**Curriculum vitae**

**Richard M. Myers, Ph.D.**

**Title** Faculty Investigator, Director and President, HudsonAlpha Institute for Biotechnology, Huntsville, Alabama

Adjunct Professor, Department of Genetics, University of Alabama at Birmingham School of Medicine

**Contact Information**

Address: HudsonAlpha Institute for Biotechnology

601 Genome Way

Huntsville, AL 35806

Telephone: 256-327-0431

FAX: 256-327-0978

email: rmyers@hudsonalpha.org

eRA Commons: MYERS.RICHARDM

Assistant:Kathy Rader

Telephone: 256-327-0432

email: krader@hudsonalpha.org

**Personal Information**

Born: March 24, 1954

**Education, Research and Professional Experience**

2008-present Faculty Investigator, Director and President, HudsonAlpha Institute for Biotechnology, Huntsville, Alabama

Adjunct Faculty Member, Department of Genetics, University of Alabama at Birmingham Medical Center

2002-2008 Stanford W. Ascherman Professor and Chairman, Department of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine

1996-2002 Professor of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine

1993 - 1996 Associate Professor of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine

1990-1993 Associate Professor of Physiology and Biochemistry and Biophysics, and Director, Human Genome Center, University of California, San Francisco

1986-1990 Assistant Professor of Physiology and Biochemistry and Biophysics, University of California, San Francisco

1982-1985 Postdoctoral Fellow, Department of Biochemistry & Molecular Biology, Harvard University with Dr. Tom Maniatis

1977-1982 Graduate Student, Department of Biochemistry, University of California, Berkeley with Dr. Robert Tjian (awarded Ph.D. in Biochemistry, 1982)

1972-1977 Undergraduate Student, Department of Biology, University of Alabama, Tuscaloosa; research with Dr. Clifford Hand and Dr. John Hardman (awarded B.S. in Biochemistry, 1977)

**Research Interests**

Genomic and genetic analysis of human traits and diseases, including childhood genetic disorders, multiple types of cancer, Parkinson disease, psychiatric disorders, amyotrophic lateral sclerosis, autoimmune diseases, and natural variation; genome-scale analysis of *cis*-acting regulatory sequences, DNA binding proteins and epigenetic action involved in human gene regulation; genetics and genomics of differential responses to drugs and environmental agents.

**Professional Activities**

**Current Activities**

Member: HeLa Genome Data Access Working Group, National Institutes of Health and the Henrietta Lacks family. 2013 - present.

Member: Scientific Advisory Committee, Department of Energy, Joint Genome Institute, Walnut Creek, CA, 2011 - present.

Member: Scientific Advisory Board, Biogen Idec, Inc. 2011 - present.

Member: Scientific Advisory Board, New York Genome Center, New York City, 2010 - present.

Member: Scientific Advisory Board, DNAnexus, Inc. 2009 - present.

Member: Scientific Advisory Board, Bay City Capital, San Francisco. 2008 - present.

Founder and Consultant: Kailos Genetics, Inc. Huntsville, AL. 2010 - present.

Member: Board of Directors, Leadership Alabama. 2010 - present.

Member: Research Advisory Board, Auburn University. 2010 - present.

Member: Biotechnology Association of Alabama. 2009 - present.

Associate Editor: Genome Research (Cold Spring Harbor Laboratory Press). 1995 - present.

Member: Human Genome Reference Consortium, National Human Genome Research Institute, National Institutes of Health. 2007 - present.

**Past Activities**

Member: External Grant Review Panel. California Institute for Regenerative Medicine. State of California. 2015.

Member: External Advisory Panel, Pharmacogenomics Research Network. National Institutes of Health. 2011 - 2014.

Member and Chair: Ad hoc Study Section, National Human Genome Research Institute, National Institutes of Health. 2014 (two sessions).

Member: Intramural Research Program Blue Ribbon Advisory Panel. National Human Genome Research Institute, National Institutes of Health. 2011 - 2013.

Member: Coordinating Committee for Prioritization of Sequencing Targets, National Human Genome Research Institute, National Institutes of Health. 2003 - 2013.

Member: External Advisory Group, Wisconsin Center of Excellence in Genome Sciences. 2010 - 2013.

Member: NIH Intramural Sequencing Center Working Group, National Human Genome Research Institute, National Institutes of Health. 2006 - 2013.

Founder and Advisor: SwitchGear Genomics, Inc. Menlo Park, CA. 2005 - 2013.

Member: Advisory Council, National Human Genome Research Institute, National Institutes of Health. 2009 - 2012.

Member and Co-chair: ENCODE Data Analysis Working Group, National Human Genome Research Institute, National Institutes of Health. 2008 - 2012.

Chair: Genomics of Gene Expression Workshop, National Human Genome Research Institute, National Institutes of Health. October 2009.

Member: Scientific Director Search Committee, National Human Genome Research Institute, National Institutes of Health. 2009 - 2010.

Member and Chair: ENCODE Data Release Working Group, National Human Genome Research Institute, National Institutes of Health. 2007 - 2011.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 - 2008.

Member: Biotech Advisory Board, Gunn High School, Palo Alto, 2005 - 2009.

Member: Biology and Biotechnology Program Advisory Committee, U.S. Department of Energy. 2001 - 2008.

Member: Scientific Advisory Board, HudsonAlpha Institute for Biotechnology, 2005 - 2008.

Member: Board of Directors, Open Biosystems, Inc. 2007 - 2008.

Member: Scientific Advisory Board, Pharmacogenetics Knowledge Base, Stanford University School of Medicine. 2001- 2008.

Member: Diversity Committee, Stanford University School of Medicine, 2002 - 2008.

Member and Chair: Review Group, Large-scale DNA Sequencing Centers, National Human Genome Research Institute, National Institutes of Health. 2003 - 2006.

Member and Chair: HapMap Advisory Committee, National Human Genome Research Institute, National Institutes of Health. 2002 - 2006.

Member: Advisory Council, National Human Genome Research Institute, National Institutes of Health. 2003 - 2006.

Member: Genome Centers Review Committee, Genome Canada. 2003, 2004.

Member: ENCODE Advisory Committee, National Human Genome Research Institute, National Institutes of Health. 2002 - 2004.

Member and Chair: Industry Liaison Committee, American Society of Human Genetics. 2002 - 2004.

Member: GRASPP (Genome Resources and Sequencing Prioritization Panel), National Human Genome Research Institute, National Institutes of Health. 2001 - 2003.

Member: Web Site Committee, American Society of Human Genetics. 2001 - 2003.

Member: Committee on Functional Genomics, Genetics and Biocomputation, Stanford University School of Medicine, 1999 - 2002.

Member (and Chair 1999 - 2002): Genome Research Review Committee, National Human Genome Research Institute, National Institutes of Health. 1998 - 2002.

Member: Ad hoc Study Section, Sequencing of additional Drosophila Genomes, National Human Genome Research Institute, National Institutes of Health. 2001.

Member: Grant Review Committee, U.S. Department of Energy. 1999.

Member: Board of Directors, American Society of Human Genetics. 1997 - 2001.

Member: Safety Committee, Stanford University, 1996 - 2000.

Member: Ad hoc Study Section, Sequencing of the Rat Genome, National Human Genome Research Institute, National Institutes of Health. 2000.

Member: Intellectual Property Rights Committee, The Human Genome Organization. 1996 - 2000.

Editorial Board Member: Human Molecular Genetics (Oxford University Press). 1992 - 2000.

Member: Special Dean’s Review Committee, Department of Genetics, Duke University School of Medicine. 2000.

Member: Study Section, National Human Genome Research Institute, National Institutes of Health. 1994 - 1998.

Member: Mouse Genomics and Genetics Subgroup, Preclinical Models for Cancer Working Group, National Cancer Institute, National Institutes of Health. 1997 - 1998.

Member: Committee on Stanford University School of Medicine/UCSF Academic Priorities and Strategies for Collaboration, Stanford University, 1996 - 1999.

Member (and Chair, 1995-1996): Program Committee, American Society of Human Genetics, 1993 - 1996.

Co-organizer (with Dr. C. Robertson): Biotechnology Training Grant Symposium, Stanford University, 1995.

Member: Advisory Board, Program in Molecular and Genetic Medicine, Stanford University School of Medicine, 1995 - 1999.

Member: Radioisotope Committee, Stanford University School of Medicine, 1994 - 1999.

Co-organizer (with Dr. G. Barsh), Genetics Seminar Series, 1995.

Member: Initial Review Group, National Center for Human Genome Research, National Institutes of Health. Four site visits, 1990 - present.

Member: Review Committee for Sanger Centre, Wellcome Trust, Cambridge, England. 1995.

Member: GESTEC Review Committees, National Center for Human Genome Research (Washington University GESTEC; Whitehead Institute GESTEC): 1994 - 1996.

Member: Board of Scientific Counselors, National Center for Human Genome Research Intramural Research Program. 1994 - 1996.

Member: Scientific Advisory Board, Neurogenetics Center, Duke University School of Medicine, Research Triangle Park, NC, 1994 - 1995.

Ad hoc Council member, National Center for Human Genome Research, National Institutes of Health, 1993 and 1995.

Associate Editor: PCR: Methods and Applications (Cold Spring Harbor Laboratory Press). 1991 - 1995.

Meeting Co-Organizer: Genome Mapping and Sequencing Meeting, Cold Spring Harbor Laboratory, three years (1992 - 1994).

Meeting Organizer: Human Chromosome 4 Workshop, Stanford University, 1993.

Member of 38 University committees, UCSF. 1986 - 1993.

Co-organizer and Session Chair, "Winding Your Way Through DNA", a joint UCSF-Exploratorium Symposium for the public on understanding the scientific and societal impact of the recombinant DNA revolution. 1992.

**Awards, Fellowships and Honors**

AAAS Fellow, The American Association for the Advancement of Science. 2011.

Leadership Alabama Inductee, Class 20, 2009.

Honorary Doctorate in Humane Letters, December 2005 (University of Alabama).

Blount Initiative Award, October 2003 (University of Alabama).

Pritzker Foundation Award, April 2002 (University of Michigan).

Darden Lecture Award, March 2002 (University of Alabama).

Wills Foundation Award, 1986 - 2003 (at UCSF/Stanford).

Searle Scholar, 1987 - 1990 (at UCSF).

Basil O'Connor Starter Scholar Research Award, 1988 (at UCSF).

Leukemia Society of America Senior Postdoctoral Fellowship, 1984 - 1985 (at Harvard).

Damon Runyon-Walter Winchell Cancer Fund Fellowship, 1982 - 1984 (at Harvard).

Honor Students' Society, 1980 - 1981 (at UC Berkeley).

Regents Fellowship, 1979 - 1980 (at UC Berkeley).

Abraham Rosenberg and Kaiser Fellowships, 1977 - 1978 (at UC Berkeley).

Phi Beta Kappa, 1975 (at University of Alabama).

**Teaching**

Lecturer in Genomics, a graduate course in genomics in the Department of Genetics, University of Alabama at Birmingham School of Medicine, 2010 - present.

Lecturer in Genomic Science, a 4-day short course funded by the NIH to provide training on next-generation DNA sequencing and analysis, with HudsonAlpha and University of Alabama at Birmingham School of Medicine faculty, 2011 - present.

Co-instructor (with Chris Gunter, Neil Lamb and Adam Hott) of BYS400/600, an undergraduate and masters-level graduate course in introductory neuroscience, University of Alabama in Huntsville, Winter/Spring semester, 2010.

Co-instructor (with Mike Cherry, Arend Sidow and Gavin Sherlock) of Genetics 211 ("Genomics”, a course for graduate students), Stanford University School of Medicine, each Winter Quarter, 2002 - 2007.

Co-instructor (with Bob Simoni) of Genetics 106Q, a course in the logic of biological science for undergraduate sophomores at Stanford University, Winter Quarter, 1999 - 2007.

Co-instructor (with Jim Ford, Greg Barsh and other Stanford faculty) and Co-director of Genetics 202 ("Medical Genetics”, a course for first year medical students), Stanford University School of Medicine, each Fall Quarter, 2003 - 2007.

Co-instructor (with Andy Fire) of “Stanford Graduate Summer Institute”, a “boot-camp” to expose beginning Stanford Graduate Students to areas outside their chosen fields, Summer 2006.

Director: Stanford Genome Training Program, Stanford University School of Medicine, 1995 - 2008.

Co-director: Genetics and Developmental Biology Training Program, Stanford University School of Medicine, 2002 - 2008.

Co-instructor of Human Biology 2A (a year-long introductory biology course for undergraduates), Stanford University, 2005 - 2006.

Co-instructor (with Doug Vollrath) of Genetics 222 ("Method and Logic in Experimental Genetics", a course for graduate students), Stanford University School of Medicine, each Winter Quarter, 1995 - 2002; guest lecturer 2003, 2005.

Guest Lecturer: BMI 234 (“Medical Genomics”, a course for graduate students and medical students), Stanford University School of Medicine, Winter Quarter, 2002.

Guest Lecturer: HRP (a course in genetic epidemiology), Stanford University, 2001 - 2005.

Guest Lecturer: Biology 2S (an undergraduate course in biology and bioethics), Stanford University, 2001 - 2007.

Guest Lecturer: Genetics 208 (“Human Genetics”, a course for graduate and medical students), Stanford University School of Medicine, each Spring Quarter, 1999 - 2003.

Director: Genetics Graduate Program, Stanford University School of Medicine, 1993 - 2001.

Guest Lecturer: Course in Genetic Epidemiology, Cold Spring Harbor Laboratories, 2000, 2002.

Co-instructor (with Bob Simoni, David Siegmund, David Cox and David Botstein) of SME2A, B, C (Science, Mathematics and Engineering), a three-quarter course in the principles of science and mathematics for undergraduate non-science majors at Stanford University, 1996 - 1999.

Organizer of the Genome Seminar Series, a three-quarter series for graduate students and postdoctoral fellows in genome science, as part of the Genome Training Program, 1997 - 2000.

Guest Faculty Instructor, CAM Course for first year graduate students, Stanford University, School of Medicine, 1994 and 1995.

Examiner in Qualifying Exams for 59 graduate students at UCSF and Stanford, 1986 - 2009.

Member of Dissertation Committees for 67 graduate students at UCSF and Stanford University, 1986 - 2009.

Co-instructor of Biochemistry 210A and 210B (a course in regulation of biological systems for first year graduate students), Department of Biochemistry & Biophysics, UCSF, seven years (1986-1993).

Co-instructor of Physiology 101 (a course in endocrinology and GI physiology for medical students), Department of Physiology, UCSF, four years (1989-1992).

Co-instructor of Advanced Molecular Cloning Course (a three-week laboratory and lecture course), Cold Spring Harbor Laboratory, four years (1988-1991).

Tutor in the Biochemical Sciences, teaching biochemistry and molecular biology to undergraduates, Harvard University; 1982 - 1985.

Director of a six week laboratory course on DNA cloning techniques, Department of Biology, University of Alabama, 1982.

Teaching Assistant, Department of Biochemistry, University of California, Berkeley, 1979 and 1980.

**Patents**

U.S. Patent Number 4,946,773, August 7, 1990, “Detection of base pair mismatches using RNAase A”, Thomas P. Maniatis and Richard M. Myers.

U.S. Patent Number 6,432,635, August 13, 2002, "Mutations in the cystatin B gene in Progressive Myoclonus Epilepsy", Richard M. Myers, David R. Cox, Len A. Pennacchio, Anna-Elina Lehesjoki and Albert de la Chapelle.

U.S. Patent Number 7,410,759, August 12, 2008, “Compositions and Methods for Diagnosing and Treating Mood Disorders”, Akil, Huda; Bunney, Jr. William E.; Choudary, Prabhakara V.; Evans, Simon J.; Jones, Edward G.; Li, Jun; Lopez, Juan F.; Thompson, Robert C.; Myers, Richard; Tomita, Hiroaki; Vawter, Marquis P.; Watson, Stanley.

**Education Outreach, Community Service and Other Activities**

Lecturer: Biotech 101 and 102, courses for adult non-scientists led by Dr. Neil Lamb at HudsonAlpha Institute. Twice yearly, 2008 - present.

Lab mentor: High school and undergraduate students, HudsonAlpha BioTrain Program, two students each summer, 2008 - present.

Lecturer: High school and middle school classes, several per year, 1990 - 2010.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 - 2008 (see http://genetics.stanford.edu/techmuseum/).

Member: Biotech Advisory Board, Gunn High School Biotechnology Program, Palo Alto, 2005 - 2009.

Coach: Palo Alto YMCA Boys’ Basketball, 1996 - 2001.

Coach: Palo Alto YMCA Girls’ Basketball, 2000 - 2003.

Coach: Palo Alto YBAL Boys’ Baseball, 1995 - 1996.

Coach and organizer: Palo Alto Boys’ Baseball league, 1997 - 2003.

Presented science lessons and laboratory tours for Bay Area primary, middle and high schools, each year 1995 - 2008.

Volunteer: L. M. Nixon Elementary School, Palo Alto, 1995 - 2005.

Volunteer: Terman Middle School, Palo Alto, 2005 - 2008.

Workshop Presenter: Sally Ride Science Festivals, Stanford University, October, 2003 - 2006.

**Refereed Publications**

1. Hand, C. W. and Myers, R. M. (1976). Arrhenius parameters for the reaction of oxygen atoms with dicyanoacetylene. J. Physical Chemistry. 80: 557-558.

2. Hodo, H. G., Murphy, J., Hardman, J. K. and Myers, R. M. (1977). Substrate interactions with the alpha-subunit of the *Escherichia coli* tryptophan synthase. Arch. Biochem. Biophys. 181: 419-427. PMID: 332076.

3. Rio, D., Robbins, A., Myers, R. and Tjian, R. (1980). Regulation of simian virus 40 early transcription *in vitro* by a purified tumor antigen. Proc. Natl. Acad. Sci. USA 77: 5706-5710. PMID: 6255460. PMCID: PMC350138.

4. Myers, R. M. and Tjian, R. (1980). Construction and analysis of simian virus 40 origins defective in tumor antigen binding and DNA replication. Proc. Natl. Acad. Sci. USA 77: 6491-6495. PMID: 6256739. PMCID: PMC350311.

5. Myers, R. M., Rio, D. C., Robbins, A. K., and Tjian, R. (1981). SV40 gene expression is modulated by the cooperative binding of T antigen to DNA. Cell. 25: 373-384. PMID: 6269743.

6. Myers, R. M., Kligman, M. and Tjian, R. (1981). Does simian virus 40 T antigen unwind DNA? J. Biol. Chem. 256: 10156-10160. PMID: 6268627.

7. Myers, R. M., Williams, R. C. and Tjian, R. (1981). Oligomeric structure of a simian virus 40 T antigen in free form and bound to DNA. J. Mol. Biol. 148: 347-353. PMID: 6273580.

8. Brock, P. W., Myers, R., Baker, D. C. and Hardman, J. K. (1983). Photoaffinity labeling of the indole sites on the *Escherichia coli* tryptophan synthase a-subunit. Arch. Biochem. Biophys. 220: 435-443. PMID: 6337554.

9. Fisher, E. F., Feist, P. L., Beaucage, S. L., Myers, R. M., Tjian, R. and Caruthers, M. H. (1984). Interaction of AD2+D2 protein and simian virus 40 large T antigen with the large tumor antigen binding site I. Biochemistry. 23: 5938-5944. PMID: 6098305.

10. Jones, K. A., Myers, R. M., and Tjian, R. (1984). Mutational analysis of simian virus 40 large T antigen binding sites. EMBO J. 3: 3247-3255. PMID: 6098470. PMCID: PMC557845.

11. Myers, R. M., Lumelsky, N., Lerman, L. S. and Maniatis, T. (1985). Detection of single base substitutions in total genomic DNA. Nature. 313: 495-498. PMID: 3969155.

12. Myers, R. M., Fischer, S. G., Maniatis, T. and Lerman, L.S. (1985). Modification of the melting properties of duplex DNA by attachment of a GC-rich DNA sequence as determined by denaturing gradient gel electrophoresis. Nucleic Acids Res. 13: 3111-3130. PMID: 2987873. PMCID: PMC341224.

13. Myers, R. M., Fischer, S. G., Lerman, L. S. and Maniatis, T. (1985). Nearly all single base substitutions in DNA fragments joined to a GC-clamp can be detected by denaturing gradient gel electrophoresis. Nucleic Acids Res. 13: 3131-3146. PMID: 4000972. PMCID: PMC341225.

14. Myers, R. M., Lerman, L. S. and Maniatis, T. (1985). A general method for saturation mutagenesis of cloned DNA fragments. Science 229: 242-247. PMID: 2990046.

15. Myers, R. M., Larin, Z. and Maniatis, T. (1985). Detection of single base substitutions by ribonuclease cleavage of mismatches in RNA:DNA duplexes. Science. 230: 1242-1246. PMID: 4071043.

16. Myers, R. M., Tilly, K. and Maniatis, T. (1986). Fine structure genetic analysis of a beta-globin promoter. Science. 232: 613-618. PMID: 3457470.

17. Milton, D. L., Napier, M. L., Myers, R. M. and Hardman, J. K. (1986). *In vitro* mutagenesis and overexpression of the *E. coli trpA* gene and the partial characterization of the resultant tryptophan synthase mutant alpha-subunits. J. Biol. Chem. 261: 16604-16615. PMID: 3023357.

18. Collins, M. and Myers, R. M. (1987). Alterations in DNA helix stability due to base modifications can be evaluated using denaturing gradient gel electrophoresis. J. Mol. Biol. 198: 737-744. PMID: 3430628.

19. Cowie, A. and Myers, R. M. (1988). DNA sequences involved in transcriptional regulation of the mouse beta-globin promoter in murine erythroleukemia cells. Molec. Cell. Biol. 8: 3122-3128. PMID: 3211138. PMCID: PMC363539.

20. Cox, D. R., Pritchard, C. A., Uglum, E., Casher, D., Kobori, J. and Myers, R. M. (1989). Segregation of the Huntington disease region of human chromosome 4 in a somatic cell hybrid. Genomics. 4: 397-407. PMID: 2523853.

21. Sheffield, V. C., Cox, D. R., Lerman, L. S. and Myers, R. M. (1989). Attachment of a 40-base-pair G+C-rich sequence (GC-clamp) to genomic DNA fragments by the polymerase chain reaction results in improved detection of single-base changes. Proc. Natl. Acad. Sci. USA. 86: 232-236. PMID: 2643100. PMCID: PMC286438.

22. Pritchard, C. A., Casher, D., Uglum, E., Cox, D. R., and Myers, R. M. (1989). Isolation and field- inversion gel electrophoresis analysis of DNA markers located close to the Huntington disease gene. Genomics. 4: 408-418. PMID: 2523854.

23. Yost, C. S., Lopez, C. D., Prusiner, S. B., Myers, R. M. and Lingappa, V. R. (1990). Non-hydrophobic extracytoplasmic determinant of stop transfer in the prion protein. Nature. 343: 669-672. PMID: 1968226.

24. Stuvé, L. L. and Myers, R. M. (1990). A directly repeated sequence in the beta-globin promoter regulates transcription in murine erythroleukemia cells. Molec. Cell Biol. 10: 972-981. PMID: 2304472. PMCID: PMC360947.

25. Lopez, C. D., Yost, C. S., Prusiner, S. B., Myers, R. M. and Lingappa, V. R. (1990). Unusual topogenic sequence directs prion protein biogenesis. Science. 248: 226-229. PMID: 1970195.

26. Brodsky, M. H., Warton, M., Myers, R. M. and Littman, D. R. (1990). Analysis of the site in CD4 that binds to the HIV envelope glycoprotein. J. Immunol. 144: 3078-3086. PMID: 1691226.

27. Pritchard, C. A., Casher, D., Bull, L., Cox, D. R. and Myers, R. M. (1990). A cloned DNA segment from the telomeric region of human chromosome 4p is not detectably rearranged in Huntington disease patients. Proc. Natl. Acad. Sci. USA. 87: 7309-7313. PMID: 2144903. PMCID: PMC54733.

28. Cox, D. R., Burmeister, M., Price, E. R., Kim, S. and Myers, R. M. (1990). Radiation hybrid mapping: A somatic cell genetic method for constructing high-resolution maps of mammalian chromosomes. Science. 250: 245-250. PMID: 2218528.

29. Duyk, G. M., Kim, S., Myers, R. M. and Cox, D. R. (1990). Exon trapping: A genetic screen to identify transcribed sequences in cloned mammalian genomic DNA. Proc. Natl. Acad. Sci. USA. 87: 8995-8999. PMID: 2247475. PMCID: PMC55087.

30. Burmeister, M., Cox, D. R. and Myers, R. M. (1990). Dinucleotide repeat polymorphism located at D21S120. Nucleic Acids Res. 18: 4969. PMID: 2395674. PMCID: PMC332044.

31. deLange, T., Shiue, L., Myers, R. M., Cox, D. R., Naylor, S. L., Killery, A. M. and Varmus, H. E. (1990). Structure and variability of human chromosome ends. Molec. Cell Biol. 10: 518-527. PMID: 2300052. PMCID: PMC360828.

32. Burmeister, M., Cox, D. R. and Myers, R. M. (1991). TaqI RFLP at D21S137. Nucleic Acids Res. 19: 4020. PMID: 1677761. PMCID: PMC328526.

33. Burmeister, M., diSibio, G., Cox, D. R. and Myers, R. M. (1991). Identification of polymorphisms by genomic denaturing gradient gel electrophoresis: application to the proximal region of human chromosome 21. Nucleic Acids Res. 19: 1475-1481. PMID: 1674130. PMCID: PMC333904.

34. Burmeister, M., Kim, S., Price, E. P., de Lange, T., Tantravahi, U., Myers, R. M. and Cox, D. R. (1991). A map of the distal region of the long arm of human chromosome 21 constructed by radiation hybrid mapping and pulsed-field gel electrophoresis. Genomics. 9: 19-30. PMID: 2004760.

35. Gaensler, K. M. L., Burmeister, M., Brownstein, B. H., Taillon-Miller, P. and Myers, R. M. (1991). Physical mapping of yeast artificial chromosomes containing sequences from the human beta-globin gene region. Genomics. 10: 976-984. PMID: 1916829.

36. Maricq, A. V., Peterson, A. S., Brake, A. J., Myers, R. M. and Julius, D. (1991). Primary structure and functional expression of a serotonin-gated ion channel. Science. 254: 432-437. PMID: 1718042.

37. Pritchard, C., Cox, D. R. and Myers, R. M. (1991). Dinucleotide repeat polymorphism located at D4S169. Nucleic Acids Res. 19: 6347. PMID: 1956808. PMCID: PMC329170.

38. Richard, C. W., Withers, D. A., Meeker, T. C., Maurer, S., Evans, G., Myers, R. M. and Cox, D. R. (1991). A radiation hybrid map of the proximal long arm of human chromosome 11 containing the MEN-1 and bcl-1 disease gene loci. Amer. J. Hum. Genet. 49: 1189-1196. PMID: 1684084. PMCID: PMC1686449.

39. Dugaiczyk, A., Goold, R., diSibio, G., and Myers, R. M. (1992). Improved sequencing of cosmids using new primers and linearized DNA. Nucleic Acids Res. 20: 6421-6422. PMID: 1475209. PMCID: PMC334544.

40. Frazer, K. A., Boehnke, M., Budarf, M. L., Wolff, R. K., Emanuel, B. S., Myers, R. M., and Cox, D. R. (1992). A radiation hybrid map of the region on human chromosome 22 containing the neurofibromatosis type 2 locus. Genomics. 14: 574-584. PMID: 1427886.

41. Law, A., Richard, C. W., Cottingham, R. W., Lathrop, G. M., Cox, D. R. and Myers, R. M. (1992). Genetic linkage analysis of bipolar affective disorder in an Old Order Amish pedigree. Hum. Genet. 88: 562-568. PMID: 1551659.

42. Pritchard, C., Zhu, N., Zuo, J., Bull, L., Pericak-Vance, M. A., Vance, J. M., Roses, A. D., Milatovich, A., Francke, U., Cox, D. R. and Myers, R. M. (1992). Recombination of 4p16 DNA markers in an unusual family with Huntington disease. Amer. J. Hum. Genet. 50: 1218-1230. PMID: 1350884. PMCID: PMC1682573.

43. Rajpara, S. M., Garcia, P. D., Roberts, R., Eliassen, J. C., Owens, D. F., Maltby, D., Myers, R. M. and Mayeri, E. (1992). Identification and molecular cloning of a neuropeptide Y homolog that produces prolonged inhibition in *Aplysia* neurons. Neuron. 9: 505-513. PMID: 1524828.

44. Sheffield, V. C., Beck, J. S., Stone, E. M. and Myers, R. M. (1992). A simple and efficient method for attachment of a 40-base pair, GC-rich sequence to PCR-amplified DNA. BioTechniques. 12: 386-387. PMID: 1571147.

45. Zuo, J., Robbins, C., Taillon-Miller, P., Cox, D. R. and Myers, R. M. (1992). Cloning of the Huntington disease region in yeast artificial chromosomes. Hum. Molec. Genet. 1 149-159. PMID: 1303170.

46. Hartzog, G. and Myers, R. M. (1993). Discrimination among potential activators of the beta-globin CACCC element by correlation of binding and transcriptional properties. Molec. Cell. Biol. 13: 44-56. PMID: 8417342. PMCID: PMC358883.

47. Bull, L. N., Hewitt, J. E., Cox, D. R. and Myers, R. M. (1993). Sensitivity of *Hinc*II to CpG methylation. Nucleic Acids Res. 21: 2021. PMID: 8493118. PMCID: PMC309454.

48. Stuvé, L. L. and Myers, R. M. (1993). Identification and characterization of a beta-globin promoter-binding factor from murine erythroleukemia cells. Molec. Cell. Biol. 13: 4311-4322. PMID: 8321233. PMCID: PMC359987.

49. Zuo, J., Robbins, C., Baharloo, S., Cox, D. R., and Myers, R. M. (1993). Construction of cosmid contigs and high-resolution restriction mapping of the Huntington disease region of chromosome 4. Hum. Molec. Genet. 2: 889-899. PMID: 8364572.

50. Goold, R. D., diSibio, G. L., Xu, H., Lang, D. B., Dadgar, J., Magrane, G. G., Dugaiczyk, A., Smith, K. A., Cox, D. R., Masters, S.B. and Myers, R. M. (1993). The development of sequence-tagged sites for human chromosome 4. Hum. Molec. Genet. 2: 1271-1288. PMID: 8401509.

51. Richard III, C. W., Boehnke, M. Berg, D. J. Lichy, J. J., Meeker, T. C., Hauser, E., Myers, R. M. and Cox, D. R. (1993). A radiation hybrid map of the distal short arm of human chromosome 11, containing the Beckwith-Weidemann and associated embryonal tumor disease loci. Am. J. Hum. Genet. 52: 915-921. PMID: 8387721. PMCID: PMC1682045.

52. Garcia, P. D. and Myers, R. M. (1994). Pituitary cell line GH3 expresses two somatostatin receptor subtypes that inhibit adenylyl cyclase: Molecular cloning and functional expression in HEK 293 cells of rat somatostatin receptor subtypes SSTR1 and SSTR2. Molec. Pharmacol. 45: 402-409. PMID: 8145727.

53. Fan, J.-B., DeYoung, J., Lagacé, R., Lina, R. A., Xu, Z., Murray, J. C., Buetow, K. H., Weissenbach, J., Goold, R. D., Cox, D. R. and Myers, R. M. (1994). Isolation of yeast artificial chromosome clones from 54 polymorphic loci mapped with high odds on human chromosome 4. Hum. Molec. Genet. 3: 243-246. PMID: 8004089.

54. John, R. M., Robbins, C. A. and Myers, R. M. (1994). Identification of genes within CpG-enriched DNA from human chromosome 4p16.3. Hum. Molec. Genet. 3: 1611-1616. PMID: 7530549.

55. Patil, N., Peterson, A., Rothman, A., de Jong, P. J., Myers, R. M. and Cox, D. R. (1994). A high resolution physical map of 2.5 Mbp of the Down Syndrome region on human chromosome 21. Hum. Molec. Genet. 3: 1811-1817. PMID: 7849705.

56. Peterson, A., Patil, N., Robbins, C., Wang, L., Cox, D. R. and Myers, R. M. (1994). A transcript map of the Down Syndrome critical region on human chromosome 21. Hum. Molec. Genet. 3: 1735-1742. PMID: 7849696.

57. Jou, Y.-S., Goold, R. D. and Myers, R. M. (1994). Localization of the beta-2-macroglobulin receptor-associated protein 1 gene (LRPAP1) and other gene fragments to human chromosome 4p16.3 by direct cDNA selection. Genomics. 24: 410-413. PMID: 7535288.

58. Jou, Y.-S. and Myers, R. M. (1995). Evidence from antibody studies that the CAG-repeat in the Huntington disease gene is expressed in the protein. Hum. Mol. Genet. 4: 465-469. PMID: 7795604.

59. Patil, N., Cox, D. R., Bhat, D., Faham, M., Myers, R. M. and Peterson, A. S. (1995). A potassium channel mutation in weaver mice implicates membrane excitability in granule cell differentiation. Nature Genet. 11: 126-129. PMID: 7550338.

60. Stone, N.E., Fan, J.B., Willour, V., Pennacchio, L.A., Warrington, J., Hu, A., de la Chapelle, A., Lehesjoki, A.E., Cox, D.R. and Myers, R.M. (1996). Construction of a 750 kb bacterial clone contig and restriction map in the region of human chromosome 21 containing the Progressive Myoclonus Epilepsy (EPM1) gene. Genome Res. 6: 218-225. PMID: 8963899.

61. Burke, J., R., Enghild, J. J., Martin, M. E., Jou, Y. S., Myers, R. M., Roses, A. D., Vance, J. M. and Strittmatter, W. J. (1996). Huntingtin and DRPLA proteins selectively interact with the enzyme GAPDH. Nature Med. 2: 347-350. PMID: 8612237.

62. Pennacchio, L. A., Lehesjoki, A. E., Stone, N. E., Willour, V. L., Virtaneva, K., Miao, J., D'Amato, E., Ramirez, L., Faham, M., Koskiniemi, M., Warrington, J., Norio, R., de la Chapelle, A., Cox, D.R. and Myers, R. M. (1996). Mutations in the gene encoding cystatin B in Progressive Myoclonus Epilepsy (EPM1). Science. 271: 1731-1734. PMID: 8596935.

63. Johnson, R. L., Rothman, A. L., Xie, J., Goodrich, L. V., Bare, J. W., Bonifas, J. M., Quinn, A. G., Myers, R. M., Cox, D. R., Epstein, E. H. and Scott, M. P. (1996). Human homolog of *patched*, a candidate gene for the basal cell nevus syndrome. Science. 272: 1668-1671. PMID: 8658145.

64. Mastrianni, J. A., Iannicola, C., Myers, R. M., DeArmond, S. and Prusiner, S. B. (1996). Mutation of the prion protein gene at codon 208 in familial Creutzfeldt-Jakob disease. Neurology. 47: 1305-1312. PMID: 8909447.

65. Virtaneva, K., Miao, J., Traskelin, A. L., Stone, N., Warrington, J., Weissenbach, J., Myers, R. M., Cox, D.R., Sistonen, P., de la Chapelle and Lehesjoki, A-E. (1996). Progressive myoclonus epilepsy EPM1 locus maps to a 175 kb interval in distal 21q. Am. J. Hum. Genet. 58: 1247-1253. PMID: 8651302. PMCID: PMC1915057.

66. Pennacchio, L.A. and Myers, R.M. (1996). Isolation and characterization of the mouse cystatin B gene. Genome Res. 6: 1103-1109. PMID: 8938434.

67. Schuler, G. D., Boguski, M. S., Stewart, E. A., Stein, L. D., Gyapay, G., et al., Myers, R. M., Cox, D. R., James, M. R., Bentley, D., Deloukas, P., Lander E. S. and Hudson, T. J. (1996). A gene map of the human genome. Science. 274: 540-546. PMID: 8849440.

68. Bell, S. M., Zuo, J., Myers, R. M. and Knowles, M. A. (1996). Fluorescence in situ hybridization deletion mapping at 4p16.3 in bladder cancer cell lines refines the localisation of the critical interval to 30 kb. Genes, Chromosomes and Cancer. 17: 108-117. PMID: 8913728.

69. Stewart, E. A., McKusick, K. B., Aggarwal, A., Bajorek, E., Brady, S., Chu, A., Fang, N., Hadley, D., Harris, M., Hussain, S., Lee, R., Maratukulam, A., O'Connor, K., Perkins, S., Piercy, M., Qin, F., Reif, T., Sanders, C, She, X., Sun, W-L, Tabar, P., Voyticky, S., Cowles, S., Fan, J. B., Mader, C, Quackenbush, J., Myers, R. M. and Cox, D. R. (1997). An STS-based radiation hybrid map of the human genome. Genome Res. 7: 422-433. PMID: 9149939.

70. Virtaneva, K., D’Amato, E., Miao, J., Koskiniemi, M., Norio, R., Avanzini, G., Franceschetti, S., Michelucci, R., Tassinari, C. A., Omer, S., Pennacchio, L. A., Myers, R. M. Dieguez-Lucena, J. L., Krahe, R., de la Chapelle, A. and Lehesjoki, A. E. (1997). Unstable minisatellite expansion causing recessively inherited myoclonus epilepsy, EPM1. Nature Genet. 15: 393-396. PMID: 9090386.

71. Aaltonen, J., Horelli-Kuitunen, N., Fan, J. B., Bjorses, P., Perheentupa, J., Myers, R., Palotie, A. and Peltonen, L. (1997). High-resolution physical and transcriptional mapping of the autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy locus on chromosome 21q22.3 by FISH. Genome Res. 7: 820-829. PMID: 9267805.

72. Bell, S. M., Shaw, M. Jou, Y. S., Myers, R. M. and Knowles, M. A. (1997). Identification and characterisation of the human homologue of SH3BP2, an SH3 binding domain protein within a common region of deletion at 4p16.3 involved in bladder cancer. Genomics. 44: 163-170. PMID: 9299232.

73. Karlovich, C. A., John, R. M., Ramirez, L., Stainier, D. Y. R. and Myers, R. M. (1998). Characterization of the Huntington disease (HD) gene homolog in the zebrafish Danio rerio. Gene. 217: 117-125. PMID: 9795179.

74. Pennacchio, L. A., Bouley, D. M., Higgins, K. M., Scott, M. P., Noebels, J. L., and Myers, R. M. (1998). Progressive ataxia, myoclonic epilepsy, and cerebellar apoptosis in cystatin B-deficient mice. Nature Genet. 20: 251-258. PMID: 9806543.

75. Deloukas, P., Schuler, G. D., Gyapay, G., Beasley, E. M., et al., Myers, R. M., Cox, D. R., Weissenbach, J., Boguski, M. S. and Bentley, D. R. (1998). A physical map of 30,000 human genes. Science. 282: 744-746. PMID: 9784132.

76. Shelbourne, P. F., Killeen, N., Hevner, R. F., Johnston, H. M., Tecott, L., Lewandoski, M., Ennis, M., Ramirez, L., Li, A., Iannicola, C., Littman, D. R. and Myers, R. M. (1999). A Huntington's disease CAG expansion at the muring *Hdh* locus is unstable and associated with behavioural abnormalities in mice. Hum. Molec. Genet. 8: 763-774. PMID: 10196365.

77. Usdin, M., Shelbourne, P. F., Myers, R. M. and Madison, D. V. (1999). Impaired synaptic plasticity in mice carrying the Huntington’s disease mutation. Hum. Molec. Genet. 8: 839-846. PMID: 10196373.

78. Rogers, T., Kalaydijieva, L., Hallmayer, J., et al., Risch, N. and Myers, R. M. (1999). Exclusion of linkage to the HLA region in ninety multiplex families with autism. J. Autism and Develop. Disorders 29: 195-201. PMID: 10425582.

79. Salmon, B., Hallmayer, J., Rogers, T., Kalaydijieva, L., Peterson, P. B., Nicholas, P., Pingree, C., McMahon, W., Spiker, D., Lotspeich, L., Kraemer, H., McCague, P., Dimiceli, S., Nouri, N., Pitts, T., Yang, J., Hinds, D., Myers, R. M. and Risch, N. (1999). Absence of linkage and linkage disequilibrium to chromosome 15q11-q13 markers in 139 multiplex families with autism. Amer. J. Med. Genet. 88: 551-556. PMID: 10490715.

80. Risch, N., Spiker, D., Lotspeich, L., Nouri, N., Hinds, D., Hallmayer, J., et al. and Myers, R. M. (1999). A genomic screen of autism: Evidence for a multi-locus etiology. Am. J. Hum. Genet. 65: 493-507. PMID: 10417292. PMCID: PMC1377948.

81. Li, Z., Karlovich, C. A., Fish, M., Scott, M. P. and Myers, R. M. (1999). A putative *Drosophila* homolog of the Huntington’s disease gene. Hum. Molec. Genet. 8: 1807-1815. PMID: 10441347.

82. Wu, Q., Zhang, T., Chen, J. C., Kim, Y., Grimwood, J., Schmutz, J., Dickson, M., Noonan, J., Zhang, M. Q., Myers, R. M. and Maniatis, T. (2001). Comparative DNA sequence analysis of mouse and human protocadherin gene clusters. Genome Res. 11: 389-404. PMID: 11230163. PMCID: PMC311048.

83. International Human Genome Sequencing Consortium. (2001). Initial sequencing and analysis of the human genome. Nature. 409: 860-921. PMID: 11237011.

84. The International Human Genome Mapping Consortium. (2001). A physical map of the human genome. Nature. 409: 934-941. PMID: 11237014.

85. Olivier, M., et al. (2001). A high resolution radiation hybrid map of the human genome. Science 298: 1298-1302. PMID: 11181994.

86. Lieuallen, K., Pennacchio, L. A., Park, M., Myers, R. M., Lennon, G. G. (2001). Cystatin B-deficient mice have increased expression of apoptosis and glial activation genes. Hum. Molec. Genet. 10: 1867-1871. PMID: 11555622.

87. Spiker, D., Lotspeich, L. J., Dimiceli, S., Szatmari, P., Myers, R. M. and Risch, N. (2001). Birth order effects on nonverbal IQ scores in autism multiplex families. J. Autism Devel. Disord. 31: 449-460. PMID: 11794410.

88. Li, J., Tabor, H., Gleason, C., Nguyen, L., Lotspeich, L., Spiker, D., Risch, N. and Myers, R. M. (2002). Lack of association between HoxA1 and HoxB1 gene variants and autism in 110 multiplex families. Amer. J. Med. Genet.: Neuropsychiatric Genet. 114: 24-30. PMID: 11840501.

89. Spiker, D., Lotspeich, L. J., Dimiceli, S., Myers, R. M. and Risch, N. (2002). Behavioral variation in autism multiplex families: Evidence for a continuous severity gradient. Amer. J. Med. Genet.: Neuropsychiatric Genet. 114: 129-136. PMID: 11857572.

90. Shannon, P., Pennacchio, L. A., Houseweart, M. K., Minassian, B. A., and Myers, R. M. (2002). Neuropathological changes in a murine model of Progressive Myoclonus Epilepsy: Cystatin B deficiency and Unverricht-Lundborg disease. J. Neuropath. Exp. Neurol. 61: 1085-1091. PMID: 12484571.

91. Stickney, H. L., Schmutz J., Woods, I. G., Holtzer C. C., Dickson, M. C., Kelly, P. D., Myers, R. M. and Talbot, W. S. (2002). Rapid mapping of zebrafish mutations with SNPs and oligonucleotide microarrays. Genome Res. 12: 1929-1934. PMID: 12466297. PMCID: PMC187572.

92. MGC Program Team. (2002). Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proc. Natl. Acad. Sci. USA. 99: 16899-16903. PMID: 12477932. PMCID: PMC139241.

93. Trinklein, N., Force Aldred, S., Saldanha, A. and Myers, R. M. (2003). Identification and functional analysis of human transcriptional promoters. Genome Res. 13: 308-312. PMID: 12566409. PMCID: PMC420378.

94. Noonan, J. P., Li, J., Nguyen, L., Caoile, C., Dickson, M., Grimwood, J., Schmutz, J., Feldman, M. W. and Myers, R. M. (2003). Extensive linkage disequilibrium, a common 16.7 kb deletion and evidence of balancing selection in the human protocadherin alpha cluster. Amer. J. Hum. Genet. 72: 621-635. PMID: 12577201. PMCID: PMC1180238.

95. Khambata Ford, S., Liu, Y., Gleason, C., Dickson, M., Altman, R. B., Batzoglou, S., and Myers, R. M. (2003). Identification of promoter regions in the human genome by using a retroviral plasmid library-based functional reporter gene assay. Genome Res. 13: 1765-1774. PMID: 12805274. PMCID: PMC403750.

96. Houseweart, M. K., Pennacchio, L. A., Vilaythong, A., Peters, C., Noebels, J. L. and Myers, R. M. (2003). Cathepsin B but not cathepsin L or S contributes to the pathogenesis of Unverricht-Lundborg progressive myoclonus epilepsy (EPM1). J. Neurobiology 56: 315-327. PMID: 12918016.

97. Houseweart, M. K., Vilaythong, A., Yin, X.-M., Noebels, J. L. and Myers, R. M. (2003). Apoptosis caused by cathepsins does not require Bid signaling in an in vivo model of progressive myoclonus epilepsy (EPM1). Cell Death and Diff. 10: 1329-1335. PMID: 12934064.

98. Evans S. J., Choudary, P. V., Vawter, M. P., Li, J., Meador-Woodruff, J. H., Lopez, J. F., Burke, S. M., Thompson, R. C., Myers, R. M., Jones, E. G., Bunney, W. E., Watson, S. J., and Akil, H. (2003). DNA microarray analysis of functionally discrete human brain regions reveals divergent transcriptional profiles. Neurobiol. Dis. 14: 240-250. PMID: 14572446. PMCID: PMC3098567.

99. Murphy, E., Yu, D., Grimwood, J., Schmutz, J., Dickson, M., Jarvis, M., Hahn, G., Nelson, J. A., Myers, R. M. and Shenk, T. (2003). Coding potential of laboratory and clinical strains of human cytomegalovirus. Proc. Natl. Acad. Sci. USA. 100: 14976-14981. PMID: 14657367. PMCID: PMC299866.

100. Li, J., Nguyen, L., Gleason, C. Lotspeich, L., Spiker, D., Risch, N. and Myers, R. M. (2004). Lack of evidence for an association between WNT2 and RELN polymorphisms and autism. Amer. J. Med. Genet.: Neuropsych. Genet. 126B: 51-57. PMID: 15048648.

101. Trinklein, N. D., Force Aldred, S., Hartman, S. J., Schroeder, D. I., Otillar, R. and Myers, R. M. (2004). An abundance of bidirectional promoters in the human genome. Genome Res. 14: 62-66. PMID: 14707170. PMCID: PMC314279.

102. Tomita, H., Vawter, M. P., Walsh, D. M., Evan, S., Choudary, P. V., Li, J., Overman, K., Atz, M., Myers, R. M., Jones, E. G., Watson, S. J., Akil, H. and Bunney, W. E. (2004). Effect of agonal and postmortem factors on microarray expression profile: quality control methods in microarray analyses of postmortem human brain. Biol. Psychiatry. 55: 346-352. PMID: 14960286. PMCID: PMC3098566.

103. Cirman, T., Oresic, K., Droga Mazovec, G., Turk, V., Reed, J. C., Myers, R. M., Salvesen, G. S., and Turk, B. (2004). Selective disruption of lysosomes in HeLa cells triggers apoptosis, mediated by cleavage of Bid by multiple papain-like lysosomal cathepsins. J. Biol. Chem. 279: 3578-3587. PMID: 14581476.

104. Kingsley, D., Zhu, B., Osoegawa, K., de Jong, P. J., Schein, J., Marra, M., Peichel, C., Amemiya, C., Schluter, D., Balabhadra, S., Friedlander, B., Chan, Y. M., Dickson, M., Grimwood, J., Schmutz, J., Talbot, W. and Myers, R. M. (2004). New genomic tools for molecular studies of evolutionary change in sticklebacks. Behavior. 141: 1331-1344.

105. Trinklein, N., Chen, W. C., Kingston, R. E. and Myers, R. M. (2004). Transcriptional regulation and binding of HSF1 and HSF2 to 32 human heat shock genes during thermal stress and differentiation. Cell Stress and Chaparones. 9: 21-28. PMID: 15270074. PMCID: PMC1065302.

106. Trinklein, N. D., Murray, J. I., Hartman, S. J., Botstein, D., and Myers, R. M. (2004). The role of heat shock transcription factor 1 in the regulation of the mammalian heat shock response. Molec. Biol. Cell. 15: 1254-1261. PMID: 14668476. PMCID: PMC363119.

107. Vawter, M. P., Evans, S., Choudary, P., Tomita, H., Meador-Woodruff, J., Molnar, M., Li, J., Lopez, J. F., Myers, R., Cox, D., Watson, S. J., Akil, H., Jones, E. G., Bunney, W. E. (2004). Gender-specific gene expression in post-mortem human brain: Localization to sex chromosomes. Neuropsychopharmacology. 29: 373-384. PMID: 14583743. PMCID: PMC3130534.

108. Li, J., Vawter, M. P., Walsh, D. M., Tomita, H., Evans, S. J., Choudary, P. V., Lopez, J. F., Avelar, A., Shokoohi, V., Chung, T., Mesarwi, O., Jones, E. G., Watson, S. J., Akil, H., Bunney, W. E. and Myers, R. M. (2004). Systematic changes in gene expression in postmortem human brains associated with tissue pH and terminal medical conditions. Hum. Molec. Genet. 13: 609-616. PMID: 14734628.

109. Noonan, J. P., Grimwood, J., Schmutz, J., Dickson, M., and Myers, R. M. (2004). Gene conversion and the evolution of protocadherin gene cluster diversity. Genome Res. 14: 354-366. PMID: 14993203. PMCID: PMC353213.

110. Grimwood, J., Gordon, L.A., Terry, A., Olsen, A., Schmutz, J., Hellsten, U., Goodstein, D., Couronne, O., Tran-Gyam, M., Aerts, A., Altherr, M., Bajorek, E., Black, S., Caenepeel, S., Caoile, C., Chan, Y. M., Christensen, M., Cleland, C. A., Copeland, A., Dalin, E., Dehal, P., Denys, M., Detter, J. C., Escobar, J., Flowers, D., Fotopulos, D., Garcia, C., Glavina, T., Gomez, M., Gonzales, E., Hammon, N., Haydu, L., Ho. I., Huang, W., Israni, S., Jett, J., Kadner, K., Kimball, H., Kobayashi, A., Lopez, F., Lou, Y., Lowry, S., Martinez, D., Medina, C., Morgan, J., Nelson, K., Nolan, M., Ovcharenko, I., Pitluck, S., Pollard, M., Popkie, A. P., Ramirez, L., Rash, S., Retterer, J., Rodriguez, A., Rogers, S., Salamov, A., Salazar, A., She, X., Smith, D., Solovyev, V., Thayer, N., Tice, H., Tsai, M., Ustaszewska, A., Vo, N., Wagner, M., Wheeler, J., Wu, K., Xie, G., Yang, J., Dubchak, I., Furey, T. S., DeJong, P., Dickson, M., Gordon, D., Eichler, E. E., Pennacchio, L. A., Richardson, P., Stubbs, L., Branscomb, E., Rokhsar, D. S., Myers, R. M., Rubin, E. M., and Lucas, S. M. (2004). The DNA sequence and biology of human chromosome 19. Nature. 428: 529-535. PMID: 15057824.

111. Murray, J. I., Whitfield, M. L., Trinklein, N. D., Myers, R. M., Brown, P. O. and Botstein, D. (2004). Diverse and specific gene expression responses to stresses in cultured human cells. Molec. Biol. Cell. 5: 2361-2374. PMID: 15004229. PMCID: PMC404029.

112. Schmutz, J., Wheeler, J., Grimwood, J., Dickson, M., Yang, J., Caoile, C., Bajorek, E., Black, S., Chan, Y. M., Denys, M., Escobar, J., Flowers, D., Fotopulos, D., Garcia, C., Gomez, M., Gonzales, E., Haydu, L., Lopez, F., Ramirez, L., Retterer, J., Rodriguez, A., Rogers, S., Salazar, A., Tsai, M., and Myers, R. M. (2004). Quality assessment of the human genome sequence. Nature. 429: 365-368. PMID: 15164052.

113. Gerhard, D.S., Wagner, L., Feingold, E.A., Shenmen, C.M., Grouse, L.H., Schuler, G., Klein, S.L., Old, S., Rasooly, R., Good, P., Guyer, M., Peck, A.M., Derge, J.G., Lipman, D., Collins, F.S., Jang, W., Sherry, S., Feolo, M., Misquitta, L., Lee, E., Rotmistrovsky, K., Greenhut, S.F., Schaefer, C.F., Buetow, K., Bonner, T.I., Haussler, D., Kent, J., Kiekhaus, M., Furey, T., Brent, M., Prange, C., Schreiber, K., Shapiro, N., Bhat, N.K., Hopkins, R.F., Hsie, F., Driscoll, T., Soares, M.B., Casavant, T.L., Scheetz, T.E., Brown-stein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Piao, Y., Dudekula, D.B., Ko, M.S., Kawakami, K., Suzuki, Y., Sugano, S., Gruber, C.E., Smith, M.R., Simmons, B., Moore, T., Waterman, R., Johnson, S.L., Ruan, Y., Wei, C.L., Mathavan, S., Gunaratne, P.H., Wu, J., Garcia, A.M., Hulyk, S.W., Fuh, E., Yuan, Y., Sneed, A., Kowis, C., Hodgson, A., Muzny, D.M., McPherson, J., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madari, A., Young, A.C., Wetherby, K.D., Granite, S.J., Kwong, P.N., Brinkley, C.P., Pearson, R.L., Bouffard, G.G., Blakesly, R.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Griffith, M., Griffith, O.L., Krzywinski, M.I., Liao, N., Morin, R., Palmquist, D., Petrescu, A.S., Skalska, U., Smailus, D.E., Stott, J.M., Schnerch, A., Schein, J.E., Jones, S.J., Holt, R.A., Baross, A., Marra, M.A., Clifton, S., Makowski, K.A., Bosak, S., Malek, J.; MGC Project Team.  (2004).  The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC).  Genome Res.  10B: 2121-2127. Erratum in: Genome Res. 6: 804. Morrin, Ryan [corrected to Morin, Ryan].  PMID: 15489334. PMCID: PMC528928.

114. Schmutz, J., Martin, J., Terry, A., Couronne, O., Grimwood, J., Lowry, S., Gordon, L. A., Scott, D., Xie, G., Huang, W., Hellsten, U., Tran-Gyam, M., She, X., Prabhakar, S., Aerts, A., Altherr, M., Bajorek, E., Black, S., Branscomb, E., Caoile, C., Challacombe, J. F., Chan, Y. M., Denys, M., Detter, C., Escobar, J., Flowers, D., Fotopulos, D., Glavina, T., Gomez, M., Gonzales, E., Goodstein, D., Grigoriev, I., Groza, M., Hammon, N., Hawkins, T., Haydu, L., Israni, S., Jett, J., Kadner, K., Kimball, H., Kobayashi, A., Lopez, F., Lou, Y., Martinez, D., Medina, C., Morgan, J., Nandkeshwar, R., Noonan, J. P., Pitluck, S., Pollard, M., Predki, P., Priest, J., Ramirez, L., Rash, S., Retterer, J., Rodriguez, A., Rogers, S., Salamov, A., Salazar, A., Thayer, N., Tice, H., Tsai, M., Ustaszewska, A., Vo, N., Wheeler, J., Wu, K., Yang, J., Dickson, M., Cheng, J.-F., Eichler, E. E., Olsen, A., Pennacchio, L. A., Rokhsar, D. S., Richardson, P., Lucas, S. M., Myers, R. M. and Rubin, E. M. (2004). The DNA sequence and comparative analysis of human chromosome 5. Nature. 431: 268-274. PMID: 15372022

115. Noonan, J. P., Grimwood, J., Danke, J., Schmutz, J., Dickson, M., Amemiya, C. T. and Myers, R. M. (2004). Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. Genome Res. 12: 2397-2405. PMID: 15545497. PMCID: PMC534663.

116. Peichel, C. L., Ross, J. A., Matson, C. K., Dickson, M., Grimwood, J., Schmutz, J., Myers, R. M., Mori, S., Schluter, D. and Kingsley, D. M. (2004). The master sex-determination locus in threespine sticklebacks is on a nascent Y chromosome. Current Biol. 14: 1416-1424. PMID: 15324658.

117. International Human Genome Sequencing Consortium. (2004). Finishing the euchromatic sequence of the human genome. Nature. 431: 931-945. PMID: 15496913.

118. ENCODE Project Consortium. (2004). The ENCODE (ENCyclopedia Of DNA Elements) Project. Science. 306: 636-640. PMID: 15499007.

119. Evans, S. J., Choudary, P. V., Neal, C. R., Li, J. Z., Vawter, M. P., Tomita, H., Lopez, J. F., Thompson, R. C., Meng, F., Stead, J. D., Walsh, D. M., Myers, R. M., Bunney, W. E., Watson, S. J., Jones, E. G. and Akil, H. (2004). Dysregulation of the fibroblast growth factor system in major depression. Proc. Natl. Acad. Sci. USA. 101: 15506-15511. PMID: 15483108. PMCID: PMC523463.

120. Martin, J., Han, C., Gordon, L. A., Terry, A., Prabhakar, S., She, X., Xie, G., Hellsten, U., Man Chan, Y-M., Altherr, M., Couronne, O., Aerts, A., Bajorek, E., Black, S., Blumer, H., Branscomb, E., Brown, N. C., Bruno, W. J., Buckingham, J. M., Callen, D. F., Campbell, C. S., Campbell, M. L., Campbell, E. W., Caoile, C., Challacombe, J. F., Chasteen, L. A., Chertkov, O., Chi, H. C., Christensen, M., Clark, L. M., Cohn, J. D., Denys, M., Detter, J. C., Dickson, M., Dimitrijevic-Bussod, M., Escobar, J., Fawcett, J. J., Flowers, D., Fotopulos, D., Glavina, T., Gomez, M., Gonzales, E., Goodstein, D., Goodwin, L. A., Grady, D. L., Grigoriev, I., Groza, M., Hammon, N., Hawkins. T., Haydu, L., Hildebrand, C. E., Huang, W., Israni, S., Jett, J., Jewett, P. E., Kadner, K., Kimball, H., Kobayashi, A., Krawczyk, M-C., Leyba, T., Longmire, J. L., Lopez, F., Lou, Y., Lowry, S., Ludeman, T., Mark, G. A., McMurray, K. L., Meincke, L. J., Morgan, J., Moyzis. R. K., Mundt, M. O., A. Munk, A. C., Nandkeshwar, R. D., Pitluck, S., Pollard, M., Predki, P., Parson-Quintana, B., Ramirez, L., Rash, S., Retterer, J., Ricke, D. O., Robinson, D. L., Rodriguez, A., Salamov, A., Saunders, E. H., Scott, D., Shough, T., Stallings, R. L., Stalvey, M., Sutherland, R. D., Tapia, R., Tesmer, J. G., Thayer, N., Thompson, L. S., Tice, H., Torney, D. C., Tran-Gyamfi, M., Tsai, M., Ulanovsky, L. E., Ustaszewska, A., Vo, N., White, P. S., Williams, A. L., Wills, P. L., Wu, J-R., Wu, K., Yang, J., DeJong, P., Bruce, D., Doggett, N., Deaven, L., Schmutz, J., Grimwood, J., Richardson, P., Rokhsar, D. S., Eichler, E. E., Gilna, P., Lucas, S. M., Myers, R. M., Rubin, E. M., and Pennacchio, L. A. (2005). The sequence and analysis of duplication-rich human chromosome 16. Nature. 432: 988-994. PMID: 15616553.

121. Colosimo, P. F., Hosemann, K. E., Balabhadra, S., Villareal, G., Dickson, M., Grimwood, J., Schmutz, J., Myers, R. M., Schluter, D. and Kingsley, D. M. (2005). Widespread parallel evolution of stickleback armor plates determined by ancestral genetic variation in Ectodysplasin. Science. 307: 1928-1933. PMID: 15790847.

122. Hillier, L. W., Graves, T. A., Fulton, R. S., Fulton, L. A., Pepin, K. H., Minx, P., Wagner-McPherson, C., Layman, D., Wylie, K., Sekhon, M., Becker, M. C., Fewell, G. A., Delehaunty, K. D., Miner, T. L., Nash, W. E., Kremitzki, C., Oddy, L., Du, H., Sun, H., Bradshaw-Cordum, H., Ali, J., Carter, J., Cordes, M., Harris, A., Isak, A., van Brunt, A., Nguyen, C., Du, F., Courtney, L., Kalicki, J., Ozersky, P., Abbott, S., Armstrong, J., Belter, E. A., Caruso, L., Cedroni, M., Cotton, M., Davidson, T., Desai, A., Elliott, G., Erb, T., Fronick, C., Gaige, T., Haakenson, W., Haglund, K., Holmes, A., Harkins, R., Kim, K., Kruchowski, S. S., Strong, C. M., Grewal, N., Goyea, E., Hou, S., Levy, A., Martinka, S., Mead, K., McLellan, M. D., Meyer, R., Randall-Maher, J., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowicz-Reilly, A., Shah, N., Swearengen-Shahid, S., Snider, J., Strong, J. T. , Thompson, J., Yoakum, M., Leonard, S., Pearman, C., Trani, L., Radionenko, M., Waligorski, J. E., Wang, C., Rock, S. M., Tin-Wollam, A-M., Maupin, R., Latreille, P., Wendl, M. C., Yang, S-P., Pohl, C., Wallis, J. W., Spieth, J., Bieri, T. A., Berkowicz, N., Osborne, J., Ding, L., Meyer, R., Sabo, A., Shotland, Y., Sinha, P., Wohldmann, P. E., Cook, L. L., Hickenbotham, M. T., Eldred, J., Williams, D., Jones, T. A., She, X., Ciccarelli, F. D., Izaurralde, E., Taylor, J., Schmutz, J., Myers, R. M., Cox, D. R., McPherson, J. D., Mardis, E. R., Clifton, S. W., Warren, W. C., Chinwalla, A. T., Eddy, S. R., Marra, M. A., Ovcharenko, I., Furey, T. S., Miller, W., Eichler, E. E., Bork, P., Suyama, M., Torrents, D., Waterston, R. H. and Wilson, R. K. (2005). Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature. 434: 724-731. PMID: 15815621.

123. Kim, T. H., Barrera, L. O., Qu, C., Van Calcar, S., Trinklein, N. D., Cooper, S. J., Luna, R., Glass, C. K., Rosenfeld, M. G., Myers, R. M., and Ren, B. (2005). Direct isolation and identification of promoters in the human genome. Genome Res. 15: 830-839. PMID: 15899964. PMCID: PMC1142473.

124. Carlson, C. S., Force Aldred, S., Tracy, R. P., Schwartz, S. M., Rieder, M., Liu, K., Williams, O. D., Irribarren, C., Lewis, E. C., Fornage, M., Boerwinkle, E., Gross, M., Nickerson, D. A., Myers, R. M., Siscovick, D. S., and Reiner, A. P. (2005). Polymorphisms within the C Reactive Protein promoter region are associated with plasma CRP levels. Am. J. Hum. Genet. 77: 64-77. Erratum in: Am J Hum Genet. 2008 Jan;82(1):251. PMID: 15897982. PMCID: PMC1226195.

125. Kopitar-Jerala, N., Schweiger, A., Myers, R. M., Turk, V., Turk, B. (2005). Sensitization of stefin B-deficient thymocytes towards staurosporin-induced apoptosis is independent of cysteine cathepsins. FEBS Lett. 579: 2149-2155. PMID: 15811333. [PubMed - indexed for MEDLINE].

126. Choudary, P.V., Molnar, M., Evans, S. J., Tomita, H., Li, J.Z., Vawter, M.P., Myers, R. M., Bunney Jr., W. E., Akil, H., Watson, S. J. and Jones, E. G. (2005). Altered cortical glutamatergic and GABAergic signal transmission with glial involvement in depression. Proc. Nat. Acad. Sci. USA. 102: 15653-15658. PMID: 16230605. PMCID: PMC1257393.

127. Dai, M., Wang, P., Boyd, A. D., Kostov, G., Athey, B., Jones, E. G., Bunney, W. E., Myers, R. M., Speed, T. P., Akil, H., Watson, S. J. and Meng, F. (2005). Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. Nucleic Acids Res. 33: e175. PMID: 16284200. PMCID: PMC1283542.

128. Cooper, S. J., Trinklein, N. D., Anton, E. D., Nguyen, L. and Myers, R. M. (2006). Comprehensive analysis of transcriptional promoter structure and function in 1% of the human genome. Genome Res. 16: 1-10. PMID: 16344566. PMCID: PMC1781345.

129. Morin, R. D., Chang, E., Petrescu, A., Liao, N., Kirkpatrick, R., Griffith, M., Butterfield, Y. S., Stott, S., Barber, S., Babakaiff, R., Matsuo, C., Wong, D., Yang, G. S., Smailus, D. E., Brown-John, M., Mayo, M., Beland, J., Gibson, S., Olson, T., Tsai, M., Featherstone, R., Chand, S., Siddiqui, A. S., Jang, W., Lee, E., Klein, S. L., Prange, C., Myers, R. M., Green, E. D., Wagner, L., Gerhard, D. S., Marra, M. A., Jones, S. J. M., Holt, R. A. (2006). Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis*. Genome Res. 16: 796-803. PMID: 16672307. PMCID: PMC1479861.

130. Vawter, M. P., Tomita, H., Meng, F., Bolstad, B., Li, J., Evans, S., Choudary, P., Atz, M., Shao, L., Neal, C., Walsh, D., Burmeister, M., Speed, T., Myers, R., Jones, E. G., Watson, S. J., Akil, H. and Bunney, W. E. (2006). Mitochondrial related gene expression changes are sensitive to agonal-pH state: Implications for brain disorders. Mol. Psychiatry. 11: 615, 663-679. PMID: 16636682. PMCID: PMC3098558.

131. Mortazavi, A., Leeper Thompson, E. C., Garcia. S. T., Myers, R. M. and Wold, B. (2006). Comparative genomics modeling of the NRSF/REST repressor network: From single conserved sites to genome-wide repertoire. Genome Res. 16: 1208-1221. PMID: 16963704. PMCID: PMC1581430.

132. Elbaz, A., Nelson, L. M., Payami, H., Ioannidis, J. P. A., Fiske, B. K., Annesi, G., Carmine, A., Factor, S. A., Ferrarese, C., Hadjigeorgiou, G. M., Higgins, D., Kawakami, H., Krueger, R., Marder, K., Mayeux, R., Mellick, G., Nutt, J., Ritz, B., Samii, A., Tanner,C. M., Van Broeckhoven, C., Van Den Eeden, S. K., Wirdefeldt, K., Zabetian, C. P., Dehem, M., Montimurro, J.S., Southwick, A., Myers, R. M., and Trikalinos, T. A. (2006). Lack of replication of thirteen single-nucleotide polymorphisms implicated in Parkinson’s disease: a large-scale international study. Lancet Neurol. 5: 917-923. PMCID: PMC3636768.

133. Cooper, S. J., Trinklein, N. D., Nguyen, L. and Myers, R. M. (2007). Serum Response Factor binding sites differ in three human cell types. Genome Res. 17: 136-144. PMID: 17200232. PMCID: PMC1781345.

134. Strehlow, A. T., Li, J. Z. and Myers, R. M. (2007). Wild-type huntingtin participates in protein trafficking between the Golgi and the extracellular space. Hum. Molec. Genet. 16: 391-409. PMID: 17189290.

135. \*Johnson, D. S., \*Mortazavi, A., Myers, R. M. and Wold, B. (2007). Genome-wide mapping of in vivo protein DNA interactions. Science. 316: 1497-1502. (\*co-first authors). PMID: 17540862. See also: Perspective by Stanley Fields. Science. 316: 1441-1442.

136. Lin, J. M., Collins, P. J., Trinklein N. D., Fu, Y., Xi, H., Myers, R. M. and Weng, Z. (2007). Transcription factor binding and histone modifications in human bidirectional promoters. Genome Res. 17: 818-827. PMID: 17568000. PMCID: PMC1891341.

137. Trinklein, N. D., Karaöz, U., Wu, J., Halees, A., Force Aldred, S., Collins, P. J., Zheng, D., Zhang, Z., Gerstein, M., Snyder, M., Myers, R. M. and Weng, Z. (2007). Integrated analysis of experimental datasets reveals many novel promoters in 1% of the human genome. Genome Res. 17: 720-731. PMID: 17567992. PMCID: PMC3098557.

138. Denoeud, F., Kapranov, P., Ucla, C., Frankish, A., Castelo, R., Drenkow, J., Lagarde, J., Alioto, T., Manzano, C., Chrast, J., Dike, S., Wyss, C., Henrichsen, C. N., Holroyd, N., Dickson, M. C., Taylor, R., Hance, Z., Foissac, S., Myers, R. M., Rogers, J., Hubbard, T., Harrow, J., Guigo, R., Gingeras, T. R., Antonarakis, S. E. and Reymond, A. (2007). Prominent use of distal 5’ transcription start sites and discovery of a large number of additional exons in ENCODE regions. Genome Res. 17: 746-759. PMID: 17567994. PMCID: PMC1891335.

139. ENCODE Project Consortium. (2007). Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature. 447: 799-816. See also: News and Views by John M. Greally. Nature. 447: 782-783. PMID: 17571346. PMCID: PMC2212820.

140. Karssen, A. M., Her, S., Li, J. Z., Patel, P. D., Meng, F., Bunney, Jr., W. E., Jones, E. G., Watson, S. J., Akil, H., Myers, R. M., Schatzberg, A. F. and Lyons, D. M. (2007). Stress-induced changes in primate prefrontal profiles of gene expression. Mol. Psychiatry. 12: 1089-1102. PMID: 17893703.

141. Atz, M., Walsh, D., Cartagena. P., Li, J., Evans, S., Choudary, P., Overman, K., Stein, R., Tomita, H., Potkin, S., Myers, R., Watson, S. J., Jones, E. G., Akil, H., Bunney, W. E. Jr., Vawter, M. P. and Members of National Institute of Mental Health Conte Center and Pritzker Neuropsychiatric Disorders Research Consortium. (2007). Methodological considerations for gene expression profiling of human brain. J. Neurosci. Methods. 163: 295-309. PMID: 1751205.

142. Li, J. Z., Meng, F., Tsavaler, L., Evans, S. J., Choudary, P. V., Tomita, H., Vawter, M. P., Walsh, D., Shokoohi, V., Chung, T., Bunney, W. E., Jones, E. G., Akil, H., Watson, S. J. and Myers, R. M. (2007). Sample matching by inferred agonal stress in gene expression analyses of the brain. BMC Genomics. 8: 336. PMID: 17892578. PMCID: PMC2213675.

143. Assimes, T. L., Knowles, J. W., Priest, J. R., Basu A., Borchert, A., Volcik, K. A., Grove, M. L., Tabor, H. K., Southwick, A., Tabibiazar, R., Sidney, S., Boerwinkle, E., Go, A. S., Iribarren, C., Hlatky, M. A., Fortmann, S. P., Myers, R. M., Kuhn, H., Risch, N. and Quertermous, T. (2007). A near null variant of 12/15-LOX encoded by a novel SNP in ALOX15 and the risk of coronary artery disease. Atherosclerosis. 198: 136-144. PMID: 17959182. PMCID: PMC2440699.

144. Collins, P. J., Kobayashi, Y., Nguyen, L., Trinklein, N. D. and Myers, R. M. (2007). The ets-related transcription factor GABP directs bidirectional transcription. PLoS Genet. 3: e208. PMID: 18020712. PMCID: PMC2077898.

145. Hlatky, M. A., Quertermous, T., Boothroyd, D. B., Priest, J. R., Glassford, A. J., Myers, R. M., Fortmann, S. P., Iribarren, C., Tabor, H. K., Assimes, T. L., Tibshirani, R. J. and Go, A. S. (2007). Polymorphisms in hypoxia inducible factor 1 and the initial clinical presentation of coronary disease. Am. Heart J. 154: 1035-1042. PMID: 18035072. [PubMed - indexed for MEDLINE].

146. Hlatky, M. A., Ashley, E., Quertermous, T., Boothroyd, D. B., Ridker, P., Southwick, A., Myers, R. M., Iribarren, C., Fortmann, S. P. and Go, A. S.; for the Atherosclerotic Disease, Vascular Function and Genetic Epidemiology (ADVANCE) Study. (2007). Matrix metalloproteinase circulating levels, genetic polymorphisms, and susceptibility to acute myocardial infarction among patients with coronary artery disease. Am. Heart J. 154: 1043-1051. PMID: 18035073.

147. Knowles, J. W., Wang, H., Itakura, H., Southwick, A., Myers, R. M., Iribarren, C., Fortmann, S. P., Go, A. S., Quertermous, T. and Hlatky, M. A. (2007). Association of polymorphisms in platelet and hemostasis system genes with acute myocardial infarction. Am. Heart J. 154: 1052-1058. PMID: 18035074. PMCID: PMC4031914.

148. Sequeira, A., Meng, F., Rollins, B., Myers, R. M., Jones, E. G., Watson, S. J., Akil, H., Schatzberg, A. F., Barchas, J., Bunney, W. E. and Vawter, M. P. (2008). Coding SNPs included in exon arrays for the study of psychiatric disorders. Molec. Psych. 13: 363-365. PMID: 18347597. PMCID: PMC3098557.

149. Johnson, D. S., Li, W., Gordon, D. B., Bhattacharjee, A., Curry, B., Ghosh, J., Brizuela, L., Carroll, J. S., Brown, M., Flicek, P., Koch, C., Dunham, I., Bieda, M., Xu, X., Farnham, P., Kapranov, P., Nix, D. A., Gingeras, T., Zhang, X., Holster, H., Jing, N., Green, R., Song, J., McCuine, S. A., Anton, E., Nguyen, L., Trinklein, N. D., Ye, Z., Ching, K., Hawkins, D., Ren, B., Scacheri1, P. C., Rozowsky, J., Karpikov, A., Euskirchen, G., Weissman, S., Gerstein, M., Snyder, M., Yang, A., Moqtaderi, Z., Hirsch, H., Shulha, H. P., Fu, Y., Weng, Z., Struhl, K., Myers, R. M., Lieb, J. D., and Liu, X. S. (2008). Systematic evaluation of variability in simulated ChIP-chip experiments. Genome Res. 18: 393-403. PMID: 18258921. PMCID: PMC2259103.

150. Schroeder, D. I. and Myers, R. M. (2008). Multiple transcription start sites for FOXP2 with varying cellular specificities. Gene. 413: 42-28. PMID: 18316164.

151. \*Li, J. Z., \*Absher, D. M., Tang, H. Southwick, A. M., Casto, A. M., Ramachandran, S., Cann, H. M., Barsh, G. S., Feldman, M., Cavalli-Sforza, L. L. and Myers, R. M. (2008). Worldwide human relationships inferred from genome-wide patterns of variation. Science. 319: 1100-1104. (\*co-first authors). PMID: 18292342.

152. Shao, L., Martin, M. V., Watson, S. J., Schatzberg, A., Akil, H., Myers, R. M., Jones, E. G., Bunney W. E. and Vawter, M. P. (2008). Mitochondrial involvement in psychiatric disorders. Ann. Med. 40: 281-295. PMID: 18428021. PMCID: PMC3098560.

153. Assimes, T. L., Knowles, J. W., Basu, A., Iribarren, C., Southwick, A., Tang, H., Absher, D., Li, J., Fair, J. M., Rubin, G. D., Sidney, S., Fortmann, S. P., Go, A. S., Hlatky, M. A., Myers, R. M., Risch, N. and Quertermous, T. (2008). Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE Study. Hum. Mol. Genet. 17: 2320-2328. PMID: 18443000. PMCID: PMC2733811.

154. Valouev, A., Johnson, D. S., Sundquist, A., Medina, C., Anton, E., Batzoglou, S., Myers, R. M. and Sidow, A. (2008). Genome-wide analysis of transcription factor binding sites based on ChIP-seq data. Nat. Methods. 5: 829-834. PMID: 19160518. PMCID: PMC2917543.

155. McGowan, K. A., Li, J. Z., Park, C. Y., Beaudry, V., Tabor, H. K., Sabnis, A. J., Zhang, W., Fuchs, H., Hrabe de Angelis, M., Myers, R. M., Attardi, L. D. and Barsh. G. S. (2008). Genetics of dark skin: ribosomal protein mutations act through p53. Nat. Genet. 40: 963-970. PMID: 18641651PMCID: PMC3979291.

156. The Cancer Genome Atlas (TCGA) Research Network (2008). Comprehensive genomic characterization defines novel cancer genes and core pathways in human glioblastomas. Nature. 455: 1061-1068. PMID: 18772890. PMCID: PMC2671642.

157. Zhang, Y., Liu, T., Meyer, C. A., Eeckhoute, J., Johnson, D. S., Bernstein, B. E., Nussbaum, C., Myers, R. M., Brown, M., Li, W. and Liu, X. S. (2008). Model-based analysis of ChIP-Seq (MACS). Genome Biol. 9: R137. PMID: 18798982. PMCID: PMC2592715.

158. Ji, H., Jiang, H., Ma, W., Johnson, D. S., Myers, R. M., and Wong, W. H. (2008). An integrated system CisGenome for analyzing ChIP-chip and ChIP-seq data. Nat. Biotechnol. 26: 1293-1300. PMID: 18978777. PMCID: PMC2596672.

159. Brunner, A. L.,Johnson, D. S., Kim, S. W., Valouev, A., Reddy, T. E., Neff, N. F., Anton, E., Medina, C., Nguyen. L., Chiao, E., Oyolu, C. B., Schroth, G. P., Absher, D., Baker, J. C. and Myers, R. M. (2009). Distinct DNA methylation patterns characterize differentiated human embryonic stem cells and developing human fetal liver. Genome Res. 19: 1044-1056. PMID: 19273619. PMCID: PMC2694474.

160. Rollins, B., Martin, M. V., Sequeira, P. A., Moon, E. A., Morgan, L. Z., Watson, S. J., Schatzberg, A., Akil, H., Myers, R. M., Jones, E. G., Wallace, D. C., Bunney, W. E. and Vawter, M. P. (2009). Mitochondrial variants in schizophrenia, bipolar disorder, and major depressive disorder. PLoS ONE. 4: e4913. [Epub 2009 Mar 17]. PMID: 19290059. PMCID: PMC2654519.

161. Pickrell, J. K., Coop, G., Novembre, J., Kudaravalli, S. Li, J., Absher, D., Srinivasan, B. S., Barsh, G. S., Myers, R. M., Feldman, M. W. and Pritchard, J. K. (2009). Signals of recent positive selection in a worldwide sample of human populations. Genome Res. 19: 826-837. PMID: 19307593. PMCID: PMC2675971.

162. Itsara, A., Cooper, G. M., Baker, C., Girirajan, S., Li, J., Absher, D., Krauss, R., Myers, R. M., Mefford, H., Cann, H. S., Singleton, A. A., Nickerson, D. A. and Eichler, E. E. (2008). Population Analysis of Large Copy Number Variants and Hotspots of Human Genetic Disease. Am. J. Hum. Genet. 4: 148-161. PMID: 19166990. PMCID: PMC2668011.

163.  Scott, L.J., Muglia, P., Kong, X.Q., Guan, W., Flickinger, M., Upmanyu, R., Tozzi, F., Li, J.Z., Burmeister, M., Absher, D., Thompson, R.C., Francks, C., Meng, F., Antoniades, A., Southwick, A.M., Schatzberg, A.F., Bunney, W.E., Barchas, J.D., Jones, E.G., Day, R., Matthews, K., McGuffin, P., Strauss, J.S., Kennedy, J.L., Middleton, L., Roses, A.D., Watson, S.J., Vincent, J.B., Myers, R.M., Farmer, A.E., Akil, H., Burns, D.K., and Boehnke, M. (2009). [Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry.](http://www.ncbi.nlm.nih.gov/pubmed/19416921?ordinalpos=1&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DefaultReportPanel.Pubmed_RVDocSum) Proc. Natl. Acad. Sci. U.S.A. 106: 7501-7506. PMID: 19416921. PMCID: PMC2678639.

164. Coop, G., Pickrell, J. K., Novembre, J., Kudaravalli, S., Li, J., Absher, J., Myers, R. M., Cavalli-Sforza, L. L., Feldman, M. W. and Pritchard, J. K. (2009). The role of geography in human adaptation. PLoS Genet. 5: e1000500. PMID: 19503611. PMCID: PMC2685456.

165. Reddy, T. E., Pauli, F., Sprouse, R. O., Neff, N. F., Newberry, K. M., Garabedian, M. J. and Myers, R. M.  (2009).  Genomic determination of the glucocorticoid response reveals unexpected mechanisms of gene regulation. Genome Res. 19: 2163-2171. PMID: 19801529. PMCID: PMC2792167.

166. Kitano, J., Ross, J. A., Mori, S., Kume, M., Jones, F. C., Chan, Y. F., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M. and Peichel, C. L. (2009). A role for a neo-sex chromosome in stickleback speciation. Nature 461: 1079-1083. PMID: 19783981. PMCID: PMC2776091.

167. Hesselson, S., Matsson, P., Shima, J., Fukushima, H., Yee, S. W., Kobayashi, Y., Gow, J., Ha, C., Ma, B., Poon, A., Johns, S., Stryke, D., Castro, D., Tahara, H., Choi, J. H., Chen, L., Picard, N., Sjödin, E., Roelofs, M., Ferrin, T., Myers, R. M., Kroetz, D., Kwok, P.Y., and Giacomini, K.   (2009). Genetic variation in the proximal promoter of ABC and SLC superfamilies: Liver and kidney specific expression and promoter activity predict variation. PLos One. 4: e6942. PMID: 19742321. PMCID: PMC2735003.

168. The MGC Project Team, Temple, G., Jang, W., Wagner, L., Shenmen, C. M., Gerhard, D. S., Rasooly, R., Feingold, E. A., Good, P., Guyer, M., Robinson, C., Peck, A.M., Derge, J.G., Lewis, J., Shoaf, D., Collins, F. S., Misquitta, L., Schaefer, C. F., Buetow, K. H., Bonner, T. I., Yankie, L., Ward, M., Phan, L., Astashyn, A., Brown, G., Farrell, C., Hart, J., Landrum, M., Maidak, B., Murphy, M., Murphy, T., Rajput, B., Riddick, L., Webb, D., Weber, J., Wu, W., Pruitt, K. D., Maglott, D., Siepel, A., Brejova, B., Diekhans, M., Harte, R., Baertsch, R., Kent, J., Haussler, D., Brent, M., Langton, L., Comstock, C.L.G., Stevens, M., Wei, C., Salehi-Ashtiani, K., Murray, R. R., Ghamsari, L., Mello, E., Lin, C., Pennacchio, C., Schreiber, K., Shapiro, N., Marsh, A., Pardes, E., Moore, T., Lebeau, A., Muratet, M., Simmons, B., Kloske, D., Sieja, S., Hudson, J., Sethupathy, P., Brownstein, M., Bhat, N., Lazar, J., Gruber, C.E., Smith, M.R., McPherson, J., Garcia, A. M., Gunaratne, P. H., Wu, J., Muzny, D., Gibbs, R. A., Young, A. C., Bouffard, G. G., Blakesley, R. W., Mullikin, J., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Hirst, M., Zeng, T., Tse, K., Moksa, M., Deng, M., Ma, K., Mah, D., Pang, J., Taylor, G., Chuah, E., Deng, A., Fichter, K., Go, A., Lee, S., Wang, J., Griffith, M., Morin, R., Moore, R. A., Mayo, M., Munro, S., Wagner, S., Jones, S., Holt, R.A., Marra, M.A., Hartigan, J., Graf, M., Wagner, R., Letovsky, S., Pulido, J.C., Robison, K., Mulligan, J., Sheen, L., Esposito, D., Hartley, J. L., Wall, V. E., Hopkins, R. F., Ohara, O. and Wiemann, S. (2009). The completion of the Mammalian Gene Collection (MGC). Genome Res. 19: 2324-2333. PMID: 19767417. PMCID: PMC2792178.

169. Martin, M. V., Rollins, B., Sequeira, P. A., Mesen, A., Byerley, W., Stein, R., Moon, E. A., Akil, H., Jones, E. G., Watson, S. J., Barchas, J., Delisi, L. E., Myers, R. M., Schatzberg, A., Bunney and W. E., Vawter, M. P. (2009). Exon expression in lymphoblastoid cell lines from subjects with schizophrenia before and after glucose deprivation. BMC Med. Genomics 2: 62. PMID: 19772658. PMCID: PMC2760574.

170. Wheeler, H. E., Metter, E. J., Tanaka, T., Absher, D., Higgins, J., Zahn, J. M., Wilhelmy, J., Davis, R. W., Singleton, A. W., Myers, R. M., Ferrucci, L. and Kim, S. K. (2009). Sequential use of transcriptional profiling, expression quantitative trait mapping, and gene association implicates MMP20 in human kidney aging. PLoS Genet. 5: e1000685. doi:10.1371/journal.pgen.1000685. PMID: 19834535. PMCID: PMC2752811.

171. Zakharia, F., Basu, A., Absher, D., Assimes, T. L., Go, A. S., Hlatky, M.A., Iribarren, C., Knowles, J. W., Li, J., Narasimhan, B., Sidney, S., Southwick, A., Myers, R. M., Quertermous, T., Risch, N., and Tang, H. (2009).  Characterizing the admixed African ancestry of African Americans. Genome Biol. 10: R141. PMID: 20025784. PMCID: PMC2812948.

172.  Chan, Y. F., Marks, M. E., Jones, F. C., Villarreal Jr., G., Shapiro, M. D., Fisher, S., Southwick, A. M., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Petrov, D., Jónsson, B., Schluter, D., Bell, M. A. and Kingsley, D. M. (2010). Adaptive evolution of pelvic reduction in sticklebacks by recurrent deletion of a Pitx1 enhancer. Science 327: 302-305. PMID: 20007865. PMCID: PMC3109066.

173. Goode, D. L., Cooper, G. M., Schmutz, J., Dickson, M., Gonzales, E., Tsai, M., Karra, K., Davydov, E., Batzoglou, S., Myers, R. M. and Sidow, A. (2010). Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes. Genome Res. 20: 301-310. PMID: 20067941. PMCID: PMC2840986.

174. Amemiya, C. T., Powers, T. P., Prohaska, S. J., Grimwood, J., Schmutz, J., Dickson, M., Miyake, T., Schoenborn, M. A., Myers, R. M., Ruddle, F. H. and Stadler, P. F. (2010). Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. Proc. Natl. Acad. Sci. USA. 107: 3622-3627. PMID: 20139301. PMCID: PMC2840454.

175. Wang, C., Sanders, C. M., Yang, Q., Schroeder, Jr., H. W., Wang, E., Babrzadeh, F., Gharizadeh, B., Myers, R. M., Hudson, Jr., J. R., Davis, R. W. and Han, J.  (2010). High throughput sequencing reveals a complex pattern of dynamic interrelationships among human T cell subsets. Proc Natl Acad Sci USA. 107: 1518-1523. PMID: 20080641. PMCID: PMC2824416.

176. Ding, F., Li, H. H., Li, J., Myers, R. M. and Francke, U. (2010). Neonatal starvation response and developmental changes in gene expression revealed by hypothalamic gene expression profiling in mice. PLoS ONE. 5: e9402. PMID: 20195375. PMCID: PMC2827556.

177. Landolin, J. M., Johnson, D. S., Trinklein, N. D., Aldred, S. F., Medina, C., Shulha, H., Weng, Z., Myers, R. M. (2010). Sequence features that drive human promoter function and tissue specificity. Genome Res. 20: 890-898. PMID: 20501695. PMCID: PMC2892090.

178. Casto, A. M., Li, J. Z., Absher, D., Myers, R., Ramachandran, S. and Feldman, M. W. (2010). Characterization of X-linked SNP genotypic variation in globally distributed human populations. Genome Biol. 11: R10. PMID: 20109212. PMCID: PMC2847713.

179.  Bernard, R., Kerman, I. A., Thompson, R. C., Jones, E. G., Bunney, W. E., Barchas, J. D., Schatzberg, A. F., Myers, R. M., Akil, H. and Watson. S. J. (2010). Altered expression of glutamate signaling, growth factor, and glia genes in the locus coeruleus of patients with major depression. Mol. Psychiatry. 16: 634-646. PMID: 20386568. PMCID: PMC2927798.

180. Assimes, T. L., Holm, H., Kathiresan, S., Reilly, M. P., Thorleifsson, G., Voight, B. F., Erdmann, J., Willenborg, C., Vaidya, D., Xie, C., Patterson, C. C., Morgan, T. M., Burnett, M. S., Li, M., Hlatky, M. A., Knowles, J. W., Thompson, J. R., Absher, D., Iribarren, C., Go, A., Fortmann, S. P., Sidney, S., Risch, N., Tang, H., Myers, R. M., Berger, K., Stoll, M., Shah, S. H., Thorgeirsson, G., Andersen, K., Herrera, J. E., Faraday, N., Kim, Y., Kral, B. G., Mathias, R., Ruczinski, I., Suktitipat, B., Wilson, W. F., Yanek, L. R., Becker, L. C., Linsel-Nitschke, P., Lieb, W., König, I. R., Hengstenberg, C., Fischer, M., Stark, K., Reinhard, W., Winogradow, J., Grassl, M., Grosshennig, A., Preuss, M., Schreiber, S., Wichmann, H-E., Meisinger, C., Yee, J., Friedlander, Y., Do, R., Meigs, J. B., Williams, G., Nathan, D. M., MacRae, C. A., Qu, L., Wilensky, R. L., Matthai J. R., W. H., Qasim, A. N., Hakonarson, H., Pichard, A. D., Kent, K. M., Satler, L., Lindsay, J. M., Waksman, R., Knouff, C. W., Waterworth, D. M., Walker, M. C., Mooser, V. E., Marrugat, J., Lucas, G., Subirana, I., Sala, J., Ramos, R., Martinelli, N., Olivieri, O., Trabetti, E. Malerba, G., Pignatti, P. F., C., Mirel, D., Parkin, M., Hirschhorn, J. N., Asselta, R., Duga, S., Musunuru, K., Daly, M. J., Purcell, S., Eifert, S., Braund, P. S., Wright, B. J., Balmforth, A. J.,. Ball, S. G., Myocardial Infarction Genetics Consortium, Wellcome Trust Case Control Consortium, Cardiogenics, Ouwehand, W. H., Deloukas, P., Scholz, M., Cambien, F., Huge, A., Scheffold, T., Salomaa, V., Girelli, D., Granger, C. B., Peltonen, L., McKeown, P. P., Altshuler, D., Melander, O., Devaney, J. M., Epstein, S. E., Rader, D. J., Elosua, R., Engert, J. C., Anand, S. S., Hall, A. S., Ziegler, A., O’Donnell, C. J., Spertus, J. A., Siscovick, D., Schwartz, S. M., Becker, D., Thorsteinsdottir, U., Stefansson, K., Schunkert, H., Samani, N. J., Quertermous, T. (2010). Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies. J. Amer. Coll. Cardiol. 56: 1552-1563. PMID: 20933357.  PMCID: PMC3084526. Erratum in J. Am. Coll. Cardiol. (2011). 57: 520.

181. Mendoza-Fandino, G. A., Gee, J. M., Ben-Dor, S., Gonzalez-Quevedo, C., Lee, K., Kobayashi, Y., Hartiala, J., Myers, R. M., Leal, S. M., Allayee, H. and Patel, P. I. (2010). A Novel g.-1258G>A Mutation in a Conserved Putative Regulatory Element of PAX9 is Associated with Autosomal Dominant Molar Hypodontia. Clin. Gen. 80: 265-272. PMID: 21443745. PMCID: PMC3084526.

182. Krolewski, D. M., Medina, A., Kerman, I. A., Bernard, R., Burke, S., Thompson, R. C., Bunney, W. E. Jr., Schatzberg, A. F., Myers, R. M., Akil, H., Jones, E. G. and Watson, S. J. (2010). Expression patterns of corticotropin-releasing factor, arginine vasopressin, histidine decarboxylase, melanin-concentrating hormone, and orexin genes in the human hypothalamus. J. Comp. Neurol. 15: 4591-4611. PMID: 20886624. PMCID: PMC2965642.

183. Popat, R. A., Van Den Eeden, S. K., Tanner, C. M., Kamel, F., Umbach, D. M., Marder, K., Mayeux, R., Ritz, B., Webster Ross, G., Petrovitch, H., Topol, B., McGuire, V., Costello, S., Manthripragada, A. D., Southwick, A., Myers, R. M. and Nelson, L. M. (2011). Coffee, ADORA2A, and CYP1A2: the caffeine connection in Parkinson’s disease.  Eur. J. Neurol. 18: 756-765. PMCID: PMC3556904.

184. ENCODE Project Consortium. (2011). A user's guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biol. 9: e1001046. PMID: 21526222. PMCID: PMC3079585.

185. Greenwood, A. K., Jones, F. C., Chan, Y. F., Brady, S. D., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M., and Peichel, C. L. (2011). The genetic basis of divergent pigment patterns in juvenile threespine sticklebacks. Heredity. 107: 155-166. PMID: 21304547. PMCID: PMC3136628.

186. Kobayashi, Y., Absher, D. M., Gulzar, Z. G., Young, S., McKenney, J. K., Peehl, D., Brooks, J. D., Myers, R. M., and Sherlock, G.  (2011).  DNA methylation profiling reveals novel biomarkers and important roles for DNA methyltransferases in prostate cancer.  Genome Res. 21: 1017-1027. PMID: 21521786. PMCID: PMC3129245.

187. The Cancer Genome Atlas Research Network (2011). Integrated genomic analyses of ovarian carcinoma. Nature. 474: 609-615. PMID: 21720365. PMCID: PMC3163504.

188. McGuire, V., Van Den Eeden, S. K., Tanner, C. M.,  Kamel, F., Umbach, D. M., Marder, K., M.P.H., Mayeux, R., Ritz, B., Ross, G. W., Petrovitch, H., Topol, B., Popat, R. A., Costello, S., Manthripragada, A. D., Southwick, A., Myers, R. M., and Nelson, L. M. (2011).  Association of DRD2 and DRD3 polymorphisms with Parkinson’s disease in a multiethnic consortium.  J. Neurol. Sci.  307: 22-29. PMCID: PMC3155471.

189. Gertz, J., Varley, K., Reddy, T., Bowling, K., Pauli, F., Parker, S., Kucera, K., Willard, H. and Myers, R. M. (2011). Analysis of DNA methylation in a three-generation family reveals widespread genetic influence on epigenetic regulation. PLoS Genetics. 7: e1002228. Epub Aug 11. PMID: 21852959. PMCID: PMC3154961.

190. Simpson, N. E., Gertz, J., Imberg, K., Myers, R. M. and Garabedian, M. J. (2011). Enhanced genome-wide occupancy of estrogen receptor alpha by the co-chaperone p23 in breast cancer cells. Molec. Endocrin. 26: 194-202. PMID: 22074947. PMCID: PMC3248325.

191. Moon, E., Rollins, B., Mesén, A., Sequeira, A., Myers, R. M., Akil, H., Watson, S. J., Barchas, J., Jones, E. G., Schatzberg, A., Bunney, W. E., Delisi, L. E., Byerley, W., and Vawter, M. P.  (2011).  Lack of association to a NRG1 missense polymorphism in schizophrenia or bipolar disorder in a Costa Rican population. Schizophr. Res. 131: 52-57. PMID: 21745728. PMCID: PMC3159824.

192. Kucera, K. S., Reddy, T. E., Pauli, F., Gertz, J., Logan, J. E., Myers, R. M., and Willard, H. F. (2011). Allele-specific distribution of RNA polymerase II on female X chromosomes.  Hum. Molec. Genet.  20: 3964-3673. PMID: 21791549. PMCID: PMC3177651.

193. Sklar, P., Ripke, S., Scott, L. J., Andreassen, O. A., Cichon, S., Craddock, N., Edenberg, H. J., Nurnberger Jr, J. I., Rietschel, M., Blackwood, D., Corvin, A., Flickinger, M., Guan, W., Mattingsdal, M., McQuillin, A., Kwan, P., Wienker, T. F., Daly, M., Dudbridge, F., Holmans, P. A., Lin, D., Burmeister, M., Greenwood, T. A., Hamshere, M. L., Muglia, P., Smith, E. N., Zandi, P. P., Nievergelt, C. M., McKinney, R., Shilling, P. D., Schork, N. J., Bloss, C. S., Foroud, T., Koller, D. L., Gershon, E. S., Liu, C., Badner, J. A., Scheftner, W. A., Lawson, W. B., Nwulia, E. A., Hipolito, M., Coryell, W., Rice, J., Byerley, W., McMahon, F. J., Schulze, T. G., Berrettini, W., Lohoff, F. W., Potash, J. B., Mahon, P. B., McInnis, M. G., Zöllner, S., Zhang, P., Craig, D. W., Szelinger, S., Barrett, T. B., Breuer, R., Meier, S., Strohmaier, J., Witt, S. H., Tozzi, F., Farmer, A., McGuffin, P., Strauss, J., Xu, W., Kennedy, J. L., Vincent, J. B., Matthews, K., Day, R., Ferreira, M. A., O’Dushlaine, C., Perlis, R., Raychaudhuri, S., Ruderfer, D., Hyoun, P. L., Smoller, J. W., Li, J., Absher, D., Thompson, R. C., Meng, F. G., Schatzberg, A. F., Bunney, W. E. , Barchas, J. D., Jones, E. G., Watson, S. J., Myers, R. M., Akil, H., Boehnke, M., Chambert, K., Moran, J., Scolnick, E., Djurovic, S., Melle, I., Morken, G., Gill, M., Morris, D., Quinn, E., Mühleisen, T. W., Degenhardt, F. A., Mattheisen, M., Schumacher, J., Maier, W., Steffens, M., Propping, P., Nöthen, M. M., Anjorin, A., Bass, N., Gurling, H., Kandaswamy, R., Lawrence, J., McGhee, K., McIntosh, A., McLean, A. W., Muir, W., J., Pickard, B. S., Breen, G., St. Clair, D., Caesar, S., Gordon-Smith, K., Jones, L., Fraser, C., Green, E. K., Grozeva, D., Jones, I. R., Kirov, G., Moskvina, V., Nikolov, I., O’Donovan, M. C., Owen, M. J., Collier, D. A., Elkin, A., Williamson, R., Young, A. H., Ferrier, I. N., Stefansson, K., Stefansson, H., Steinberg, S., Gustafsson, O., Bergen, S. E, Nimgaonkar, V., Hultman, C., Landén, M., Lichtenstein, P., Sullivan, P., Schalling, M., Osby, U., Backlund, L., Frisén, L., Langstrom, N., Jamain, S., Leboyer, M., Etain, B., Bellivier, F., Petursson, H., Sigurosson, E., Müller-Mysok, B., Lucae, S., Schwarz, M., Schofield, P. R., Martin, N., Montgomery, G. W., Lathrop, M., Óskarsson, H., Bauer, M., Wright, A., Mitchell, P. B., Hautzinger, M., Reif, A., Kelsoe, J. R. and Purcell, S. M. (2011). Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nat. Genet. 43: 977-983. PMID: 21926972. PMCID: PMC3637176.

194. Ng, S-L., Friedman, B.A., Schmid, S., Gertz, J., Myers, R. M., tenOever, B. R. and Maniatis, T. (2011). IKKε regulates the balance between the type I and type II interferon responses. Proc. Natl. Acad. Sci. USA. 108: 21170-21175. PMID: 22171011. PMCID: PMC3248534.

195. Gertz, J., Varley, K. E., Davis, N. S., Baas, B. J., Goryshin, I. Y., Vaidyanathan, R., Kuersten, S. and Myers, R. M. (2012). Transposon-based construction of strand-specific RNA-seq libraries. Genome Res. 22: 134-141. PMID: 22128135. PMCID: PMC3246200.

196. Jones, F. C., Chan, Y. F., Schmutz, J., Grimwood, J., Brady, S., Southwick, A., Absher, D., Myers, R. M., Schluter, D. and Kingsley, D. M. (2012). A genome-wide SNP genotyping array reveals patterns of global and species pair divergence in sticklebacks. Curr Biol. 22: 83-90. PMID: 22197244. PMCID: PMC3319444.

197. Zimmerman J. W., Pennison, M. J., Brezovich I., Yi, N., Yang, C. T., Ramaker, R., Absher, D., Myers, R. M., Kuster, N., Costa, F. P., Barbault, A. and Pasche, B. (2012). Cancer cell proliferation is inhibited by specific modulation frequencies. Br. J. Cancer. 106: 307-313. PMID: 22134506. PMCID: PMC3261663.

198. Kirigin, F. F., Lindstedt, K., Sellars, M., Ciofani, M., Low, S. L., Jones, L., Bell, F., Pauli, F., Bonneau, R., Myers, R. M., Littman, D. R. and Chong, M. M. W. (2012). Dynamic microRNA gene transcription and processing during T cell development. J. Immunol. 188: 3257-3267. PMID: 22379031. PMCID: PMC3934760.

199. Reddy, T. E., Gertz, J., Pauli, F., Kucera, K. S., Newberry, K. M., Marinov, G. K., Mortazavi, A., Williams, B. A., Wold, B., Willard, H. F. and Myers, R. M.  (2012). Effects of sequence variation on differential allelic transcription factor occupancy and gene expression.  Genome Res. 22: 860-869. PMID: 22300769. PMCID: PMC3337432. See Research Highlight in Nature Reviews Genetics. doi:10.1038/nrg3219.

200. Jones, F. C., Grabherr, M. G., Chan, Y. F., Russell, P, Mauceli, E., Zody, M. C., Pirun, M., Johnson, J., White, S., Birney, E., Searle, S., Schmutz, J., Grimwood, J., Dickson, M. C., Myers, R. M., Miller, C. T., Summers, B. R., Knecht, A. K., Brady, S. D., Zhang, H., Pollen, A. A., Howes, T., Amemiya, C., Broad Whole Genome Sequencing Platform and Whole Genome Assembly Team, Lander, E. S., DiPalma, F., Lindblad-Toh, K. and Kingsley, D. M. (2012). The genomic basis of adaptive evolution in threespine sticklebacks. Nature 484: 55-61. PMID: 22481358. PMCID: PMC3322419. Comment in Nature 484: 46-47.

201. Chen, Y., Negre, N., Li, Q., Mieczkowska, J. O., Slattery, M., Liu, T., Zhang, Y., Kim, T., He, H., Zieba, J., Ruan, Y., Bickel, P. J., Myers, R. M., Wold, B. J., White, K. P., Lieb, J. D. and Liu, S. (2012). Systematic evaluation of factors influencing ChIP-seq fidelity. Nat. Methods. 9: 609-614. PMID: 22522655. PMCID: PMC3477507.

202. Monahan, K., Rudnick, N. D., Kehayova, P. D., Pauli, F., Newberry, K. N., Myers, R. M. and Maniatis, T. (2012). The role of CTCF and cohesin in the generation of single cell diversity of protocadherin-α gene expression. Proc. Natl. Acad. Sci. USA. 109: 9125-9130. PMID: 22550178. PMCID: PMC3384188.

203. Sequeira, A., Morgan, L., Walsh, D. M., Cartagena, P. M., Choudary, P., Li, J., Schatzberg, A. F., Watson, S. J., Akil, H., Myers, R. M., Jones, E. G., Bunney, W. E. and Vawter, M. P. (2012). Gene expression changes in the prefrontal cortex, anterior cingulate cortex and nucleus accumbens of mood disorders subjects that committed suicide. PLoS One. 7: e35367. Epub 2012 Apr 30. PMID: 22558144. PMCID: PMC3340369.

204. Pemberton, T. J., Absher, D., Feldman, M. W., Myers, R. M., Rosenberg, N. A. and Li, J. Z. (2012). Genomic patterns of homozygosity in worldwide human populations. Am. J. Hum. Genet. 91: 275-292. PMID: 22883143. PMCID: PMC3415543.

205. Hastak, K., Adimoolam, D., Trinklein, N. D., Myers, R. M. and Ford, J. M.  (2012).  Identification of a functional in vivo p53 response element in the coding sequence of the Xeroderma Pigmentosum Group C gene.  Genes & Cancer OnlineFirst.  3: 131-140. PMID: 23050045. PMCID: PMC3463920.

206. Reddy, T. E., Gertz, J., Crawford, G. E., Garabedian, M. J. and Myers, R. M.  (2012).  The hypersensitive glucocorticoid response specifically regulates period 1 and expression of circadian genes.  Mol. Cell. Biol. 32: 3756-3767. PMID: 22801371. PMCID: PMC3430195.

207. Wark, A. R., Mills, M. G., Dang, L. H., Chan, Y. F., Jones, F. C., Brady, S. D., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M., and Peichel, C. L.  (2012).  Genetic Architecture of Variation in the Lateral Line Sensory System of Threespine Sticklebacks.  G3: Genes Genomes Genetics. 2:  1047-1056. PMID: 22973542. PMCID: PMC3429919.

208. Wang, H., Maurano, M. T., Qu, H., Varley, K. E., Gertz, J., Pauli, F., Weaver, M., Lee, K., Canfield, T., Sandstrom, R., Thurman, R. E., Kaul, R., Myers, R. M. and Stamatoyannopoulos, J. A. (2012). Widespread plasticity in CTCF occupancy linked to DNA methylation. Genome Res. 22: 1680-1688. PMID: 22955980. PMCID: PMC3431485.

209. Gertz, J., Reddy, T. E., Varley, K. E., Garabedian, M. J., and Myers, R. M.  (2012).  Genistein and bisphenol A exposure cause estrogen receptor 1 to bind thousands of sites in a cell type-specific manner. Genome Res. 22: 2153-2162. PMID: 23019147. PMCID: PMC3483545.

210. Whitfield, T. W., Wang, J., Collins, P. J., Partridge, E. C., Trinklein, N. D., Myers, R. M. and Weng, Z. (2012). Functional analysis of transcription factor binding sites in human promoters. Genome Biol. 13:R50. PMID: 22951020. PMCID: PMC3491394.

211. Wang, J., Zhuang, J., Sowmya Iyer, S., Lin, X., Whitfield, T. W., Greven, M., Pierce, B. G., Dong, X., Kundaje, A., Cheng, Y., Rando, O. J., Birney, E., Myers, R. M., Noble, W. S., Snyder, M. and Weng, Z. (2012). Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Res. 22: 1798-1812. PMCID: PMC3431495.

212. The ENCODE Project Consortium. (2012). An Integrated Encyclopedia of DNA Elements in the Human Genome. Nature. 489: 57–74. PMID: 22955616. PMCID: PMC3439153.

213. Gerstein, M. B., Kundaje, A., Hariharan, M., Landt, S. G., Yan, K., Cheng, C., Mu, X., Khurana, E., Rozowsky, J., Alves, P., Abyzov, A., Addleman, N., Alexander, R., Bhardwaj, N., Boyle, A. P., Cayting, P., Charos, A., Cheng, Y., Clarke, D., Eastman, C., Euskirchen, G., Frietze, S., Gertz, J., Grubert, F., Harmanci, A., Jain, P., Kasowski, M., Lacroute, P., Leng, J., Lian, J., Min, R., Monahan, H., O'Geen, H., Ouyang, Z., Partridge, E. C., Patacsil, D., Pauli, F., Raha, D., Ramirez, L., Reddy, T. E., Reed, B., Shi, M., Slifer, T., Wang, C., Wu, L., Yang, X., Yip, K., Zilberman-Schapira, G., Batzoglou, S., Sidow, A., Farnham, P. J., Myers, R. M., Weissman, S. M., and Snyder, M.  (2012).  Architecture of the human regulatory network derived from ENCODE data.  Nature.  489: 91–100. PMID: 22955619. PMCID: PMC4154057.

214. Landt, S. J., Marinov, G. K., Kundaje, A., Kheradpour, P., Pauli, F., Batzoglou, S., Bernstein, B. E., Bickel, P., Brown, J. B., Cayting, P., Chen, Y., DeSalvo, G., Epstein, C., Fisher-Aylor, K. I., Euskirchen, G., Gerstein, M., Gertz, J., Hartemink, A. J., Hoffman, M. M., Iyer, V. R., Jung, Y. L., Karmakar, S., Kellis, M., Kharchenko, P. V., Li, Q., Liu, T., Liu, X. S., Ma, L., Milosavljevic, A., Myers, R. M., Park, P. J., Pazin, M. J., Perry, M. D., Raha, D., Reddy, T. E., Rozowsky, J., Shoresh, N., Sidow, A., Slattery, M., Stamatoyannopoulos, J. A., Tolstorukov, M. Y., White, K. P., Xi, S., Farnham, P. J., Lieb, J. D., Wold, B. J., and Snyder, M.  (2012).  ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia.  Genome Res.  22: 1813-1831.  PMID: 22955991. PMCID: PMC3431496.

215. Sumiyama, K., Miyake, T., Grimwood, J., Stuart, A., Dickson, M., Schmutz, J., Ruddle, F., Myers, R. M. and Amemiya, C.  (2012).  Theria-specific homeodomain and cis-regulatory element evolution of the Dlx3-4 bigene cluster in 12 different mammalian species.  JEZ Part B: Molec. Dev. Evol.  5: 1-12. PMID: 22951979. PMCID: PMC3651898.

216. Ciofani, M., Madar, A., Galan, C., Sellars, M., Mace, K., Pauli, F., Agarwal, A., Huang, W., Parkurst, C. N., Muratet, M., Newberry, K. M., Meadows, S., Greenfield, A., Yang, Y., Jain, P., Kirigin, F. K., Birchmeier, C., Wagner, E. F., Murphy, K. M., Myers, R. M., Bonneau, R. and Littman DR. (2012). A Validated Regulatory Network for Th17 Cell Specification. Cell. 151: 289-303. PMID: 23021777. PMCID: PMC3503487.

217. Kerman, I. A., Bernard, R., Bunney, W. E., Jones, E. G., Schatzberg, A. F., Myers, R. M., Barchas, J. D., Akil, H., Watson, S. J., and Thompson, R. C.  (2012).  Evidence for transcriptional factor dysregulation in the dorsal raphe nucleus of patients with major depressive disorder.  Frontiers in Neuroscience. 6: 135. PMID: 23087602. PMCID: PMC3475304.

218. Candille, S., Absher, D., Bauchet, M., McEvoy, B., Beleza, S., Garrison, N. A., Myers, R. M., Barsh, G. S., Tang, H. and Shriver, M. D. (2012). Genome-wide association studies of quantitatively measured skin, eye, and hair pigmentation in four European populations. PLoS ONE 7: e48294. PMID: 23118974. PMCID: PMC3485197.

219. Guo, Y., Monahan, K., Wua, H., Gertz, J., Lia, W., Myers, R. M., Maniatis, T. and Wu, Q. (2012). CTCF/Cohesin-mediated DNA looping is required for protocadherin α promoter choice. Proc. Nat. Acad. Sci. USA. 109: 21081-21086. PMID: 23204437. PMCID: PMC3529044.

220. Medina, A., Seasholtz, A. F., Sharma, V., Burke, S., Bunney, W. Jr., Myers, R. M., Schatzberg, A., Akil, H. and Watson, S. J.  (2012).  Glucocorticoid and mineralocorticoid receptor expression in the human hippocampus in major depressive disorder.  J. Psychiatr. Res.  47: 307-314.  PMID: 23219281. PMCID: PMC4248661.

221. Varley, K. E., Gertz, J., Bowling, K. M., Parker, S. L., Reddy, T. E., Pauli, F., Cross, M. K., Williams, B., Stamatoyannopoulos, J. A., Crawford, G. E., Absher, D. M., Wold, B. J. and Myers, R. M. (2013). Dynamic DNA methylation across diverse human cell lines and tissues. Genome Res. 23: 555-567. PMID: 23325432. PMCID: PMC3589544.

222. Phatnani, H. P., Guarnieri, P., Friedman, B., Carrasco, M. A., Muratet, M., O’Keeffe, S., Nwakeze, C., Pauli-Behn, F., Newberry, K. M., Meadows, S. K., Tapia, J. C., Myers, R. M., and Maniatis, T.  (2013).  An intricate interplay between astrocytes and motor neurons in ALS.  Proc. Natl. Acad. Sci. U.S.A.  110: E756-765. PMID: 23388633. PMCID: PMC3581928.

223. Tsumagari, K., Baribault, C., Varley, K. E., Gertz, J., Terragni, J., Pradhan, S., Badoo, M., Crain, C. M., Song, L., Crawford, G. E., Myers, R. M., Lacey, M., and Ehrlich, M.  (2013).  Early de novo DNA methylation and prolonged active demethylation in the muscle lineage.  Epigenetics. 15: 317-332. PMID: 23417056. PMCID: PMC3669123.

224. Li, J. Z., Bunney, B. G., Meng, F., Hagenauer, M. H., Walsh, D. M., Vawter, M. P., Evans, S. J., Choudary, P. V., Cartagena, P., Barchas, J. D., Schatzberg, A. F., Jones, E. J., Myers, R. M., Watson, Jr., S. J., Akil, H. and Bunney, W. E.  (2013).  Circadian patterns of gene expression in the human brain and disruption in major depressive disorder.  Proc. Natl. Acad. Sci. USA.  110: 9950-9955. PMID: 23671070. PMCID: PMC3683716.

225. Cross-Disorder Group of the Psychiatric Genomics Consortium, Smoller, J. W., Craddock, N.,…. Myers, R. M. ,….Zhang, P., Zitman, F. G., Zöllner, S., Craddock, N., Kendler, K.  (2013).  Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis.  Lancet.  381: 1371-1379. PMCID: PMC3714010.

226. Medina, A., Burke, S., Thompson, R. C., Bunney, W. Jr., Myers, R. M., Schatzberg, A., Akil, H., and Watson, S. J.  (2013).  Glutamate transporters: A key piece in the glutamate puzzle of major depressive disorder.  J. Psychiatr. Res.  47: 1150-1156.  PMID: 23706640.

227. Chiu, I. M., Morimoto, E. T. A., Goodarzi, H., Liao, J. T., O’Keeffe, S., Phatnani, H. P., Muratet, M., Carroll, M. C., Levy, S., Tavazoie, S., Myers, R. M., and Maniatis, T.  (2013).  A Neurodegeneration-Specific Gene-Expression Signature of Acutely Isolated Microglia from an Amyotrophic Lateral Sclerosis Mouse Model.  Cell Rep. 4: 385-401. PMCID: PMC4272581.

228. Guella, I., Sequeira, A., Rollins, B., Morgan, L., Torri, F., van Erp, T. G., Myers R. M., Barchas, J. D., Schatzberg, A. F., Watson, S. J., Akil, H., Bunney, W. E., Potkin, S. G., Macciardi, F., and Vawter, M. P. (2013). Analysis of miR-137 expression and rs1625579 in dorsolateral prefrontal cortex. J. Psychiatr. Res. 47: 1215-1221. PMID: 23786914. PMCID: PMC3753093.

229. Cross-Disorder Group of the Psychiatric Genomics Consortium, Lee, S. H., Ripke, S., Neale, B. M., Faraone, S. V., Purcell, S. M., Perlis, R. H., Mowry B. J., Thapar, A., Goddard, M. E., Witte, J. S., Absher, D., Agartz, I., Akil, H.,..., Müller-Myhsok, B., Murtha, M., Myers, R. M., Myin-Germeys, I., Neale, M. C., Nelson, S. F.,..., Devlin, B., Kelsoe, J. R., Sklar, P., Daly, M. J., O'Donovan, M. C., Craddock, N., Sullivan, P. F., Smoller, J. W., Kendler, K. S. and Wray, N. R. (2013). Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nat. Genet. 45: 984-994. PMID: 23933821. PMCID: PMC3800159.

230. Savic, D., Gertz, J., Jain P., Cooper, G. M. and Myers R. M. (2013). Mapping genome-wide transcription factor binding sites in frozen tissues. Epigenetics & Chromatin. 6: 30. PMCID: PMC3848595.

231. Gertz, J., Savic, D., Varley, K. E., Partridge, E. C., Safi, A., Jain, P., Cooper, G. M., Reddy, T. E., Crawford, G. E. and Myers R. M. (2013). Distinct properties of cell type-specific and shared transcription factor binding sites. Mol. Cell. 52: 25-36. PMID: 24076218. PMCID: PMC3811135.

232. Day, K., Waite, L. L., Thalacker-Mercer, A., West, A., Bamman, M. M., Brooks, J. D., Myers, R. M., and Absher, D.  (2013).  Differential DNA methylation with age displays both common and dynamic features across human tissues that are influenced by CpG landscape.  Genome Biol.  14: R102.  [Epub ahead of print].  PMID: 24034465. PMCID: PMC4053985.

233. Mortazavi, A., Pepke, S., Jansen, C., Marinov, G. K., Ernst, J., Kellis, M., Hardison, R. C., Myers, R.M. and Wold, B. J.  (2013).  Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps.  Genome Res.  23: 2136-2148. PMID: 24170599. PMCID: PMC3847782.

234. Guella, I., Sequeira, A., Rollins, B., Morgan, L., Myers, R. M., Watson, S. J., Akil, H., Bunney, W. E., Delisi, L. E., Byerley, W., and Vawter, M. P.  (2013).  Evidence of allelic imbalance in the schizophrenia susceptibility gene ZNF804A in human dorsolateral prefrontal cortex.  Schizophr Res.  152: 111-116.  doi: 10.1016/j.schres.2013.11.021.  PMCID: PMC3947280.

235. Tomita, H., Ziegler, M. E., Kim, H. B., Evans, S. J., Choudary, P. V., Li, J. Z., Meng, F., Dai, M., Myers, R. M., Neal, C. R., Speed, T. P., Barchas, J. D., Schatzberg, A. F., Watson, S. J., Akil, H., Jones, E. G., Bunney, W. E., and Vawter, M. P.  (2013).  G protein-linked signaling pathways in bipolar and major depressive disorders.  Front Genet.  4: 297.  PMID: 24391664.  PMCID: PMC3870297.

236. Schork, A. J., Thompson, W. K., Pham, P., Torkamani, A., Roddey, J. C., Sullivan, P. F., Kelsoe, J. R., O'Donovan, M. C., Furberg, H., Tobacco and Genetics Consortium, Bipolar Disorder Psychiatric Genomics Consortium, Schizophrenia Psychiatric Genomics Consortium, Schork, N. J., Andreassen, O. A., and Dale, A. M. (2013). All SNPs are not created equal: genome-wide association studies reveal a consistent pattern of enrichment among functionally annotated SNPs. PLoS Genet. 9: e1003449. doi: 10.1371/journal.pgen.1003449. PMID: 23637621. PMCID: PMC3636284.

237. Marinov, G. K., Williams, B. A., McCue, K., Schroth, G. P., Gertz, J., Myers, R. M., and Wold, B. J.  (2014).  From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing.  Genome Res.  24: 496-510. PMID: 24299736. PMCID: PMC3941114.

238. Kellis, M., Hardison, R. C., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Laura L. Elnitski, Farnham, P. J., Feingold, E. A., Gerstein, M., Giddings, M. C., Gilbert, D. M., Gingeras, T. R., Green, E. D., Guigo, R., Hubbard, T., Kent, J., Lieb, J. D., Myers, R. M., Pazin, M. J., Ren, B., Stamatoyannopoulos, J. A., Weng, Z., and White, K. P.  (2014).  Defining functional DNA elements in the human genome.  Proc. Natl. Acad. Sci. USA.  111: 6131-6138. PMCID: PMC4035993.

239. Turner, C. A., Thompson, R. C., Bunney, W. E., Schatzberg, A. F., Barchas, J. D., Myers, R. M., Akil, H. and Watson, S. J. (2014). Altered choroid plexus gene expression in major depressive disorder. Front Hum Neurosci. 8: 238. Published online Apr 22, 2014. doi: 10.3389/fnhum.2014.00238. PMCID: PMC4001046.

240. Gasper, W. C., Marinov, G. K., Pauli-Behn, F., Scott, M. T., Newberry, K., de Salvo, G., Ou, S., Myers, R. M., Vielmetter, J., and Wold, B.  (2014).  Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: Identifying ChIP-quality p300 monoclonal antibodies.  Sci Rep. 2014 Jun 12;4:5152. doi: 10.1038/srep05152. PMCID: PMC4053718.

241. Varley, K. E., Gertz, J., Roberts, B. S., Davis, N. S., Bowling, K. M., Kirby, M. K., Nesmith, A. S., Oliver, P. G., Grizzle, W. E., Forero-Torres, A., Buchsbaum, D. J., LoBuglio, A. F., and Myers, R. M. (2014). Recurrent read-through fusion transcripts in breast cancer. Breast Cancer Res Treat. 146: 287-297. PMCID: PMC4085473.

242. Kellis, M., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Elnitski, L. L., Farnham, P. J., Feingold, E. A., Gerstein, M., Giddings, M. C., Gilbert, D. M., Gingeras, T. R., Green, E. D., Guigo, R., Hubbard, T., Kent, J., Lieb, J. D., Myers, R. M., Pazin, M. J., Ren, B., Stamatoyannopoulos, J. A., Weng, Z., White, K. P. and Hardison, R. C. (2014). Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proc. Natl. Acad. Sci. USA. 111: E3366. PMCID: PMC4143047.

243. Julià, A., Domènech, E., Chaparro, M., García-Sánchez, V., Gomollón, F., Panés, J., Mañosa, M., Barreiro-De Acosta, M., Gutiérrez, A., Garcia-Planella, E., Aguas, M., Muñoz, F., Esteve, M., Mendoza, J. L., Vera, M., Márquez, L., Tortosa, R., López-Lasanta, M., Alonso, A., Gelpí, J. L., García-Montero, A. C., Bertanpetit, J., Absher, D., Myers, R. M., Gisbert, J. P. and Marsal, S. (2014). A genome-wide association study identifies a novel locus at 6q22.1 associated with ulcerative colitis. Hum. Mol. Genet. 23: 6927-6934. [Epub ahead of print]. PMID: 25082827.

244. Vrieze, S. I., Malone, S. M., Vaidyanathan, U., Kwong, A., Kang, H. M., Zhan, X., Flickinger, M., Irons, D., Jun, G., Locke, A. E., Pistis, G., Porcu, E., Levy, S., Myers, R. M., Oetting, W., McGue, M., Abecasis, G., Iacono, W. G. (2014). In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. Psychophysiology. 51: 1309-1320. PMCID: PMC4231480.

245. Bunney, B. G., Li, J. Z., Walsh, D. M., Stein, R., Vawter, M. P., Cartagena, P., Barchas, J. D., Schatzberg, A. F., Myers, R. M., Watson, S. J., Akil, H., and Bunney, W. E. (2014). Circadian dysregulation of clock genes: clues to rapid treatments in major depressive disorder. Mol. Psychiatry. doi: 10.1038/mp.2014.138. PMID: 25349171.

246. Lasseigne, B. N., Burwell, T. C., Patil, M. A., Absher, D. M., Brooks, J. D., and Myers, R. M. (2014). DNA methylation profiling reveals novel diagnostic biomarkers in renal cell carcinoma. BMC Medicine. BMC Med.12: 235. [Epub ahead of print]. PMID: 25472429. PMCID: PMC4265327.

247. Cirulli, E. T., Lasseigne, B. N., Petrovski, S., Sapp, P. C., Dion, P. A., Leblond, C. S., Couthouis, J., Lu, Y., Wang, Q, Keebler, J., Krueger, B. J., Ren, Z., Levy, S. E., Boone, B. E., Wimbish, J. R., Jones, L. W., Jones, A., Carulli, J. P., Day-Williams, A., Staropoli, J., Xin, W. W, Chesi, A., Raphael, A. R., McKenna-Yasek, D., Cady, J., Vianney de Jong, J. M. B., Kenna, K. P., Smith, B., Topp, S., Miller, J., Gkazi, A., FALS Sequencing Consortium, Al-Chalabi, A., van den Berg, L. H., Veldink, J., Silani, V., Ticozzi, N., Shaw, C. E., Baloh, R. H., Appel, S., Simpson, E., Lagier-Tourenne, C., Pulst, S. M., Gibson, S., Trojanowski, J. Q., Elman, L., McCluskey, L., Grossman, M., Shneider, N., Chung, W., Ravits, J. M., Glass, J. D., Sims, K. B., Van Deerlin, V., Maniatis, T., Hayes, S. D., Ordureau, A., Swarup, S., Landers, J., Baas, F., Allen, A. S., Bedlack, R. S., Harper, J. W., Gitler, A. D., Rouleau, G. A., Brown, R., Harms, M. B., Cooper, G., Harris, T., Myers, R. M., and Goldstein, D. B. (2015). Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. Science 347: 1436-1441. PMCID: PMC4437632. Comment in Science 347: 1422-1423 (2015).

248. Varley, K. E., Forero, A., Li, U., Chen, D., Grizzle, W. E., Downs-Kelly, E., Burwell, T. C., Vaklavas, C., Buchsbaum, D. J., Myers, R. M. and LoBuglio, A. F. (2014). RNA-seq Reveals Tumor MHC II Prognostic Signature in Triple Negative Breast Cancer. J. Clin. Oncolog. Under review.

249. Perez, M. V., Pavlovic, A., Wheeler, M. T., Miller, C. L., Shang, C., Liu, J., Dewey, F. E., Pan, S., Thanaporn, P. K., Absher, D., Brandimarto, J., Salisbury, H., Chan, K., Mukherjee, R. D., Konadhode, R. H., Myers, R. M., Sedehi, D., Scammell, T. E., Quertermous, T., Cappola, T., and Ashley, E.  (2015).  The neuromodulator hypocretin/orexin receptor 2 regulates cardiac function.  Science Translational Medicine.  Submitted.

250. Savic, D. Roberts, B. S., Carleton, J. B., Partridge, E. C., White, M. A., Cohen, B. A., Cooper, G. M., Gertz, J. and Myers, R. M. (2015). Promoter-distal RNA polymerase II binding discriminates active from inactive transcription factor binding sites. Submitted.

251. Paugh, S. W., Bonten, E. J., Savic, D. Ramsey, L. B., Thierfelder, W. E., Gurung, P., Subbarao Malireddi, R. K., Actis, M., Mayasundari, A., Min, J., Coss, D. R., Laudermilk, L. T., Panetta, J. C., McCorkle, J. R., Fan, Y., Crews, K. R., Stocco, G., Wilkinson, M. R., Ferreira, A. M., Cheng, C., Yang, W., Karol, S. E., Fernandez, C. A., Diouf, B., Smith, C., Hicks, J. K., Zanut, A., Giordanengo, A., Crona, D., Bianchi, J. J., Holmfeldt, L., Mullighan, C. G., den Boer, M. L., Pieters, R., Jeha, S., Dunwell, T. L., Latif, F., Bhojwani, D., Carroll, W. L., Pui, C. H., Myers, R. M., Guy, K., Kanneganti, T. D., Relling, M. V., and Evans, W. E., (2015). NALP3 inflammasome upregulation and CASP1 cleavage of the glucocorticoid receptor cause glucocorticoid resistance in leukemia cells. Nat Genet. 47: 607-614. doi: 10.1038/ng.3283. Epub 2015 May 4. PMCID: PMC4449308 [Available on 2015-12-01].

252. Maier, R., Moser, G., Chen, G. B., Ripke, S.; Cross-Disorder Working Group of the Psychiatric Genomics Consortium, Coryell, W., Potash, J. B., Scheftner, W. A., Shi, J., Weissman, M. M., Hultman, C. M., Landén, M., Levinson, D. F., Kendler, K. S., Smoller, J. W., Wray, N. R., Lee, S. H. Collaborators (364). Absher, D., Agartz, I., Akil, H., ..., Murtha, M., Myers, R. M., ... Zitman, F. G., and Zöllner, S.. (2015). Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. Am. J. Hum. Genet. 96: 283-294. doi: 10.1016/j.ajhg.2014.12.006. Epub 2015 Jan 29. PMCID: PMC4320268.

253. Sequeira, A., Rollins, B., Magnan, C., van Oven, M., Baldi, P., Myers, R. M., Barchas, J. D., Schatzberg, A. F., Watson, S. J., Akil, H., Bunney, W. E., and Vawter MP. (2015). Mitochondrial mutations in subjects with psychiatric disorders. PLoS One. 10: e0127280. doi: 10.1371/journal.pone.0127280. eCollection 2015. PMCID: PMC4444211.

254. Julià, A., Pinto, J. A., Gratacós, J., Queiró, R.,, Ferrándiz, C., Fonseca, E., Montilla, C., Torre-Alonso, J. C., Puig, L., Pérez Venegas, J. J., Fernández Nebro, A., Fernández, E., Muñoz-Fernández, S., Daudén, E., González, C., Roig, D., Sánchez Carazo, J. L., Zarco, P., Erra, A., López Estebaranz, J. L., Rodríguez, J., Ramírez, D. M., de la Cueva, P., Vanaclocha, F., Herrera, E., Castañeda, S., Rubio, E., Salvador, G., Díaz-Torné, C., Blanco, R., Willisch Domínguez, A., Mosquera, J. A., Vela, P., Tornero, J., Sánchez-Fernández, S., Corominas, H., Ramírez, J., López-Lasanta, M., Tortosa, R., Palau, N., Alonso, A., García-Montero, A. C., Gelpí, J. L., Codó, L., Day, K., Absher, D., Myers, R. M., Cañete, J. D., and Marsal, S. (2015). A deletion at ADAMTS9-MAGI1 locus is associated with psoriatic arthritis risk. Ann. Rheum. Dis. pii: annrheumdis-2014-207190. doi: 10.1136/annrheumdis-2014-207190. [Epub ahead of print]. PMID: 25990289.

255. Indjeian, V. B., Jones, F. C., Guenther, C. A., Kingman, G. A., Grimwood, J., Schmutz, J., Myers, R. M., and Kingsley, D. M. (2015). Gain and loss of GDF6 expression and the evolution of skeletal traits in fish and humans. Submitted.

256. Aurbach, E. L., Inui, E. G., Turner,C. A., Hagenauer, M. H., Prater, K. E., Li, J. Z., Absher, D. M., Shah, N., Blandino, Jr., P., Li, J. Z., Bunney, W. E., Myers, R. M., Barchas, J. D., Schatzberg, A., Watson, S. J., and Akil, H. (2015). Fibroblast growth factor 9 is a novel anxiogenic and pro-depressant agent in the hippocampus. Submitted.

257. Alonso, A., Domènech, E., Julià, A., Panés, J., García-Sánchez, V., Mateu, P. N., Gutiérrez, A., Gomollón, F., Mendoza, J. L., Garcia-Planella, E., Acosta, M. B., Muñoz, F., Vera , M., Saro, C., Esteve, M., Andreu, M., Chaparro, M., Manyé, J., Cabré, E., López-Lasanta, M., Tortosa, R., Gelpí, J. L., García-Montero, A. C., Bertranpetit, J., Absher, D., Myers, R. M., Marsal, S., and Gisbert, J. P. (2015). Identification of Risk Loci for Crohn's Disease Phenotypes Using a Genome-Wide Association Study. Gastroenterology. 148: 794-805. PMID: 25557950.

258. Julià, A., González, I., Fernández-Nebro, A., Blanco, F., Fernández-Gutierrez, B., González, A., Cañete, J. D., Maymó, J., Alperi-López, M., Olivè, A., Corominas, H., Martínez-Taboada, V., Erra, A., Sánchez, S., Alonso, A., Lopez Lasanta, M., Tortosa, R., Codó, L., Lluis Gelpi. J., García-Montero, A. C., Bertranpetit, J., Absher, D., Bridges Jr., S. L., Myers, R. M., Tornero, J., and Marsal, S. (2015). Genome-wide association study of anti-cyclic citrullinated protein-positive rheumatoid arthritis identifies a new risk locus in slc8a3. Submitted.

259. Roberts, B. S., Hardigan, D. A., Kirby, M. K., Fitz-Gerald, M. B., Wilcox, C. M., Kimberly, R. P., and Myers, R. M. (2015). Blocking of targeted microRNAs from next-generation sequencing libraries. Nucleic Acids Res. doi: 10.1093/nar/gkv724. Jul 23. pii: gkv724. PMID: 26209131.

260. Aurbach, E. L., Inui, E. G., Turner, C. A., Hagenauer, M. H., Prater, K. E., Li, J. Z., Absher, D., Shah, N., Blandino, P. Jr., Bunney, W. E., Myers, R. M., Barchas, J. D., Schatzberg, A. F., Watson, S. J. Jr., and Akil, H. (2015). Fibroblast growth factor 9 is a novel modulator of negative affect. Proc. Natl. Acad. Sci. U.S.A. 112: 11953-11958. PMID: 26351673.

261. Savic, D., Partridge, E. C., Newberry, K. M., Smith, S. B., Meadows, S. K., Roberts, B. S., Mackiewicz, M., Mendenhall, E. M., and Myers, R. M. (2015). CETCh-seq: CRISPR epitope tagging ChIP-seq of DNA-binding proteins. Genome Res. 25: 1581-1589. PMCID: PMC4579343.

262. Mamdani, F., Rollins, B., Morgan, L., Myers, R. M., Barchas, J. D., Schatzberg, A. F., Watson, S. J., Akil, H., Potkin, S. G., Bunney, W. E., Vawter, M. P., and Sequeira, P. A. Variable telomere length across post-mortem human brain regions and specific reduction in the hippocampus of major depressive disorder. (2015). Transl. Psychiatry. 5: e636. doi: 10.1038/tp.2015.134. PMID: 26371764.

263. Huang, W., Thomas, B., Gavzy, S. J., Wu, L., Kim, S. V., Rigo, F., Meadows, S., Montoya, N. R., Herrera, N., Domingos, A., Rastinejad, F., Myers, R. M., Fuller-Pace, F., Oreste, A., and Littman, D. R. (2015). DDX5 and its associated lncRNA Rmrp modulate Th17 cell effector functions. Nature. In press.

**Solicited Articles, Reviews, Chapters and Books**

1. Learned, R. M., Myers, R. M. and Tjian, R. (1981). Replication in monkey cells of plasmid DNA containing the minimal SV40 Origin. In: Structure and DNA-protein interactions of replication origins, ICN-UCLA Symposia on Molecular and Cellular Biology, Volume XX­I, (eds. Dan S. Ray and C. Fred Fox, Academic Press, New York) pp. 555-566.

2. Myers, R. M. (1982). Dissertation: T antigen : DNA interactions involved in SV40 DNA replication and regulation of viral gene expression. The University of California at Berkeley. NRLF C 2 938 630.

3. Myers, R. M. and Maniatis, T. (1986). Recent advances in the development of methods for detecting single base substitutions associated with human genetic diseases. Cold Spring Harbor Symp. Quant. Biol. 51: 275-284.

4. Myers, R. M. (1986). Generation of single and double base substitutions in cloned DNA fragments. In: Gene Transfer Vectors for Mammalian Cells. Cold Spring Harbor Press (Cold Spring Harbor, NY), pp 46-56.

5. Myers, R. M., Maniatis, T. and Lerman, L. S. (1987). Detection and localization of single base changes by denaturing gradient gel electrophoresis. Meth. Enzymol. 155: 501-527.

6. Myers, R. M., Sheffield, V., and Cox, D. R. (1988). Detection of single base changes in DNA: Ribonuclease cleavage and denaturing gradient gel electrophoresis. In: Genomic Analysis: A Practical Approach (ed. K. Davies; IRL Press Ltd, Oxford), pp. 95-139.

7. Myers, R. M., Sheffield, V. C. and Cox, D. R. (1989). PCR and denaturing gradient gel electrophoresis. In: The Polymerase Chain Reaction (eds. H. Erlich, R. Gibbs, H. Kazazian Jr; Cold Spring Harbor Press, Cold Spring Harbor, NY). pp. 177-181.

8. Myers, R. M., Cowie, A., Stuvé, L., Hartzog, G. and Gaensler, K. (1989). Genetic and biochemical analysis of the mouse beta-major globin promoter. In: Hemoglobin Switching, Part A: Transcriptional Regulation (eds. G. Stamatoyanopolous and A. Nienhuis; A.R. Liss, Inc., New York). pp 117-127.

9. Pritchard, C. A., Cox, D. R. and Myers, R. M. (1989). Methylation at the Huntington disease-linked D4S95 locus. Amer. J. Hum. Genet. 45: 335-336.

10. Myers, R. M., Sheffield, V. C. and Cox, D. R. (1989). Mutation detection by PCR, GC-clamps and denaturing gradient gel electrophoresis. In: PCR Technology: Principles and Applications for DNA Amplification (ed. H. Erlich; Stockton Press, New York). pp 71-88.

11. Sheffield, V. C., Cox, D. R. and Myers, R. M. (1990). Strategies for identifying DNA polymorphisms in PCR-amplified genomic DNA by denaturing gradient gel electrophoresis. In: PCR-Protocols and Applications: A Laboratory Manual (eds. M. Innis, D. Gelfand, J. Sninsky and T. White; Academic Press, San Diego). pp. 206-218.

12. Pritchard, C. A., Cox, D. R. and Myers, R. M. (1991). Invited editorial: The end in sight for Huntington disease? Amer. J. Hum. Genet. 49: 1-6.

13. Cox, D. R. and Myers, R. M. (1992). Bridging the gaps. Current Biology. 2: 338-339.

14. Myers, R. M. (1993). The Pluses of Subtraction (Perspective). Science 259: 942-943.

15. Neel, J. V., Satoh, C. and Myers, R. M. (1993). Report of a workshop on the application of molecular genetics to the study of mutation in the children of atomic bomb survivors. Mut. Research 291: 1-20.

16. Pritchard, C. A., Zhu, N., Cox, D. R. and Myers, R. M. (1993). Molecular Genetics of Huntington Disease. In: Advances in Genome Biology, Second Edition (ed. R. Verma; JAI Press). pp. 157-205.

17. Myers, R. M., Goold, R. D. and van Ommen, G.-J. (1994). Report of the Third International Workshop on Human Chromosome 4. Cytogenetics and Cell Genetics 66: 217-236.

18. Cox, D. R., Green, E. D., Cohen, D., Lander, E., and Myers, R. M. (1994). Assessing mapping progress in the Human Genome Project. Science. 265: 2031-2032.

19. Green, E. D., Cox, D. R. and Myers, R. M. (1995). The Human Genome Project and Its Impact on the Study of Human Disease. In: The Metabolic Basis of Inherited Disease, Seventh Edition. (eds. C.R. Scriver, A.L. Beaudet, W.S. Sly, and D. Valle; McGraw-Hill, Inc.) pp. 401-436.

20. Estabrooks, L. L., Breg, W. R., Hayden, M. R., Ledbetter, D. H., Myers, R. M., Wyandt, H. E., Yang-Feng, T. L., and Hirschhorn, K. (1995). Summary of the 1993 ancillary meeting "Recent research on chromosome 4p syndromes and genes". Amer. J. Hum. Genet. 55: 453-458.

21. Cox, D. R. and Myers, R. M. (1996). A map to the future. Nature Genet. 12: 117-118.

22. Boguski, M. S., Cox, D. R. and Myers, R. M., editors. (1996). Genomes and Evolution. Current Opinion in Genetics & Development 6 (6).

23. Boguski, M., Chakravarti, A., Gibbs, R., Green, E., and Myers, R. M. (1996). The end of the beginning: the race to begin human genome sequencing [editorial]. Genome Res. 6: 771-772.

24. Eisen, J. A., Kaiser, D. and Myers, R. M. (1997). Gastrogenomic delights: a movable feast. Nature Med. 3: 1076-1078.

25. Green, E. D., Birren, B., Klapholz, S., Myers, R. M. and Hieter, P., eds. (1997). Genome Analysis: A Laboratory Manual. Cold Spring Harbor Laboratory Press. Vol. 1: Analyzing DNA.

26. Goodman, L., Boguski, M., Chakravarti, A., Gibbs, R., Green, E., and Myers, R. M. (1997). Genome horizons [editorial]. Genome Res. 7: 567-568.

27. Birren, B., Green, E. D., Klapholz, S., Myers, R. M. and Roskams, J., eds. (1998). Genome Analysis: A Laboratory Manual. Cold Spring Harbor Laboratory Press. Vol. 2: Detecting Genes.

28. Myers, R. M., Hedrick, L. and Hayashi, K. (1998). Detection of DNA Variation, in Genome Analysis: A Laboratory Manual. Vol. 4. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. pp. 287-384.

29. Beasley, E. M., Myers, R. M., Cox, D. R. and Lazzeroni, L. C. (1999). Statistical refinement of primer design parameters. In: PCR Applications: Protocols for Functional Genomics. (eds. Michael Innis, David Gelfand & John Sninsky, Academic Press). pp. 55-71.

30. Birren, B., Green, E. D., Klapholz, S., Myers, R. M., Riethman, H. and Roskams, J., eds. (1999). Genome Analysis: A Laboratory Manual. Cold Spring Harbor Laboratory Press. Vol. 3: Cloning Systems.

31. Birren, B., Green, E. D., Hieter, P., Klapholz, S., Myers, R. M. Riethman, H. and Roskams, J., eds. (1999). Genome Analysis: A Laboratory Manual. Cold Spring Harbor Laboratory Press. Vol. 4: Mapping Genomes.

32. Serratosa, J. M., Gardiner, R. M., Lehesjoki, A. E., Pennacchio, L. A., Myers, R. M. (1999). The Molecular Genetic bases of the Progressive Myoclonus Epilepsies; Lippincot-Raven Publisher; Delgado-Escueta, A.V., Wilson, W., Olsen, R., and Porter, R. Eds. Basic Mechanisms of the Epilepsies, Second Edition. Advances in Neurology 79: 383-398. PMID: 10514828.

33. Matise, T. C., Wasmuth, J. J., Myers, R. M., and McPherson, J. D. (1999). Somatic Cell Genetics and Radiation Hybrid Mapping, in Genome Analysis: A Laboratory Manual. Vol. 4. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. pp. 259-302.

34. Tabor, H. K., Risch, N. J. and Myers, R. M. (2002). OPINION: Candidate gene approaches for studying complex genetic traits: practical considerations. Nat. Rev. Genet. 3: 391-397. PMID: 11988764.

35. Schmutz, J., Grimwood, J. and Myers, R. M. (2004). Assembly of DNA sequencing data. In: Methods in Molecular Biology, "Bacterial Artificial Chromosomes: Methods and Protocols", eds. S. Zhao and M. Stodolsky. Humana Press. 255: 319-332. PMID: 15020835.

36. Schmutz, J., Grimwood, J. and Myers, R. M. (2004). Sequence finishing. In: Methods in Molecular Biology, "Bacterial Artificial Chromosomes: Methods and Protocols", eds. S. Zhao and M. Stodolsky. Humana Press. 255: 333-342. PMID: 15020836.

37. Schmutz, J., Grimwood, J. and Myers, R. M. (2004). Quality assessment of finished BAC sequences. In: Methods in Molecular Biology, "Bacterial Artificial Chromosomes: Methods and Protocols", eds. S. Zhao and M. Stodolsky. Humana Press. 255: 343-350. PMID: 15020837.

38. Bunney, W. E., Bunney, B. G., Vawter, M. P., Tomita, H., Li, J., Evans, S. J., Choudary, P. V., Myers, R. M., Jones, E. G., Watson, S. J., Akil, H. (2003). Microarray technology: a review of new strategies to discover candidate vulnerability genes in psychiatric disorders. Am. J. Psychiatry. 160: 657-666.

39. Schmutz, J., Wheeler, J., Grimwood, J., Dickson, M., and Myers, R. M. (2003). Assessing the quality of finishedgenomic sequence. Cold Spring Harb. Symp. Quant. Biol. 68: 31-37. PMID: 15338600.

40. Karssen\*, A. M., Li\*, J. Z., Her, S., Patel, P. D., Meng, F., Evans, S. J., Vawter, M. P., Tomita, H., Choudary, P. V., Bunney, Jr., W. E., Jones, E. G., Watson, S. J., Akil, H., Myers, R. M., Schatzberg, A. F. and Lyons, D. M. (2006). Application of microarray technology in primate behavioral neuroscience research. Methods. 38: 227-234. (\*co-first authors). PMID: 16469505.

41. Watson, J. D., Caudy, A. A., Myers, R. M. and Witkowski, J. A. (2007). Recombinant DNA: Genes and Genomes, 3rd Edition. W. H. Freeman Press. ISBN 0-7167-2866-4.

42. Wold, B. and Myers, R. M. (2008). Sequence census methods for functional genomics. Nature Meth. 5: 19-21. PMID: 18165803. [PubMed - indexed for MEDLINE].

43. Akil, H., Evans, S. J., Turner, C. A., Perez, J., Myers, R. M., Bunney, W. E., Jones, E. G., Watson, S. J. and the Pritzker Consortium. (2008). The fibroblast growth factor family and mood disorders. Novartis Found. Symp. 289: 94-96; discussion 97-100, 193-195. PMID: 18497097.

44. Pasche, B. and Myers, R. M. (2009). One step forward toward identification of the genetic signature of glioblastomas. (Review). [JAMA.](javascript:AL_get(this,%20'jour',%20'JAMA.');) 302: 325-326. PMID: 19602695. [PubMed - in process].

45. Lamb, N. E., Myers, R. M. and Gunter, C. (2009). Education and personalized genomics: deciphering the public's genetic health report. (Perspective). Personalized Med. 6: 681-690. PMID: 20161675. PMCID: PMC2821046.

46. Barsh, G. S. and Myers, R. M. (2013). Obituary: David R. Cox 1946-2013. Nature. 45: 716. PMID: 23800862.

**Selected News, Commentary and Reporting**

1. Cook-Deegan, R. (1989). The Alta summit, December 1984. Genomics. 5: 661-663. PMID: 2613249.

2. Palca, J. (2005). DNA: The Machinery Behind Human Beings - Part 1. <http://www.npr.org/templates/story/story.php?storyId=4953053>.

3. Smaglik, P. (2007). Career View. Nature 450: p. 758.

4. Check, E. (2008). Largest yet survey of human genetic diversity. Nature. doi:10.1038/news.2008.614.

5. Palca, J. (2008). [Mapping Human Genetic Diversity](http://www.sciencefriday.com/segment/02/22/2008/mapping-human-genetic-diversity.html). <http://www.sciencefriday.com/guests/richard-myers.html#page/full-width-list/1>.

**Biographical Information for Dr. Richard M. Myers**

Dr. Richard M. Myers received his B.S. in Biochemistry from the University of Alabama in 1977, his Ph.D. in Biochemistry from the University of California, Berkeley in 1982, and did his post-doctoral training at Harvard University. He joined the faculty of the UCSF Medical Center in 1986 moved to Stanford University in 1993, where he served as Professor and Chair in the Department of Genetics. Since 2008, Dr. Myers has been [President, Director and a Faculty Investigator](https://www.linkedin.com/vsearch/p?title=President%2C+Director+and+Faculty+Investigator&trk=prof-exp-title) of the [HudsonAlpha Institute for Biotechnology](https://www.linkedin.com/vsearch/p?company=HudsonAlpha+Institute+for+Biotechnology&trk=prof-exp-company-name), a non-profit research and teaching enterprise in Huntsville, Alabama. The Myers laboratory studies the human genome, with goals of understanding how allelic variation and gene expression changes contribute to human traits, including diseases, behaviors and other phenotypes. His group uses high-throughput genomic methods, including DNA sequencing, genotyping, chromatin immunoprecipitation, mRNA expression profiling, transcriptional promoter and DNA methylation measurements, as well as computational and statistical tools, to identify, characterize and understand the functional elements encoded in our genomes, and how they work together at the molecular level in normal and pathological conditions. His group also sequences whole genomes, whole exomes and targeted regions of the genome with ultrahigh-throughput DNA sequencing technologies to identify DNA sequence variants relevant to clinical and basic biological problems. The lab integrates these functional genomics, epigenetic and genetic data to understand how our genomes are involved in cancer, brain disorders, ALS, children born with developmental disorders, autoimmune diseases and other traits.

**Detailed Biography**

**College and Graduate Education and Research**

I obtained my undergraduate education at the University of Alabama in Tuscaloosa, graduating in 1977 with a B.S. in Biochemistry. There, I did research in physical chemistry and in enzymology. The work in physical chemistry was under the guidance of Dr. Clifford Hand, a remarkable teacher who helped me understand the scientific method and the excitement of doing research to answer basic questions about how the universe works. We studied the kinetics of gas phase reactions by using a flow reactor and mass spectrometry (all on homemade equipment!).

I began to get exposure to biology, particularly biochemistry and molecular biology, so I changed into a different lab, and did research my last two years in college in Dr. John Hardman's lab, a biochemist who studied how enzymes work. My project was to study of the mechanisms of enzyme action and allostery, using *E. coli* tryptophan synthase as a model system. I synthesized an affinity substrate to label the enzyme and used it to probe the reaction kinetics in the last step of tryptophan biosynthesis.

In 1977, I moved to Berkeley, California to do my graduate work in the Department of Biochemistry at the University of California at Berkeley. I obtained my Ph.D. in 1982 in the laboratory of Dr. Robert Tjian (“Tij”), who arrived there in my second year as a beginning faculty member. I studied SV40 T antigen, including its DNA binding properties, its role in DNA replication, and the mechanisms of transcriptional regulation imparted by its binding to the viral genome. My projects involved purifying and studying proteins, similar to my undergraduate work, but also introduced me to molecular biology (DNA cloning, which had just been invented), and studying protein:DNA interactions, an interest that continues to today.

**Postdoctoral Work**

In 1982, after graduate school, I joined Dr. Tom Maniatis’s lab at Harvard University in the Department of Biochemistry and Molecular Biology to do my postdoctoral work. When I began my project, I studied mammalian gene expression, using the -globin locus to probe elements that control transcription of the gene cluster in erythroid cells. We developed a new method for generating single base mutations in cloned segments of DNA, and used it to saturate the -globin gene promoter with more than 150 mutations. I tested these mutations for their effect on transcription by transferring plasmid constructs carrying them into cultured human and mouse cells, which gave a detailed picture of the *cis-*acting elements that contribute to levels of mRNA of the gene.

The mutagenesis method involved treating naked DNA fragments with various mutagens, cloning the fragments as a pool into a plasmid vector, and then purifying the mutant promoters from the wild type (which was the vast majority) by using an unusual gel system that had just been developed by Dr. Leonard Lerman, a biophysicist with whom Tom Maniatis had done his graduate work, then at SUNY Albany. This electrophoretic method was called denaturing gradient gel electrophoresis (DGGE), and it has the remarkable property of separating DNA fragments differing by only a single base pair in a polyacrylamide gel, based on the melting behavior of the DNA.

It occurred to us that the separation could be used not only to purify mutant fragments, but also as a way to detect mutations, so I spent much of my postdoc work (and some of the first few years of my first faculty appointment) developing this and another method involving cleavage of mismatched RNA:DNA hybrids (called RNase cleavage) for mutation detection. I began to learn about human genetics for the first time, and applied the two detection methods we developed to identifying people who carried mutations as well as neutral polymorphisms in their genomes. Such methods were sorely needed, because, at the time, the only ways to detect mutations or polymorphisms were to clone and sequence the fragments from each person or to use restriction enzymes, or to use expensive (at the time) oligonucleotides and gel electrophoresis followed by Southern blotting.

Because we began to talk about these methods in seminars and at scientific meetings, Tom was invited to attend a small conference in Alta, Utah concerned with human genetics, and sponsored by the U.S. Department of Energy and the International Commission for Protection Against Environmental Mutagens and Carcinogens. His interest was more in gene expression, and, being a very generous postdoctoral advisor, he sent me instead. In December 1984, I, along with a group of 18 other researchers met at a ski resort (I don’t ski, so I mostly just tried to stay warm in the hotel) to discuss a difficult problem that had basic science as well as tremendous social significance. The question was, is it possible to determine whether the Hiroshima and Nagasaki atomic bomb blasts at the end of World War II increased the rate of mutations in the sperm or eggs of survivors of the bombings, in other words, did the exposure to high doses of irradiation increase the germline mutation rate? The question was whether any methods were available to measure mutations in the offspring of survivors, and to determine whether the number of mutations was higher than in unexposed people. A variety of cell-based mutation assays and other approaches by the folks who had been working in this field for a long time were discussed, and I presented the methods we had developed for mutation detection. It was clear that the problem was huge; the baseline rate of mutation in people was so low that we did not have a clear number based on data. So how could we determine whether there was an increase in offspring of exposed individuals if we didn’t know the rate of mutation in people not exposed to radiation? The problem was so vexing that someone at the meeting (not me, I’m sad to say!) commented that “the rate is so low that we would have to sequence the entire human genome to know the answer”. After the laughter died down, it is clear that the D.O.E. folks, and probably others at the meeting, took this concept clearly, as not long after, that very entity proposed the basis for the Human Genome Project, which began in earnest in 1990. I take no credit for this vision, but was very excited to be part of the meeting and to rub elbows with a new (to me) community of scientists who eventually became my colleagues. I especially owe a debt to Drs. Maynard Olson and Jim Neel, two gentlemen who were experts in genetics and who encouraged me to move into the field of human genetics and provided early and continuing mentorship that helped me find my way in this new field.

**Faculty Positions at UCSF and Stanford University**

I began my first faculty position at the University of California in San Francisco in late 1985, with my primary appointment in the Department of Physiology and my secondary appointment in the Department of Biochemistry and Biophysics. I set up my lab to continue studying globin gene expression, and some of my graduate students and postdocs worked on both *cis*- and *trans*-acting components that regulate transcription of the gene for the next six years. I also wanted to learn more about human genetics, and was interested in identifying the gene that is mutated in people with Huntington disease (gene hunting by positional cloning had just been developed, and the disease was compelling to me). During my first months, I had the very good fortune to meet Dr. David Cox, a brilliant physician-scientist who was a medical geneticist and also had a Ph.D. in yeast genetics. We immediately joined forces, and for 15 years our laboratories were essentially a joint lab. I learned a tremendous amount about inheritance and quantitative biology from David, and we not only worked on Huntington disease, but also other diseases of the nervous system. We developed and improved several technologies for gene hunting, including radiation hybrid mapping, a method that used high-energy x-rays to fragment human chromosomes that were recovered in somatic cell hybrids and then used to determine the locations of DNA markers in our genome. This led us to apply for and have awarded one of the first NIH grants to establish a human genome center in 1990, as one of the inaugural labs participating in the public Human Genome Project (HGP).

In early 1993, David and I moved our laboratories and the Human Genome Center to the Department of Genetics at Stanford University School of Medicine. Our labs continued to work on inherited human diseases, including not only brain diseases and phenotypes, but also others. We identified the genes for an inherited form of childhood progressive epilepsy (called “EPM1”), for a key step in development of the cerebellum (the “weaver” gene), and with others, genes involved in inherited skin cancer, hemochromatosis, and an autoimmune disease. My lab generated and studied mouse models of Huntington disease and EPM1 during those years.

At the Stanford Human Genome Center, we applied radiation hybrid and other mapping technologies to human chromosomes as part of the HGP, but also began collaborating with the Joint Genome Institute (JGI) in Walnut Creek to sequence human genomic DNA with funding from the U.S. Department of Energy. Ultimately, this led to maps of the entire genome that were instrumental in piecing the entire sequence together, as well as to a substantial amount of finished, contiguous DNA sequence. By the time we reached the finish line in 2003, our group was responsible for genome-wide maps, and with the JGI, for 11% of the finished human genome sequence, including the entirety of chromosomes 5, 16 and 19. We also contributed to the final sequence of human chromosome 4 with Washington University’s Genome Center.

In 2000, David left Stanford for industry (Perlegen and then Pfizer), and, sadly, died unexpectedly in 2012. I continued to run the Stanford Human Genome Center, as well as a lab of about 15 graduate students and postdocs working on human genetics and genomics. In addition, I was Vice Chair and then Chair of the Department of Genetics during my last 11 years at Stanford. During that time, I began to combine genome-wide approaches with my old interest in transcriptional regulation, which led to a close and still-active collaboration with Dr. Barbara Wold and her lab at Caltech. Our groups have worked together to develop and apply methods for measuring gene expression, protein:DNA interactions and epigenetic events on a genome-wide scale, including chromatin immunoprecipitation (ChIP), mRNA and microRNA expression, transcriptional promoter and methylation measurements, and computational and statistical tools to study human biology. We are one of the initial groups who comprise the ENCODE Consortium, which has the goal of identifying and understanding all the functional elements in the human genome. The techniques and knowledge we have gained from this work are important components of our projects to understand diseases and our interactions with the environment, including variable responses to drugs, as discussed below.

**HudsonAlpha Institute**

In 2008, I moved my laboratory and Genome Center from Stanford University to Huntsville Alabama to become the Director of a new enterprise called the HudsonAlpha Institute for Biotechnology. This non-profit research institute, located in Cummings Research Park next to NASA headquarters and home to several hundred engineering, computer and biotechnology companies, uses genomics and genetics to make and apply discoveries for solving important problems in human health, energy and environmental science. At HudsonAlpha Institute, we have continued work that my laboratory started at Stanford, while working collaboratively with faculty at the institute and with other researchers on a wide range of scientific and biomedical problems.

A large part of our efforts are towards the study of an array of human diseases. These include disorders of the nervous system, notably Parkinson disease, bipolar disorder, schizophrenia, major depression and ALS, as well as several types of cancer, including breast, prostate, kidney, and pancreatic cancer. We also work on autoimmune diseases, with emphasis on rheumatoid arthritis, Crohn's disease, lupus and psoriasis. These studies involve identifying DNA sequence differences, as well as differences in functional readout of the genome, between affected and unaffected individuals in an effort to understand the genetic basis of the disease.

My lab is part of the Pritzker Consortium, a collaboration between six laboratories around the U.S., where we study psychiatric disorders by assessing gene expression and DNA methylation patterns in post mortem brain tissues, as well as blood specimens, from people with the disease compared to individuals who are not affected. With Shawn Levy at HudsonAlpha, we also collaborate with Dr. Mike Boehnke, Dr. Goncalo Abecasis, and colleagues at the University of Michigan and several other universities to study the genetics of bipolar disorder, in a very large study where we sequenced the entire genomes of 4,000 people, half with bipolar and half without. The goals of our psychiatric research are to understand the genetic and genomic bases of the disorders, in hopes of identifying pathways that will lead to predictive biomarkers for the disorders and responses to treatments, as well as to new targets for therapies.

In collaboration with scientists at HudsonAlpha, Stanford University, the University of Alabama at Birmingham, and the Mitchell Cancer Center at the University of South Alabama in Mobile, we are applying these approaches to several cancer projects to provide a comprehensive genomic comparison of tumors compared to non-tumor tissues. These studies include breast cancer (ER+PR+ as well as triple negative breast cancer), kidney cancer, prostate cancer and pancreatic cancer. In the case of breast cancer, we are also using genomic approaches to understand the basis of response and non-response to new therapies in clinical trials; these are in collaboration with Drs. Andres Forero, Al LoBuglio and Don Buchsbaum at UAB and with Dr. K-T Varley, a former postdoc in my lab now on the faculty at the University of Utah. These experiments include measuring copy number variation, exome sequence variants, the immune repertoire, and genome-wide DNA methylation, mRNA, microRNA, and chromatin modifications. With Drs. Devin Absher and Shawn Levy at HudsonAlpha, we have also begun to apply this type of comprehensive genomic analysis to autoimmune disease, including lupus, rheumatoid arthritis (with Dr. Sara Marsal at Vall d'Hebron Hospital in Barcelona, Spain and Dr. Louis Bridges at UAB) and Parkinson disease (with Dr. David Standaert and colleagues at UAB). With Dr. David Goldstein, then at Duke University, and Dr. Tim Harris, at Biogen Idec, Inc. in Cambridge, MA, we are sequencing the exomes of thousands of individuals with ALS, and these studies have identified new genes that contribute to the disease that are also potential targets for new drugs. In related studies, we have collaborated with Drs. Tom Maniatis and Neil Shneider at Columbia University to apply functional genomics methods to human cells and mouse models of ALS to elucidate the mechanisms of the disease.

The sequencing group we built at the Stanford Human Genome Center moved to HudsonAlpha as well, now led by HudsonAlpha faculty investigators Jane Grimwood and Jeremy Schmutz. They continue to collaborate with the Joint Genome Institute and have developed their own research programs, mostly concerned with the genomics of plants, organisms with complex and difficult-to-sequence genomes, with particular interests in crop improvement, other agricultural problems, bioenergy and the environment.

We have continued our basic science interest in gene expression, applying genetics and functional genomics methods to probe a wide range of human cells for both cis- and trans-acting elements that regulate transcription. We continue to collaborate with Dr. Barbara Wold and others on the ENCODE Project. In addition to contributing to the ENCODE encyclopedia, we are studying particular transcription factors and networks of factors involved in interesting human biological problems, including responses to hormones such as glucocorticoids and sex hormones, the stress response, and neuronal development.

In addition to my research, I participate in a variety of teaching, educational outreach, and institutional and national service activities. At UCSF and Stanford, I taught in several courses in genetics and genomics to undergraduate, medical and graduate students, as well as to non-science majors. I helped established a partnership between the Department of Genetics and the San Jose Tech Museum, which develops scientific exhibits as well as providing a venue for training graduate students and postdoctoral fellows in the art of teaching to the public. I have had a long-standing special interest and have participated in numerous activities to increase and foster diversity in research and education, with particular emphasis in under-represented groups. We have continued and greatly expanded these types of activities at HudsonAlpha Institute, where we have a team of science education professionals, led by Dr. Neil Lamb, who work with faculty, students and postdocs at HudsonAlpha to develop, test, and implement a wide variety of programs that teach the importance of science in our everyday lives at every age level, from young children to adults. These programs provide services, ideas, excitement and tools throughout the State of Alabama and the country (see http://www.hudsonalpha.org/education).

I serve on a variety of advisory panels and editorial boards, including panels for the National Institutes of Health, the Department of Energy, several universities, and the Pharmacogenomics Research Network. I am a member of the HeLa Genome Data Access Working Group, led by the National Institutes of Health. I am an Associate Editor of Genome Research and participate in strategic planning and grant reviews for the NIH, DOE and other agencies. I am also an advisor to two biotech companies that work on genomics-related problems; these are Kailos Genetics, Inc., located on the HudsonAlpha campus, and DNAnexus, Inc. In Mountain View, CA. I serve on the Scientific Advisory Boards of The Joint Genome Center in Walnut Creek, CA, Bay City Capital in San Francisco, CA, Biogen Idec, Inc. in Cambridge, MA, and the New York Genome Center in New York City.