1101/gr.4074106] [PubMed:16344561], pp. 123–131.

[83] S. Davis and P. S. Meltzer. "Ewing's sarcoma: general insights from a rare model". In: *Cancer Cell* 9.5 (May 2006). [DOI:10.1016/j.ccr.2006.05.003] [PubMed:16697953], pp. 331–332.

[84] P. C. Scacheri, G. E. Crawford, and S. Davis. "Statistics for ChIP-chip and DNase hypersensitivity experiments on NimbleGen arrays". In: *Meth. Enzymol.* 411 (2006). [DOI:10.1016/S0076-6879(06)11014-9] [PubMed:16939795], pp. 270–282.

[85] P. C. Scacheri, S. Davis, D. T. Odom, G. E. Crawford, S. Perkins, M. J. Halawi, S. K. Agarwal, S. J. Marx, A. M. Spiegel, P. S. Meltzer, and F. S. Collins. "Genome-wide analysis of menin binding provides insights into MEN1 tumorigenesis". In: *PLoS Genet.* 2.4 (Apr. 2006). [PubMed Central:PMC1428788] [DOI:10.1371/journal.pgen.0020051] [PubMed:16604156], e51.

[86] K. Baird, S. Davis, C. R. Antonescu, U. L. Harper, R. L. Walker, Y. Chen, A. A. Glatfelter, P. H. Duray, and P. S. Meltzer. "Gene expression profiling of human sarcomas: insights into sarcoma biology". In: *Cancer Res.* 65.20 (Oct. 2005). [DOI:10.1158/0008-5472.CAN-05-1699] [PubMed:16230383], pp. 9226–9235.

[87] S. Durinck, Y. Moreau, A. Kasprzyk, S. Davis, B. De Moor, A. Brazma, and W. Huber. "BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis". In: *Bioinformatics* 21.16 (Aug. 2005). [DOI:10.1093/bioinformatics/bti525] [PubMed:16082012], pp. 3439–3440.

[88] C. G. Son, S. Bilke, S. Davis, B. T. Greer, J. S. Wei, C. C. Whiteford, Q. R. Chen, N. Cenacchi, and J. Khan. "Database of mRNA gene expression profiles of multiple human organs". In: *Genome Res.* 15.3 (Mar. 2005). [PubMed Central:PMC551571] [DOI:10.1101/gr.3124505] [PubMed:15741514], pp. 443–450.

[89] S. Davis and V. L. Nimgaonkar. "Impact of overlapping recruitment on linkage analysis of complex disorders: simulation studies". In: *Am. J. Med. Genet.* 105.2 (Mar. 2001). [PubMed:11304826], pp. 141–144.

[90] R. H. Duerr, M. M. Barmada, L. Zhang, S. Davis, R. A. Preston, L. J. Chensny, J. L. Brown, G. D. Ehrlich, D. E. Weeks, and C. E. Aston. "Linkage and association between inflammatory bowel disease and a locus on chromosome 12". In: *Am. J. Hum. Genet.* 63.1 (July 1998). [PubMed Central:PMC1377250] [DOI:10.1086/301929] [PubMed:9634527], pp. 95–100.

[91] S. Davis, E. Sobel, M. Marinov, and D. E. Weeks. "Analysis of bipolar disorder using affected relatives". In: *Genet. Epidemiol.* 14.6 (1997). [DOI:3.0.CO;2-Y] [PubMed:9433550], pp. 605–610.

[92] S. Davis and D. E. Weeks. "Comparison of nonparametric statistics for detection of linkage in nuclear families: single-marker evaluation". In: *Am. J. Hum. Genet.* 61.6 (Dec. 1997). [PubMed Central:PMC1716077] [DOI:10.1086/301635] [PubMed:9399893], pp. 1431–1444.

[93] C. Julier, M. Delepine, B. Keavney, J. Terwilliger, S. Davis, D. E. Weeks, T. Bui, X. Jeunemaitre, G. Velho, P. Froguel, P. Ratcliffe, P. Corvol, F. Soubrier, and G. M. Lathrop. "Genetic susceptibility for human familial essential hypertension in a region of homology with blood pressure linkage on rat chromosome 10". In: *Hum. Mol. Genet.* 6.12 (Nov. 1997). [PubMed:9328471], pp. 2077–2085.

[94] J. R. O'Connell, S. Davis, and D. E. Weeks. "Analysis of a complex oligogenic disease". In: *Genet. Epidemiol.* 14.6 (1997). [DOI:3.0.CO;2-K] [PubMed:9433591], pp. 861–866.

[95] D. E. Weeks, S. Davis, M. Schroeder, and L. R. Goldin. "Nonparametric simulation based linkage statistics for general pedigrees". In: *J. Rheumatol.* 24.1 (Jan. 1997). [PubMed:9002040], pp. 206–207.

[96] S. Davis, M. Schroeder, L. R. Goldin, and D. E. Weeks. "Nonparametric simulation-based statistics for detecting linkage in general pedigrees". In: *Am. J. Hum. Genet.* 58.4 (Apr. 1996). [PubMed Central:PMC1914666] [PubMed:8644751], pp. 867–880.

Publicly Available Software

In total, my software is downloaded by more than 40,000 users per year. Visit listed URL for more details.

GenomicDataCommons	`https://github.com/Bioconductor/GenomicDataCommons`
wdlRunR	`https://github.com/seandavi/wdlRunR`
RCircos	`http://cran.r-project.org/web/packages/RCircos/index.html`
GEOquery	`http://www.bioconductor.org/packages/release/bioc/html/GEOquery.html`
ACME	`http://www.bioconductor.org/packages/release/bioc/html/ACME.html`
biomaRt	`http://www.bioconductor.org/packages/release/bioc/html/biomaRt.html`
methylumi	`http://www.bioconductor.org/packages/release/bioc/html/methylumi.html`

GEOmetadb	http://www.bioconductor.org/packages/release/bioc/html/GEOmetadb.html
SRAdb	http://www.bioconductor.org/packages/release/bioc/html/SRAdb.html
ngCGH	https://github.com/seandavi/ngCGH
Complete Genomics Tools	https://github.com/seandavi/CompleteGenomicsTools

Social Media Reach

Twitter	https://twitter.com/seandavis12, 2,100 followers, bioinformatics, genomics, data science, R, and scientific IT
Biostars	https://www.biostars.org/u/287/, An online community for informatics questions and answers, my contributions rank 7 out of 18,000 users
Bioconductor	https://support.bioconductor.org/u/490/, An online support community for Bioconductor, my contributions rank 3 out of 8,000 users
GitHub	https://github.com/seandavi