Sean Davis

Curriculum Vita

2009– Present 2007–2008 2005–2007 2002–2005 9531 Rommel Drive Columbia, MD 21046 ⊠ sdavis2@mail.nih.gov 'n http://seandavi.github.io/

Google Scholar–i10-index: 75; h-index: 45; 16,227 citations

Staff Scientist, Center for Cancer Research, National Cancer Institute.
Research Fellow, National Cancer Institute.
Research Fellow, National Human Genome Research Institute.
Clinical Fellow, Combined Johns Hopkins and National Cancer Institute Pe-
diatric 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

Education and Professional Experience

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, NIH Intramural Representative, NIH Data Commons working group 2017
 - December, Co-organizer, NIH Hour of Code, Data Science Special Interest Group, NIH, 2017 Bethesda, MD
 - November, NIH Representative to US Department of Agriculture, Blueprint for USDA Ef-2017 forts in Agricultural Animal Genomics, Beltsville, MD
- August, 2017 NIH Intramural Representative, NIH Data Commons Review Committee
 - February, Organizer, NIH/NIST Medical Devices Cybersecurity Workshop, Bethesda, MD 2017
- January, Cancer Moonshot Blue Ribbon Panel Implementation Working Group, National 2017-present Cancer Data Ecosystem
 - January, Organizer,Globus Data Platform Hackathon and Workshop, NIH, Bethesda, 2017 $\,$ MD

January,	$NCI\ Representative,$	NHLBI To	pMed Data	Commons	Planning	Workshop
2017						

December, Founding Member, NIH Data Science Special Interest Group 2016-present

July, $\it NCI \, Representative, NIH$ Data Commons Reference Dataset Working Group 2016-July,

2017

- 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- Presidential Subcommittee on AI and Machine Learning, Cancer Moonshot November, Initiative 2016
- December, NCI representative and panel member, FDA Informatics and Precision Medicine 2015 Workshop
 - January, Co-organizer, NCBI Genomics and Bioinformatics Hackathon 2016
- November, NCI Cancer Cloud Pilot, Leading Intramural Research Program evaluation and 2015-present 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, CCR Representative to CBIIT Strategic Planning Committee 2015-present
 - $2015 \quad {\rm NCI\,Intramural\,Research\,Program\,Representative,\,NCI\,Cancer\,Cloud\,Initiative}$
 - 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, Intramural NIH representative, BD2K Software Development Conference $2014\,$
 - January, *Organizer and Instructor*, Bioinformatics Summer Course, Riberão Preto Med-2014 ical 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, NIH Representative, Big Data Conference, Agricultural Research Service, 2013 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
 - ${\it 2009-2010~Chair, Center~for~Cancer~Research~Bioinformatics~Planning~and~Implementation} \\ {\it Committee}$
 - ${\bf September},\ \textit{NIH}\ \textit{Representative},\ {\bf NIFA},\ {\bf USDA},\ {\bf Genomics}\ {\bf and}\ {\bf Bioinformatics}\ {\bf Workshop},$
 - 2010 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, A Data Ecosystem for Biomedical Big Data, Grand Rounds, Wake Forest School
 - 2018 of Medicine, Winston-Salem, NC
- November, Thoughts on Components of an Agricultural Data Ecosystem, Blueprint for
 - 2017 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, A cloud-based data ecosystem for cancer research, Dana Farber Cancer Institute, 2017 Boston, MA
 - January, Open APIs with R and Bioconductor, Harvard/Boston R/Bioconductor Meetup, 2017 Boston, MA
 - October, Big data science careers in Government, University of California, Riverside, CA 2016
 - October, Democratizing access to Big Cancer Data, Midatlantic Bioinformatics Confer-2016 ence, 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, Introduction to RNA-Seq Data Analysis, NCI $2016\,$
 - January, Introduction to Bioconductor: Code and Practice, DataCommunityDC, Wash-2016 ington DC
 - October, Course organizer and faculty: Harvard School of Engineering and Applied Sci-2015 ence: CS290 Extreme Computing
 - September, BioIT: A Symbiotic Relationship Between Biological Research and IT Infras-2015 tructure, 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, Introduction to RNA-Seq Data Analysis, NCI 2015
 - January, Introduction to R and Bioconductor, NCI 2015
 - December, Introduction to R for Data Manipulation and Visualization, NIH 2014
 - June, 2014 Course Organizer, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
 - February, One-day course on RNA-seq data analysis and visualization, CIT, NIH 2014

- February, Reproducible research using the Snakemake workflow toolkit on Biowulf, CIT, $2014\,$ NIH
- January, *Course Organizer*, Bioinformatics Summer Course, Riberão Preto Medical 2014 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, Planning for High Performance and Scientific Computing at the NIH, Agricul-2013 tural Research Service, USDA, Beltsville, MD
- November 6, Introduction to Next Generation Sequencing Technologies, Bioinformatics 2012 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, AACR Molecular Biology in Clinical Oncology (one-week course), Aspen & except 2008 Snowmass, CO
 - March 28, Featured Speaker, Bioinformatics for Medical Genetics Symposium, American 2012 College of Medical Genetics, Charlotte, NC
 - February Advanced R and Bioconductor Workshop on High-Throughput Genetic Analy-27-28, 2012 sis, Fred Hutchinson Cancer Research Center, Seattle, WA
 - January 13, Introduction to Next-Generation Sequencing: Mapping and Counting, Center 2012 of Excellence in Integrative Cancer Biology and Genomics Seminar Series, NCI
 - November High-resolution Views of the Cancer Genome Using Next-Generation Sequenc-18, 2011 ing 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, Complete Genomics Data Tutorial, Center for Cancer Research, NCI 2011
- October 22, BioConductor: Tools for the Comprehension of Genomic Data, Translational 2010 Genomics Conference, Center of Excellence in Integrative Cancer Biology and Genomics annual meeting
- October 22, Bioinformatics at the Center for Cancer Research, An Update, Center of Excel-2010 lence in Integrative Cancer Biology and Genomics annual meeting
- September 9, Potential Applications of Genomics in Agriculturally Important Species, NIFA, 2010 U.S. Department of Agriculture

- Spring, 2010 Microarray Data Analysis Using R and Bioconductor, Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University
- February 23, Genomic Technologies for Viewing the Cancer Genome, Georgetown University 2010
 - July, 2010 Course Organizer, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
 - November Structural Variant Discovery in Short Read Sequencing using R and Bioconduc-
 - 18, 2009 tor, Fred Hutchinson Cancer Research Center, Seattle, WA
 - November Instructor, High throughput sequence analysis tools and approaches with Bio-
 - 18-20, 2009 conductor, Fred Hutchinson Cancer Research Center, Seattle, WA
 - March 17, High-resolution Views of the Cancer Genome: Tools for examining the genome
 - 2009 in a high-throughput way, Case Western Reserve University, Cleveland, OH
- February 12, Genomics for the Pediatrician: An Overview of Genomics Technologies, Pedi-
 - 2009 atric 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
- o Breast Cancer Research
- Cancer Research
- o Clinical Cancer Research
- Database
- Endocrine-Related Cancer
- EURASIP Journal on Bioinformat- PLoS Computational Biology ics and Systems Biology
- Genetic Epidemiology
- o Genomics

- Genome Research
- Gigascience
- Molecular Carcinogenesis
- Molecular Cancer Research
- Nature Methods
- Nucleic Acids Research
- o Pigment Cell & Melanoma Research
- 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).
- 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.
- 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.
- 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.
- 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.
- 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].
- Sean Davis and Ewy Mathe, eds. Statistical Genomics. Springer, 2016.

- [8] 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.
- [9] 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.
- [10]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.
- [11] 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.
- [12] 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.
- [13] 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.
- [14] 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 Can-*

- cer Res. Treat. 150.2 (Apr. 2015). [PubMed Central:PMC4989123] [DOI:10.1007/s10549-015-3314-6] [PubMed:25773928], pp. 457–466.
- [15] 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.
- [16] 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.
- [17] 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.
- [18] 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.
- [19] 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.
- [20] 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.
- [21] 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 compara-

- tive genomic hybridization (CGH) arrays". In: $PLoS\ ONE\ 10.3\ (2015)$. [PubMed Central:PMC4357472] [DOI:10.1371/journal.pone.0116078] [PubMed:25764003], e0116078.
- [22] 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.
- [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* (Apr. 2015). [DOI:10.18632/oncotarget.3268] [PubMed:25929339].
- [24] 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. Mc-Cleish, 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.
- [25] 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. "Genomewide 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.
- [26] 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.
- [27] 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.
- [28] 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.
- [29] 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 Cen-

- $tral: PMC4893961] \ [DOI: 10.1158/0008-5472. CAN-12-3342] \ [PubMed: 23856246], pp.\ 4372-4382.$
- [30] 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.
- [31] 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.
- [32] 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. "Wholegenome 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.
- [33] 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.
- [34] 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.
- [35] 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.
- [36] 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] 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.
- [39] 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.
- [40] 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.
- [41] 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.
- [42] 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
- [43] 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 paraffinembedded tissue samples". In: *Methods Mol. Biol.* 823 (2012). [DOI:10.1007/978-1-60327-216-2₈] [PubMed:22081342], pp. 107–118.
- [44] 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.

- [45] 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 Κ gene due to activation of Wnt/Κ-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.
- [46] G. Zoppoli, S. Solier, W. C. Reinhold, H. Liu, J. W. Connelly, A. Monks, R. H. Shoe-maker, 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.
- [47] 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.
- [48] 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.
- [49] 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.
- [50] 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.
- [51] 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.
- [52] 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.

- [53] 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-γlinksultravioletradiationtomelanomagenesis In: Nature 469.7331 (Jan. 2011). [PubMed Central:PMC3140101] [DOI:10.1038/nature09666] [PubMed:21248750], pp. 548–553.
- [54] 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.
- [55] 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.
- [56] 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.
- [57] 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.
- [58] 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.
- [59] 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.
- [60] 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.
- [61] 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.
- [62] 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.
- [63] 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.
- [64] 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.
- [65] 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.
- [66] 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.
- [67] 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.
- [68] 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.

- [69] 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.
- [70] 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.
- [71] 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.
- [72] 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.
- [73] 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.
- [74] 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.
- [75] 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.
- [76] 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.
- [77] 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.
- [78] 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.

- [79] 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.
- [80] 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.
- [81] 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.
- [82] 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.
- [83] 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.
- [84] 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
- [85] 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.
- [86] 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.
- [87] 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.
- [88] 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.

- [89] 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.
- [90] 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.
- [91] 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.
- [92] 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.
- [93] 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.
- [94] 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.
- [95] 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.

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