updated 10/25/18

DONALD F. CONRAD | CURRICULUM VITAE

Associate Professor and Chief, Division of Genetics
Oregon National Primate Research Center
Oregon Health & Science University
Portland, OR 97239

Phone: 503-346-5432
Cell: 314-452-3893
Email: conradon@ohsu.edu
Web: www.genetics.wustl.edu/dclab

EDUCATION

A.B., Biochemistry and Molecular Biology – Dartmouth College	1999
M.Sc., Epidemiology, advised by Julie Parsonnet and Atsuko Shibata – Stanford School of Medicine	2000
Ph.D., Human Genetics, advised by Jonathan Pritchard – The University of Chicago	2007
Postdoctoral fellow, advised by Matt Hurles – Wellcome Trust Sanger Institute, Cambridge, UK	2007-2010

ACADEMIC POSITIONS/ EMPLOYMENT

Associate Professor and Chief, Division of Genetics, Oregon National Primate Research Center	2018-present
Associate Professor, Genetics and Pathology & Immunology, Washington University, St Louis, MO	2017-2018
Assistant Professor, Genetics and Pathology & Immunology, Washington University, St Louis, MO	2011-2017
Statistical Programmer, Genaissance Pharmaceuticals, New Haven, CT	2002
Epidemiologist, DzGenes LLC, St. Louis, MO	2002-2002

UNIVERSITY APPOINTMENTS AND COMMITTEES

Pediatrics Department Search Committee, Director of Genetics Division, Washington University	2016-2017
Genetics Department Seminar Series Director, Washington University	2012-2018
Genetics Department Faculty Search Committee, Washington University	2012-2015

HONORS AND AWARDS

Fulbright Specialist Grant	2017
Inducted into Dartmouth College Sports Hall of Fame	2014
Finalist for Postdoctoral Trainee (Basic) award, ASHG	2008
Best Dissertation in Biological Sciences (honorable mention), The University of Chicago	2008
NCAA DI Champion Track and Field (Team), Stanford University	2000
Ranked 14th in the USA (Individual, 10k)	2000
Captain of the Dartmouth Track and Field, Cross-Country teams (4 times)	1997-1999
Ivy League Champion Track and Field (Individual, 10k)	1997

EDITORIAL RESPONSIBILITIES

Editorial board of *Genome Research*	2014-present
Editorial board of *Biology of Reproduction*	2013-present

Editorial board of *Andrology* 2012-present

Articles or proposal refereed

146 articles for 39 Journals: Nature (13x), Science, American Journal of Human Genetics, Andrology, Bioinformatics, Biological Psychiatry, Biology of Reproduction, BMC Biology, Briefings in Functional Genomics, Cell & Tissue Research, Chromosome Research, CSH Protocols, Development, EMBO Molecular Medicine, European Journal of Human Genetics, Fertility & Sterility, Forensic Science International: Genetics, Genetics, Genome Biology, Genome Research, Human Heredity, Human Molecular Genetics, Human Mutation, Journal of Clinical Investigation, Journal of Pharmacogenomics, Molecular Biology and Evolution, Molecular Ecology, Nature Communications, Nature Genetics, Nature Methods, Nature Reviews Genetics, Neurogenetics, Pediatrics, PLoS Genetics, PLoS ONE, PNAS, Systems Biology in Reproductive Medicine, Trends in Genetics.

United States-Israel Binational Agricultural Research and Development Fund (BARD). National Science Foundation of Switzerland

PROFESSIONAL SOCIETIES AND ORGANIZATIONS

American Society of Andrology	2010-present
American Society of Human Genetics	2005-present
Society for the Study of Reproduction	2018-present

INVITED PROFESSORSHIPS AND LECTURESHIPS

ASA-EAA Exchange Lecture, European Congress of Andrology, Budapest	2018
Department Seminar, Johns Hopkins University	2018
Institute of Genomic Medicine, University of Newcastle, UK	2017
Human Genome and Healthcare, Royal Society in London, UK	2017
International Congress of Andrology, Copenhagen	2017
Department Seminar, University of Tartu, Estonia	2017
Department Seminar, ONPRC, Oregon Health and Science University	2017
Society for Reproductive Investigation, Orlando	2017
Department Seminar, Dept. of Human Genetics, University of Michigan	2017
Broad Institute Medical & Population Genetics Seminar	2016
Department Seminar, Indiana State University	2016
Greenwald Symposium, University of Kansas	2016
Department Seminar, Medical College Wisconsin	2016
Portugalia Geneticae, Porto, Portugal	2016
Leena Peltonen School of Human Genetics, Sanger Institute	2015-2017
Eliot B. Shoolman Visiting Professor, Harvard Medical School	2015
Department Seminar, Biology, Columbia University	2014
Invited Seminar, Hayward Genetics Center, Tulane University	2014
Dept. Seminar, Center for Molecular Medicine, Wayne State University	2014
Banbury Center Meeting, Cold Spring Harbor Labs	2014
XXIII North American Testis Workshop, San Antonio	2013

Department Seminar, Dept. of Human Genetics, University of Chicago	2013
Department Seminar, IPATIMUP, Porto, Portugal	2011
Keystone Symposium, Functional Impact of Structural Variation, Steamboat Springs, CO	2011
Department Seminar, Genetics, University College London, UK	2010
anEUploidy Workshop, Split, Croatia	2010
Personal Genomes (session co-chair), Cold Spring Harbor Laboratory, NY	2010
Department of Genetics, Washington University School of Medicine, MO	2010
COGS Symposium, Cambridge Research Institute, Cambridge, UK	2010
Department of Genetics, MD Anderson Cancer Center, Houston, TX	2010
Genomic Disorders Meeting, Cambridge, UK	2010
Department of Genetics and Genomics, Mt. Sinai School of Medicine, NY	2010
Department of Genetics, Albert Einstein College of Medicine, NY	2010
Division of Human Biology, Fred Hutchinson Cancer Research Center, WA	2010
Division of Medical Genetics, University of Geneva School of Medicine, Switzerland	2009
Genetic Anthropology at Fine Scales, Honolulu, HI	2009
Amer. Soc. of Human Genetics (from submitted abstract), Honolulu, HI	2009
CNV Workshop, University of Leicester, UK	2009
Geneforum 2009, Tartu, Estonia)	2009
5th International Meeting on Cryptic Chromosomal Rearrangements in Mental Retardation and Autism, Troina, Sicily	2009
Division of Medical Genetics, University of Geneva School of Medicine, Switzerland	2009
American Society of Human Genetics (from submitted abstract), Philadelphia, PA	2008
anEUploidy Workshop, Geneva, Switzerland	2008
DECIPHER Symposium, Cambridge, UK	2008
Department of Statistics, Oxford University, UK	2007
Human Genome Variation 2007, Barcelona, Spain	2007
Genetics of Complex Traits and Isolated Populations, Turin, Italy	2007
American Society of Human Genetics (from submitted abstract), New Orleans, LA	2006
Department of Human Genetics, University of Pecs, Pecs, Hungary	2006
American Society of Human Genetics (from submitted abstract), Salt Lake City, UT	2005

CONSULTING RELATIONSHIPS AND BOARD MEMBERSHIPS

Site reviewer, March of Dimes Prematurity Research Center	2018
NHGRI/NICHD Workshop on Reproductive Genetics, Discussion Group Co-lead	2018
NICHD Study Section, CHHD-R: Reproduction, Andrology & Gynecology, standing member	2013-present
Consultant, PierianDx	2015-2017
NICHD Special Emphasis Panel, ZHD1 DSR-L 50 1	2017

NICHD/CDC Workshop, Fertility Status and Overall Health, invited participant	2016
NICHD Special Emphasis Panel, ZHD1 DSR-L 50 1	2016
NIH/CSR Genomics of Health and Disease, *ad hoc* reviewer	2016
Consultant, CDC, Served as a consultant on the design of a novel CGH array-based system for newborn screening from blood spots	2012
NIH Study Section, NICHD P01, *ad hoc* reviewer, invited 4 times	2012
NHGRI Special Emphasis Panel, ENCODE technology development, *ad hoc* reviewer	2011

RESEARCH SUPPORT

Governmental

PI, R01HD078641 Genomics Of Spermatogenic Impairment	$2.71M	09/10/14 – 05/31/19
PI, R01MH101810 Modeling The Effects Of Structural Variation In GTEX Data And Mendelian Disease	$1.14M	07/25/13 – 06/30/18
PI, R01MH101810-03S1 Modeling The Effects Of Structural Variation In GTEX Data And Mendelian Disease	$118K	07/01/16 – 06/30/18
PI, R01HG007178 Analysis Of *De Novo* Mutation From Sequencing Of Related Individuals And Cells	$2.05M	05/08/14 – 02/28/19
PI, R01HG007178-04S1 Analysis Of *De Novo* Mutation From Sequencing Of Related Individuals And Cells	$46K	14/09/17 – 02/28/19
Co-I, R01MH100027 Autism Genetics, Phase II: Increasing Representation of Human Diversity	$27.5K	03/25/13 – 02/28/18
Co-I, U54HD087011-01 Washington University Intellectual and Developmental Disabilities Research Center	$32.5K	09/01/15 – 08/31/20

Non-governmental

PI, Research Contract with PierianDx, Variant Clinical Relevance Scoring	$130K	05/01/15 –12/31/16
Co-I, Grant from Children's Discovery Institute of St. Louis Children's Hospital, MC-II-2016-533 Sex-specific Super Enhancer Activity in Glioblastoma	$150K	02/01/16 – 01/31/19

TEACHING RESPONSIBILITIES

Co-director, Bio5488: Genomics, Washington University School of Medicine	2012-2018
Lecturer, Bio621: Computational Statistical Genetics, Washington University School of Medicine	2011-2018
Lecturer, Bio5285: Mammalian Genetics, Washington University School of Medicine	2011-2018
Lecturer, Bio5488: Genomics, Washington University School of Medicine	2011
Guest Lecturer, Wellcome Trust Advanced Course: Design and Analysis of Genetic-based Association Studies	2009-2010
Instructor, Core Bio Writing Course, The University of Chicago	2007
Teaching assistant, The X and the Y, The University of Chicago	2006
Teaching assistant, Human Variation and Disease, The University of Chicago	2004
Teaching assistant, Human Heredity, The University of Chicago	2004
Teaching assistant, Molecular Biology, Dartmouth College	1997

BIBLIOGRAPHY

Peer reviewed manuscripts

1. Kasak L, Punab M, … , **Conrad DF**, Laan M. Bi-allelic Recessive Loss-of-Function Variants in FANCM Cause Non-obstructive Azoospermia. Am J Hum Genet. 103(2):200-212. 2018.
2. Nagirnaja L, Aston KI, **Conrad DF**. Genetic intersection of male infertility and cancer. Fertil Steril. 109(1):20-26. 2018.
3. GTEx Consortium. Genetic effects on gene expression across human tissues. Nature. 550(7675):204-213. 2017.
4. Tan MH, Li Q, … , **Conrad DF**, Samuel CE, O'Connell MA, Walkley CR, Nishikura K, Li JB. Dynamic landscape and regulation of RNA editing in mammals. Nature. 550(7675):249-254. 2017.
5. Lima AC, **Conrad DF**. The long and short of translational control in male germ cells. Biol Reprod. 97(1):2-4. 2017.
6. Lima AC, Jung M, Rusch J, Usmani A, Lopes AM, **Conrad DF**. A Standardized Approach for Multispecies Purification of Mammalian Male Germ Cells by Mechanical Tissue Dissociation and Flow Cytometry. J Vis Exp. (125). 2017.
7. Nagirnaja L, Vigh-Conrad K, **Conrad DF.** How to map the genetic basis for conditions that are comorbid with male infertility. Semin Reprod Med. 35(3):225-230. 2017.
8. Chiang C, Scott AJ, Davis JR, Tsang EK, Li X, Kim Y, Hadzic T, Daman F, Ganel L, GTEx Consortium, Montgomery SB, Battle A, **Conrad DF***, Hall IM*. The impact of structural variation on human gene expression. Nat Genet. 49(5):692-699. 2017.
9. Wu SH, Schwartz RS, Winter DJ, **Conrad DF**, Cartwright RA. Estimating error models for whole genome sequencing using mixtures of dirichlet multinomial distributions. Bioinformatics. Mar 15. 2017.
10. Ho NR, Usmani AR, Yin Y, Ma L, **Conrad DF**. Multiplex shRNA screening of germ cell development by in vivo transfection of mouse testis. G3. 7(1):247-255. 2017.
11. Wilfert AB, Chao KR, Kaushal M, Jain S, Zollner S, Adams DR, **Conrad DF**. Genome-wide significance testing of variation from single case exomes. Nat Genet. 48(12): 1455-1461, 2016.
12. Lima AC, Jung M, Rusch J, Usmani A, Lopes A, **Conrad DF**. Multispecies purification of testicular germ cells. Biol Reprod. Aug 14 2016.
13. Wong SY, Beamer LJ, …., **Conrad DF**, Kozicz T, Morava E. Defining the phenotype and assessing the severity in phosphoglucomutase-1 deficiency. J Pediatr. 175:130-168. 2016.
14. Ho NR, Huang N, **Conrad DF**. Improved detection of disease-associated variation by sex-specific characterization and prediction of genes required for fertility. Andrology. 3(6):1140-9, 2015.
15. Ni B, Lin Y, Sun L, Zhu M, Li Z, Wang H, Yu J, Guo X, Zuo X, Dong J, Xia Y, Wen Y, Wu H, Li H, Zhu Y, Ping P, Chen X, Dai J, Jiang Y, Xu P, Du Q, Yao B, Weng N, Lu H, Wang Z, Zhu X, Yang X, Xiong C, Ma H, Jin G, Xu J, Wang X, Zhou Z, Liu J, Zhang X, **Conrad DF**, Hu Z, Sha J. Low-frequency germline variants across 6p22.2-6p21.33 are associated with non-obstructive azoospermia in Han Chinese men. Hum Mol Genet. 24(19):5628-36, 2015.
16. Lima AC, Carvalho F, Gonçalves J, Fernandes S, Marques PI, Sousa M, Barros A, Seixas S, Amorim A, **Conrad DF**, Lopes AM. Rare double sex and mab-3-related transcription factor 1 regulatory variants in severe spermatogenic failure. Andrology. 3(5):825-33, 2015.
17. Huang N, Wen Y, Guo X, Li Z, Dai J, Ni B, Yu J, Lin Y, Zhou W, Yao B, Jiang Y, Sha J, **Conrad DF***, Hu Z*. A Screen for Genomic Disorders of Infertility Identifies MAST2 Duplications Associated with Nonobstructive Azoospermia in Humans. Biol Reprod. 93(3):61, 2015.
18. Nikolskiy I, **Conrad DF**, Chun S, Fay JC, Cheverud JM, Lawson HA. Using whole-genome sequences of the LG/J and SM/J inbred mouse strains to prioritize quantitative trait genes and nucleotides. BMC Genomics, 6:415, 2015.
19. Rivas MA, Pirinen M, **Conrad DF**,…,MacArthur DG. Impact of predicted protein-truncating genetic variants on the human transcriptome. Science, 8;348(6235):666-9, 2015.
20. Hughes AE, …, **Conrad DF**, …,Graubert TA. Clonal architecture of secondary acute myeloid leukemia defined by single-cell sequencing. PLoS Genetics, 10(7):e1004462. 2014.

21. Byrois J,…, **Conrad DF**,…,Dermitzakis ET. Cis and trans effects of human genomic variants on gene expression. PLoS Genetics,10(8):e1004461. 2014.

22. Jain S, Noordam MJ, Hoshi M, Vallania FL, **Conrad DF**. Validating single cell genomics for the study of renal development. Kidney International, 86(5):1049-55. 2014.

23. MacArthur DG, Manolio TA, Dimmock DP, Rehm HL, Shendure J, Abecasis GR, Adams DR, Altman RB, Antonarakis SE, Ashley EA, Barrett JC, Biesecker LG, **Conrad DF**, Cooper GM, Cox NJ, Daly MJ, Gerstein MB, Goldstein DB, Hirschhorn JN, Leal SM, Pennacchio LA, Stamatoyannopoulos JA, Sunyaev SR, Valle D, Voight BF, Winckler W, Gunter C. Guidelines for investigating causality of sequence variants in human disease. Nature. 508(7497):469-76. 2014.

24. Mulle JG, Pulver AE, McGrath JA, Wolyniec PS, Dodd AF, Cutler DJ, Sebat J, Malhotra D, Nestadt G, **Conrad DF**, …, Warren ST. Reciprocal duplication of the Williams-Beuren syndrome deletion on chromosome 7q11.23 is associated with schizophrenia. Biol Psychiatry. 75(5):371-7, 2014.

25. Grozeva D, Kirov G, **Conrad DF**, Barnes CP, Hurles M, Owen MJ, O'Donovan MC, Craddock N. Reduced burden of very large and rare CNVs in bipolar affective disorder. Bipolar Disord. 15(8):893-8, 2013.

26. Ramu A, Noordam MJ, Schwartz RS, Wuster A, Hurles ME, Cartwright RA, **Conrad DF**. DeNovoGear: de novo indel and point mutation discovery and phasing. Nat Methods. 10(10):985-7, 2013.

27. A. M. Lopes, K. I. Aston, E. Thompson, F. Carvalho, J. Goncalves, N. Huang, R. Matthiesen, M. J. Noordam, I. Quintela, A. Ramu, C. Seabra, A. B. Wilfert, J. Dai, J. M. Downie, S. Fernandes, X. Guo, J. Sha, A. Amorim, A. Barros, A. Carracedo, Z. Hu, M. E. Hurles, S. Moskovtsev, C. Ober, D. A. Paduch, J. D. Schiffman, P. N. Schlegel, D. T. Carrell, **D.F. Conrad**. Human Spermatogenic Failure Purges Deleterious Mutation Load from the Autosomes and Both Sex Chromosomes, including the Gene DMRT1. PLoS Genetics. 9(3):e1003349, 2013.

28. M. Hu, Q. Ayub, J.A. Guerra-Assunção, Q. Long, Z. Ning, N. Huang, I. G. Romero, L. Mamanova, P. Akan, X. Liu, A. J. Coffey, D. J. Turner, H. Swerdlow, J. Burton, M. A. Quail, **D. F. Conrad**, A. J. Enright, C. Tyler-Smith, Y. Xue. Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. Hum Genet. 131(5):665-74, 2012.

29. D. Grozeva, **D. F. Conrad**, C. P. Barnes, M. Hurles, M. J. Owen, M. C. O'Donovan, N. Craddock, G. Kirov. Independent estimation of the frequency of rare CNVs in the UK population confirms their role in schizophrenia. Schizophr Res. 135(1-3):1-7, 2012.

30. D. G. MacArthur, S. Balasubramanian, A. Frankish, N. Huang, J. Morris, K. Walter, L Jostins, Habegger L, Pickrell JK, Montgomery SB, Albers CA, Zhang ZD, **D. F. Conrad**, Lunter G, Zheng H, Ayub Q, DePristo MA, Banks E, Hu M, Handsaker RE, Rosenfeld JA, Fromer M, Jin M, Mu XJ, Khurana E, Ye K, M Kay, G. Saunders, M. M. Suner, T. Hunt, I.H. Barnes, C. Amid, D. Carvalho-Silva, A.H. Bignell, C. Snow, B. Yngvadottir, S. Bumpstead, D. N. Cooper, Y. Xue, I. G. Romero; 1000 Genomes Project Consortium, J. Wang, Y. Li, R. A. Gibbs, S. A. McCarroll, E. T. Dermitzakis,J. K. Pritchard, J.C. Barrett, J. Harrow , M.E. Hurles, M. B. Gerstein, and C. Tyler-Smith. A systematic survey of loss-of-function variants in human protein-coding genes. Science. 335:823-8, 2012.

31. **D. F. Conrad**, J. E. Keebler, M. A. DePristo, S. J. Lindsay, Y. Zhang, F. Casals, Y. Idaghdour, C. L. Hartl, C. Torroja, K. V. Garimella, M. Zilversmit, R. Cartwright, G. A. Rouleau, M. Daly, E. A. Stone, M. E. Hurles, and P. Awadalla. Variation in genome-wide mutation rates within and between human families. Nat Genet, 43:712-4, 2011.

32. R. E. Mills, K. Walter, C. Stewart, R. E. Handsaker, K. Chen, C. Alkan, A. Abyzov, S. C. Yoon, K. Ye, R. K. Cheetham, A. Chinwalla, **D. F. Conrad**, Y. Fu, F. Grubert, I. Hajirasouliha, F. Hormozdiari, L. M. Iakoucheva, Z. Iqbal, S. Kang, J. M. Kidd, M. K. Konkel, J. Korn, E. Khurana, D. Kural, H. Y. Lam, J. Leng, R. Li, Y. Li, C. Y. Lin, R. Luo, X. J. Mu, J. Nemesh, H. E. Peckham, T. Rausch, A. Scally, X. Shi, M. P. Stromberg, A. M. Sttz, A. E. Urban, J. A. Walker, J. Wu, Y. Zhang, Z. D. Zhang, M. A. Batzer, L. Ding, G. T. Marth, G. McVean, J. Sebat, M. Snyder, J. Wang, K. Ye, E. E. Eichler, M. B. Gerstein, M. E. Hurles, C. Lee, S. A. McCarroll, and J. O. Korbel. Mapping copy number variation by population-scale genome sequencing. Nature, 470:59-65, 2011.

33. The 1000 Genomes Project Consortium. A map of human genome variation from population scale sequencing. Nature, 467:1061-73, 2010.

34. A. W. Pang, J. R. Macdonald, D. Pinto, J. Wei, M. A. Ra q, **D. Conrad**, H. Park, M. Hurles, C. Lee, J. C. Venter, E. Kirkness, S. Levy, L. Feuk, and S. W. Scherer. Towards a comprehensive structural variation map of an individual human genome. Genome Biol, 11:R52, 2010.

35. K. A. Vigh-Conrad, **D. F. Conrad**, and D. Preuss. A protein allergen microarray detects specific IgE to pollen surface, cytoplasmic and commerical allergen extracts. PLoS One, 5:e10174, 2010.

36. **D. F. Conrad**, C. P. Bird, B. Blackburne, S. Lindsay, L. Mamanova, C. Lee, D. J. Turner, and M. E. Hurles. Mutation spectrum revealed by sequencing human germline CNVs. Nat Genet, 42:385-91, 2010.

37. Wellcome Trust Case Control Consortium. Genome-wide association study of copy number variation in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 464:713-20, 2010.

38. B. Schuster-Bckler, **D. Conrad**, and A. Bateman. Dosage sensitivity shapes the evolution of copy-number varied regions. PLoS One, 5:e9474, 2010.

39. **D. F. Conrad*,** D. Pinto*, R. Redon, L. Feuk, O. Gokcumen, Y. Zhang, J. Aerts, T. D. Andrews, C. Barnes, P. Campbell, T. Fitzgerald, M. Hu, C. H. Ihm, K. Kristiansson, D. G. MacArthur, J. R. MacDonald, I. Onyiah, A. W. C. Pang, S. Robson, K. Stirrups, A. Valsesia, K. Walter, J. Wei, C. Tyler-Smith, N. Carter, C. Lee, S. Scherer, and M. Hurles. Origins and functional impact of copy number variation in the human genome. Nature, 464:704-12, 2010.

40. Y. Xue, X. Zhang, N. Huang, A. Daly, C. J. Gillson, D. G. Macarthur, B. Yngvadottir, A. C. Nica, C. Woodwark, Y. Chen, **D. F. Conrad**, Q. Ayub, S. Q. Mehdi, P. Li, and C. Tyler-Smith. Population differentiation as an indicator of recent positive selection in humans: an empirical evaluation. Genetics, 183:1065-77, 2009.

41. A. E. Murmann, **D. F. Conrad**, H. Mashek, C. A. Curtis, R. I. Nicolae, C. Ober, and S. Schwartz. Inverted duplications on acentric markers: mechanism of formation. Hum Mol Genet, 18:2241-56, 2009.

42. K. B. Schroeder, M. Jakobsson, M. H. Crawford, T. G. Schurr, S. M. Boca, **D. F. Conrad**, R. Y. Tito, L. P. Osipova, L. A. Tarskaia, S. I. Zhadanov, J. D. Wall, J. K. Pritchard, R. S. Malhi, D. G. Smith, and N. A. Rosenberg. Haplotypic background of a private allele at high frequency in the Americas. Mol Biol Evol, 26:995-1016, 2009.

43. T. J. Pemberton, M. Jakobsson, **D. F. Conrad**, G. Coop, J. D. Wall, J. K. Pritchard, P. I. Patel, and N. A. Rosenberg. Using population mixtures to optimize the utility of genomic databases: linkage disequilibrium and association study design in India. Ann Hum Genet, 72:535{46, 2008.

44. R. A. Kumar, S. KaraMohamed, J. Sudi, **D. F. Conrad**, C. Brune, J. A. Badner, T. C. Gilliam, N. J. Nowak, Cook E. H., W. B. Dobyns, and S. L. Christian. Recurrent 16p11.2 microdeletions in autism. Hum Mol Genet, 17:628-38, 2008.

45. R. Redon, S. Ishikawa, K. R. Fitch, L. Feuk, G. Perry, T. D. Andrews, H. Fiegler, M. H. Shapero, A. R. Carson, W. Chen, E. K. Cho, S. Dallaire, J. Freeman, … , **D. F. Conrad**, X. Estivill, C. Tyler-Smith, N. P. Carter, H. Aburatani, C. Lee, K. W. Jones, S. W. Scherer, and M. E. Hurles. Global variation in copy number in the human genome. Nature, 444:444-454, 2006.

46. **D. F. Conrad*,** M. Jakobsson*, G. Coop*, X. Wen, J. D. Wall, N. A. Rosenberg, and J. K. Pritchard. A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. Nat Genet, 38:1251-1260, 2006.

47. D. Falush, M. Torpdahl, X. Didelot, **D. F. Conrad**, D. J. Wilson, and M. Achtman. Mismatch induced speciation in salmonella. Philos Trans R Soc Lond B Biol Sci, 361:2045-2053, 2006.

48. **D. F. Conrad**, T. D. Andrews, N. P. Carter, M. E. Hurles, and J. K. Pritchard. A high-resolution survey of deletion polymorphism in the human genome. Nat Genet, 38:75-81, 2006.

49. J. Goldman, **D. F. Conrad**, C. Ley, D. Halperin, M. delaLuzSanchez, R. Villacorta, and J. Parsonnet. Validation of Spanish language dyspepsia questionnaire. Dig Dis Sci, 47:624-40, 2002.

Invited publications (reviews, book chapters)

1. K. I. Aston and **D. F. Conrad**. The sperm genome: effect of aneuploidies, structural variation, single nucleotide changes, and DNA damage on embryogenesis and development, chapter in: Paternal influences on human reproductive success (ed. DT Carrell). Cambridge University Press, 2013.

2. K. I. Aston and **D. F. Conrad**. A review of genome-wide approaches to study the genetic basis for spermatogenic defects. Methods Mol Biol. 927:397-410. 2013.

3. **D. F. Conrad**. Meeting on big mutations addresses big questions in human genetics. Genome Med, 3:12, 2011.

4. **D. F. Conrad** and M. E. Hurles. The population genetics of structural variation. Nat Genet, 39:S30-6, 2007.

5. **D. F. Conrad** and J. K. Pritchard. Population Genetics and Disease, chapter in: Genes and common diseases-genetics in modern medicine (eds. AF Wright and ND Hastie). Cambridge University Press, 2007.

Movies, videotapes, etc.

1. **D. F. Conrad.** "Copy number variation and association studies", in Marchini, J. (ed.), Statistical Methods for the Analysis of Genome-Wide Association Studies: Practical advice and guidance, The Biomedical & Life Sciences Collection, Henry Stewart Talks Ltd, London (online at https://hstalks.com/t/873/copy-number-variation-and-association-studies/?biosci), 2008.
2. **D. F. Conrad.** "Population genetics of structural variation", in Scherer, S. (ed.), Copy Number Variation: , The Biomedical & Life Sciences Collection, Henry Stewart Talks Ltd, London (online at https://hstalks.com/t/1396/population-genetics-of-structural-variation/?biosci), 2009.