CURRICULUM VITAE

Michael Boehnke

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PERSONAL INFORMATION

Born:	May 16, 1956, Eugene, Oregon
Married:	Betsy Foxman
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EDUCATION

B.A. Honors College in Mathematics with Distinction, University of Oregon, 1977

Coursework in Mathematics and Biology, Albert-Ludwigs-Universität, Freiburg, West Germany, 1977-1978

Ph.D. in Biomathematics, University of California, Los Angeles, 1983
Dissertation: Advances in Pedigree Analysis: Ascertainment, Goodness of Fit, and Optimization. Advisor: Kenneth Lange.

PROFESSIONAL EXPERIENCE

Research Associate, Cedars-Sinai Medical Center, 1979-1980

Teaching Assistant, Department of Biology, UCLA, 1979-1981

Research Assistant, Department of Biomathematics, UCLA, 1980-1983

Assistant Professor, Department of Biostatistics, University of Michigan, 1984-1989

Associate Professor, Department of Biostatistics, University of Michigan, 1989-1993

Professor, Department of Biostatistics, University of Michigan, 1993-present

Director, University of Michigan Genome Science Training Program, 1995-present

Director, University of Michigan Center for Statistical Genetics, 1999-present

Visiting Scholar, Department of Human Genetics, UCLA, 2007-2008

Visiting Scholar, Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, 2008

HONORS

Phi Beta Kappa, 1976

DeCou Prize Winner as Outstanding Mathematics Undergraduate at the University of Oregon, 1977

Fulbright Scholar in Freiburg, West Germany, 1977-1978

National Institutes of Health Pre-Doctoral Trainee, 1978-1983

Snedecor Award for Outstanding Statistical Applications Paper, American Statistical Association, 1993, joint with Kenneth Lange

Myrto Lefkopolou Distinguished Lecturer, Harvard University School of Public Health, 1994

University of Michigan School of Public Health Excellence in Research Award, 1999

Pharmacia Research Professor of Biostatistics, 1999-2005

Bernard Greenberg Lecturer, Department of Biostatistics, University of North Carolina School of Public Health, 2002

Fellow, American Statistical Association, 2002-present

Richard G. Cornell Collegiate Professor of Biostatistics, 2005-2008

Member, Institute of Medicine of the National Academies, 2006-present

Benjamin Stapleton Lecturer, University of Colorado at Denver and Health Sciences Center, Denver, Colorado, 2007

Richard G. Cornell Distinguished University Professor of Biostatistics, 2008-present

Fellow, American Association for the Advancement of Science, 2010-present

Prize for outstanding paper in *Genetic Epidemiology*, 2013

PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science

American Society of Human Genetics

International Genetic Epidemiology Society

PUBLICATIONS

Publications which have received peer review

1. **Boehnke M**, Guzman M, Hehmann R, Leibold W, and Gatti RA (1980) HLA-D typing with lymphoblastoid cell lines. VIII. Cut points and gene frequency estimates by multiple testing analysis. *Tissue Antigens* 16:161-168.

2. Lange K, **Boehnke M**, and Carson R (1981) Moment computations for subcritical branching processes. *Journal of Applied Probability* 18:52-64.

3. Lange K and **Boehnke M** (1982) How many polymorphic genes will it take to span the human genome? *American Journal of Human Genetics* 34:842-845.

4. Lange K and **Boehnke M** (1983) Extensions to pedigree analysis. IV. Covariance components models for multivariate traits. *American Journal of Medical Genetics* 14:513-524.

5. Lange K and **Boehnke M** (1983) Some combinatorial problems of DNA restriction fragment length polymorphisms. *American Journal of Human Genetics* 35:177-192.

6. **Boehnke M**, Conneally PM, and Lange K (1983) Two models for a maternal factor in the inheritance of Huntington disease. *American Journal of Human Genetics* 35:845-860.

7. Lange K and **Boehnke M** (1983) Extensions to pedigree analysis. V. Optimal calculation of Mendelian likelihoods. *Human Heredity* 33:291-301.

8. **Boehnke M** and Greenberg DA (1984) The effects of conditioning on probands to correct for multiple ascertainment. *American Journal of Human Genetics* 36:1298-1308.

9. **Boehnke M** and Lange K (1984) Ascertainment and goodness of fit of variance component models for pedigree data. *Progress in Clinical and Biological Research* 147:173-192.

10. Gatti RA, **Boehnke M,** Crist M, and Sparkes RS (1985) Genetic linkage studies in ataxia-telangiectasia: Gm markers. *Kroc Foundation Series* 19:163-172.

11. **Boehnke M**, Moll PP, Lange K, Weidman WH, and Kottke BA (1986) Univariate and bivariate analyses of cholesterol and triglyceride levels in pedigrees. *American Journal of Medical Genetics* 23:775-792.

12. Hodge SE and **Boehnke M** (1986) A note on Cannings and Thompson's sequential sampling scheme for pedigrees. *American Journal of Human Genetics* 39:274-281.

13. **Boehnke M** (1986) Estimating the power of a proposed linkage study: a practical computer simulation approach. *American Journal of Human Genetics* 39:513-527.

14. **Boehnke M**, Moll P, Kottke B, and Weidman W (1987) Partitioning the variability of fasting plasma glucose levels in pedigrees. Genetic and environmental factors. *American Journal of Epidemiology* 125:679-689.

15. Bird TD, **Boehnke M**, Schellenberg GD, Deeb SS, and Lipe HP (1987) The use of apolipoprotein CII as a genetic marker for myotonic dystrophy. *Archives of Neurology* 44:273-275.

16. Schellenberg GD, Deeb SS, **Boehnke M**, Bryant EM, Martin GM, Lampe TH, and Bird TD (1987) Association of an apolipoprotein CII allele with familial dementia of the Alzheimer type. *Journal of Neurogenetics* 4:97-108.

17. Diehl SR, **Boehnke M**, Collins FS, Erickson RP, Karolyi IJ, Ploughman LM, Pericak-Vance MA, Aylsworth AS, and Roses AD (1987) Linkage analysis of peripheral neurofibromatosis to DNA markers on chromosome 8. *Journal of Medical Genetics* 24:532-534.

18. Bird TD, **Boehnke M**, Anderson J, Lampe TH, Schellenberg GD, and Larson EB (1987) The frequency of C4B variants of complement in familial and sporadic Alzheimer disease. *Alzheimer Disease and Associated Disorders* 1:251-255.

19. Diehl SR, **Boehnke M**, Erickson RP, Baxter AB, Bruce MA, Lieberman JL, Platt DJ, Ploughman LM, Seiler KA, Sweet AM, and Collins FS (1987) Linkage analysis of von Recklinghausen neurofibromatosis to DNA markers on chromosome 17. *Genomics* 1:361-363.

20. Hanash SM, **Boehnke M**, Chu EH, Neel JV, and Kuick RD (1988) Non-random distribution of structural mutants in ethylnitrosourea-treated cultured human lymphoblastoid cells. *Proceedings of the National Academy of Sciences USA* 85:165-169.

21. Chu EH, **Boehnke M**, Hanash SM, Kuick RD, Lamb BJ, Neel JV, Niezgoda W, Pivirotto S, and Sundling G (1988) Estimation of mutation rates based on the analysis of polypeptide constituents of cultured human lymphoblastoid cells. *Genetics* 119:693-703.

22. Schwartz AG, **Boehnke M**, and Moll PP (1988) Family risk index as a measure of familial heterogeneity of cancer risk. A population-based study in metropolitan Detroit. *American Journal of Epidemiology* 128:524-535.

23. **Boehnke M**, Young MR, and Moll PP (1988) Comparison of sequential and fixed-structure sampling of pedigrees in complex segregation analysis of a quantitative trait. *American Journal of Human Genetics* 43:336-343.

24. Schellenberg GD, Bird TD, Wijsman EM, Moore DK, **Boehnke M**, Bryant EM, Lampe TH, Nochlin D, Sumi SM, Deeb SS, Beyreuther K, and Martin GM (1988) Absence of linkage of chromosome 21q21 markers to familial Alzheimer's disease. *Science* 241:1507-1510.

25. Tarlo KS, **Boehnke M**, and Chin B (1988) Synergism of mutant frequencies in the mouse lymphoma cell mutagenicity assay by binary mixtures of methyl methanesulfonate and ethyl methanesulfonate. *Mutation Research* 206:239-246.

26. Lange K, Weeks D, and **Boehnke M** (1988) Programs for Pedigree Analysis: MENDEL, FISHER, and dGENE. *Genetic Epidemiology* 5:471-472.

27. Young MR, **Boehnke M**, and Moll PP (1988) Correcting for single ascertainment by truncation for a quantitative trait. *American Journal of Human Genetics* 43:705-708.

28. Diehl SR, **Boehnke M**, Erickson RP, Ploughman LM, Seiler KA, Lieberman JL, Clarke HB, Bruce MA, Schorry EK, Pericak-Vance MA, O'Connell P, and Collins FS (1989) A refined genetic map of the region of chromosome 17 surrounding the von Recklinghausen neurofibromatosis (NF1) gene. *American Journal of Human Genetics* 44:33-37.

29. **Boehnke M** and Moll PP (1989) Identifying pedigrees segregating at a major locus for a quantitative trait: an efficient strategy for linkage analysis. *American Journal of Human Genetics* 44:216-224.

30. Ploughman LM and **Boehnke M** (1989) Estimating the power of a proposed linkage study for a complex genetic trait. *American Journal of Human Genetics* 44:543-551.

31. Olson JM, **Boehnke M**, Neiswanger K, Roche AF, and Siervogel RM (1989) Alternative genetic models for the inheritance of the phenylthiocarbamide taste deficiency. *Genetic Epidemiology* 6:423-434.

32. **Boehnke M**, Arnheim N, Li H, and Collins FS (1989) Fine-structure genetic mapping of human chromosomes using the polymerase chain reaction on single sperm: experimental design considerations. *American Journal of Human Genetics* 45:21-32.

33. Ping AJ, Reeve AE, Law DJ, Young MR, **Boehnke M**, and Feinberg AP (1989) Genetic linkage of Beckwith-Wiedemann syndrome to 11p15. *American Journal of Human Genetics* 44:720-723.

34. **Boehnke M**, Omoto KH, and Arduino JM (1990) Selecting pedigrees for linkage analysis of a quantitative trait: the expected number of informative meioses. *American Journal of Human Genetics* 46:581-586.

35. Kwon JM, **Boehnke M**, Burns TL, and Moll PP (1990) Commingling and segregation analyses: comparison of results from a simulation study of a quantitative trait. *Genetic Epidemiology* 7:57-68.

36. Roth MS, Weiner GJ, Allen EA, Terry VH, Harnden CE, **Boehnke M**, Kaminski MS, and Ginsburg D (1990) Molecular characterization of anti-idiotype antibody-resistant variants of a murine β-cell lymphoma. *Journal of Immunology* 145:768-777.

37. **Boehnke M** (1990) Sample-size guidelines for linkage analysis of a dominant locus for a quantitative trait by the method of lod scores. *American Journal of Human Genetics* 47:218-227.

38. Olson JM and **Boehnke M** (1990) Monte Carlo comparison of preliminary methods for ordering multiple genetic loci. *American Journal of Human Genetics* 47:470-482.

39. Eto K, Sumi SM, Bird TD, McEvoy-Bush T, **Boehnke M**, and Schellenberg G (1990) Family with dominantly inherited ataxia, amyotrophy, and peripheral sensory loss: Spinopontine atrophy or Machado-Joseph Azorean disease in another non-Portuguese family? *Archives of Neurology* 47:968-974.

40. Sieving PA, Bingham EL, Roth MS, Young MR, **Boehnke M**, Kuo CY, and Ginsburg D (1990) Linkage relationship of X-linked juvenile retinoschisis with Xp22.1-p22.3 probes. *American Journal of Human Genetics* 47:616-621.

41. Iannuzzi MC, Hidaka N, **Boehnke M**, Bruck ME, Hanna WT, Collins FS, and Ginsburg D (1991) Analysis of the relationship of von Willebrand disease (vWD) and hereditary hemorrhagic telangiectasia and identification of a potential type IIA vWD mutation. *American Journal of Human Genetics* 48:757-763.

42. **Boehnke M** (1991) Allele frequency estimation from data on relatives. *American Journal of Human Genetics* 48:22-25.

43. **Boehnke M**, Lange K, and Cox DR (1991) Statistical methods for multipoint radiation hybrid mapping. *American Journal of Human Genetics* 49:1174-1188.

44. Richards JE, Kuo C, **Boehnke M**, and Sieving PA (1991) Rhodopsin Thr58Arg mutation in a family with autosomal dominant retinitis pigmentosa. *Ophthalmology* 98:1797-1805.

45. Sowers MR, **Boehnke M**, Jannausch ML, Crutchfield M, Corton G, and Burns TL (1992) Familiality and partitioning the variability of femoral bone mineral density in women of child-bearing age. *Calcified Tissue International* 50:110-114.

46. **Boehnke M** (1992) Genetic Analysis Workshop 7: radiation hybrid and somatic cell hybrid mapping of chromosome 21. *Cytogenetics and Cell Genetics* 59:74-76.

47. **Boehnke M** (1992) Radiation hybrid mapping by minimization of the number of obligate chromosome breaks. *Cytogenetics and Cell Genetics* 59:96-98.

48. Schellenberg GD, **Boehnke M**, Wijsman EM, Moore DK, Martin GM, and Bird TD (1992) Genetic association and linkage analysis of the apolipoprotein CII locus and familial Alzheimer's disease. *Annals of Neurology* 31:223-227.

49. Lange K and **Boehnke M** (1992) Bayesian methods and optimal experimental design for gene mapping by radiation hybrids. *Annals of Human Genetics* 56:119-144.

50. Altherr MR, Plummer S, Bates G, MacDonald M, Taylor S, Lehrach H, Frischauf AM, Gusella J, **Boehnke M**, and Wasmuth JJ (1992) Radiation hybrid map spanning the Huntington disease gene region of chromosome 4. *Genomics* 13:1040-1046.

51. **Boehnke M** (1992) Multipoint analysis for radiation hybrid mapping. *Annals of Medicine* 24:383-386.

52. Frazer KA, **Boehnke M**, Budarf ML, Wolff RK, Emanuel BS, Myers RM, and Cox DR (1992) A radiation hybrid map of the region on human chromosome 22 containing the neurofibromatosis type 2 locus. *Genomics* 14:574-584.

53. Gorski JL, **Boehnke M**, Reyner EL, and Burright EN (1992) A radiation hybrid map of the proximal short arm of the human X chromosome spanning incontinentia pigmenti 1 (IP1) translocation breakpoints. *Genomics* 14:657-665.

54. Spence MA, Bishop DT, **Boehnke M**, Elston RC, Falk C, Hodge SE, Ott J, Rice J, Merikangas K, and Kupfer D (1993) Methodological issues in linkage analyses for psychiatric disorders: secular trends, assortative mating, bilineal pedigrees. *Human Heredity* 43:166-172.

55. Richard CW III, **Boehnke M**, Berg DJ, Lichy JH, Meeker TC, Hauser E, Myers RM, and Cox DR (1993) A radiation hybrid map of the distal short arm of human chromosome 11, containing the Beckwith-Wiedemann and associated embryonal tumor disease loci. A*merican Journal of Human Genetics* 52:915-921.

56. Chamberlain JS, **Boehnke M**, Frank TS, Kiousis S, Xu J, Guo SW, Hauser ER, Norum RA, Helmbold EA, Markel DS, Keshavarzi SM, Jackson CE, Calzone K, Garber J, Collins FS, and Weber BL (1993) *BRCA1* maps proximal to D17S579 on chromosome 17q21 by genetic analysis. *American Journal of Human Genetics* 52:792-798.

57. Biesecker BB, **Boehnke M**, Calzone K, Markel DS, Garber JE, Collins FS, and Weber BL (1993) Genetic counseling for families with inherited susceptibility to breast and ovarian cancer. *Journal of the American Medical Association* 269:1970-1974.

58. Abel KJ, **Boehnke M**, Prahalad M, Ho P, Flejter WL, Watkins M, VanderStoep J, Chandrasekharappa SC, Collins FS, Glover TW, and Weber BL (1993) A radiation hybrid map of the *BRCA1* region of chromosome 17q12-21. *Genomics* 17:632-641.

59. Flejter WL, Barcroft CL, Guo SW, Lynch ED, **Boehnke M**, Chandrasekharappa S, Hayes S, Collins FS, Weber BL, and Glover TW (1993) Multicolor FISH mapping with Alu-PCR amplified YAC clone DNA determines the order of markers in the *BRCA1* region on chromosome 17q12-q21. *Genomics* 17:624-631.

60. Schork NJ, **Boehnke M**, Terwilliger JD, and Ott J (1993) Two-trait-locus linkage analysis: a powerful strategy for mapping complex genetic traits. *American Journal of Human Genetics* 53:1127-1136.

61. Richards JE, Lichter PR, **Boehnke M**, Uro JL, Torrez D, Wong D, and Johnson AT (1994) Mapping of a gene for autosomal dominant juvenile-onset open-angle glaucoma to chromosome 1q. *American Journal of Human Genetics* 54:62-70.

62. McDonald MT, Papenberg KA, Ghosh S, Glatfelter AA, Biesecker BB, Helmbold EA, Markel DS, Zolotor A, McKinnon WC, Vanderstoep JL, Jackson CE, Iannuzzi M, Collins FS, **Boehnke M**, Porteous ME, Guttmacher AE, and Marchuk DA (1994) A disease locus for hereditary haemorrhagic telangiectasia maps to chromosome 9q33-34. *Nature Genetics* 6:197-204.

63. Yu CE, Payami H, Olson JM, **Boehnke M**, Wijsman EM, Orr HT, Kukull WA, Goddard KA, Nemens E, White JA, Alonso ME, Taylor TD, Ball MJ, Kaye J, Morris J, Chui H, Sadovnick AD, Martin GM, Larson EB, Heston LL, Bird TD, and Schellenberg GD (1994) The apolipoprotien E/CI/CII gene cluster and late-onset Alzheimer disease. *American Journal of Human Genetics* 54:631-642.

64. Lunetta KL and **Boehnke M** (1994) Multipoint radiation hybrid mapping: comparison of methods, sample size requirements, and optimal study characteristics. *Genomics* 21:92-103.

65. **Boehnke M** (1994) Limits of resolution of genetic linkage studies: implications for the positional cloning of human disease genes. *American Journal of Human Genetics* 55:379-390.

66. Couch FJ, Abel KJ, Brody LC, **Boehnke M**, Collins FS, and Weber BL (1994) Localization of the gene for ATP citrate lyase (ACLY) distal to gastrin (GAS) and proximal to D17S856 on chromosome 17q12-q21. *Genomics* 21:444-446.

67. Oshima J, Yu CE, **Boehnke M**, Weber JL, Edelhoff S, Wagner MJ, Wells DE, Wood S, Disteche CM, Martin GM, and Schellenberg GD (1994) Integrated mapping analysis of the Werner Syndrome region of chromosome 8. *Genomics* 23:100-113.

68. Maliarik M, Kost J, Harrington D, Major M, Popovich J, **Boehnke M**, and Iannuzzi MC (1994) Linkage analysis of major histocompatibility genes in familial sarcoidosis. *Sarcoidosis* 11:236-239.

69. Ford D, Easton DF, Bishop DT, Narod SA, Goldgar DE, Haites N, Milner B, Allan L, Ponder BAJ, Peto J, Smith S, Stratton M, Lenoir GM, Feunteun J, Lynch H, Arason A, Barkardottir R, Egilsson V, Black DM, Kelsell D, Spurr N, Devilee P, Cornelisse CJ, Varsen H, Birch JM, Skolnick M, Santibanezkoref MS, Teare D, Steel M, Porter D, Cohen BB, Carothers A, Smyth EM, Weber B, Newbold B, **Boehnke M**, Collins FS, Cannon-Albright LA, and Goldgar D (1994) Risks of cancer in *BRCA1*-mutation carriers. *Lancet* 343:692-695.

70. Lange K, **Boehnke M**, Cox DR, and Lunetta KL (1995) Statistical methods for polyploid radiation hybrid mapping. *Genome Research* 5:136-150.

71. Lunetta KL, **Boehnke M**, Lange K, and Cox DR (1995) Experimental design and error detection for polyploid radiation hybrid mapping. *Genome Research* 5:151-163.

72. Pawar H, Bingham EL, Lunetta KL, Segal M, Richards JE, **Boehnke M**, and Sieving PA (1995) Refined genetic mapping of juvenile X-linked retinoschisis. *Human Heredity* 45:206-210.

73. Couch FJ, Garber J, Kiousis S, Calzone K, Hauser ER, Merajver SD, Frank TS, **Boehnke M**, Chamberlain JS, Collins FS, and Weber BL (1995) Genetic analysis of eight breast-ovarian cancer families with suspected *BRCA1* mutations. *Journal of the National Cancer Institute* 17:9-14.

74. **Boehnke M** and Hulbert-Shearon T (1995) Recombination fraction estimate of zero in the presence of apparent recombinants: effects of incomplete penetrance and sporadic cases. *Genetic Epidemiology* 12:509-513.

75. Easton DF, Ford D, Bishop DT, Haites N, Milner B, Allan L, Easton DF, Ponder BAJ, Peto J, Smith S, Ford D, Stratton M, Narod SA, Lenoir GM, Feunteun J, Lynch H, Arason A, Barkdardottir R, Egilsson DV, Bishop DT, Black DM, Kelsell D, Spurr NK,

Devilee P, Cornelisse CJ, Varsen H, Birch JM, Santibanezkoref MS, Teare MD, Steel M, Porter D, Cohen BB, Carothers A, Smyth E, Weber B, **Boehnke M**, Collins FS, Cannon-Albright LA, Goldgar D, and Skolnick M (1995) Breast and ovarian-cancer incidence in *BRCA1*-mutation carriers. *American Journal of Human Genetics* 56:265-271.

76. Narod SA, Ford D, Devilee P, Barkardottir RB, Lynch HT, Smith SA, Ponder BAJ, Weber BL, Garber JE, Birch JM, Cornelis RS, Kelsell DP, Spurr NK, Smyth E, Haites N, Sobol H, Bignon YJ, Chang-claude J, Hamann U, Lindblom A, Borg A, Piver MS, Gallion HH, Struewing JP, Whittemore A, Tonin P, Goldgar DE, Easton DF, Milner B, Allan L, Simard J, Rommens J, McGillivray B, Green R, Ives E, Boyd N, Rosen B, Cole D, Morgan K, Moslehi R, Ponder B, Peto J, Smith S, Stratton M, Dicioccio RA, Gallion H, Santibanezkoref MS, Teare MD, Evans DG, Stoppalyonnet D, Lalle P, Bonaiti C, Essioux L, Girodet C, Maugardlouboutin C, Nicolleau G, Longy M, Toulouse C, Horstein I, Birnbaum D, Eisinger F, Karengueven F, Noguchi T, Hardouin A, Rio P, Machelardroumagnac M, Nogues C, Cohenhaguenauer O, Lortholary A, Bay Jo, Arason A, Barkdardottir RB, Egilsson V, Bishop DT, Kelsell D, Murday VA, Solomon E, Spurr N, Turner G, Lenoir G, Feunteun J, Lynch H, Lynch J, Watson P, Conway T, Bonnardel C, Serova O, Torchard D, Larsson C, Vasen H, Vanleeuwen I, Cornelisse CJ, Steel M, Porter D, Cohen BB, Carothers A, Cannon-Albright LA, Goldgar D, Skolnick M, Becher H, Johannsson O, Weber B, Collins FS, **Boehnke M**, Garber J, and Li F (1995) An evaluation of genetic-heterogeneity in 145 breast-ovarian-cancer families. *American Journal of Human Genetics* 56:254-264.

77. Ho PP, Couch FJ, Brody LC, Abel KJ, **Boehnke M,** Shearon TH, Chandrasekharappa SC, Collins FS, and Weber BL (1995) Localization of the human homolog of the yeast cell division control 27 gene (*CDC27*) proximal to *ITGB3* on human chromosome 17q21.3. *Somatic Cell and Molecular Genetics* 21:351-355.

78. Hulbert-Shearon T, **Boehnke M**, and Lange K (1996) Lod score curves for phase-unknown matings. *Human Heredity* 46:55-57.

79. Hauser ER, **Boehnke M**, Guo SW, and Risch N (1996) Affected-sib-pair interval mapping and exclusion for complex genetic traits: sampling considerations. *Genetic Epidemiology* 13:117-137.

80. Griffith AJ, Burgess DL, Kohrman DC, Yu J, Blaschak J, Blanton SH, **Boehnke M**, Hecht JT, Overhauser J, and Meisler MH (1996) Localization of the homolog of a mouse craniofacial mutant to human chromosome 18q11 and evaluation of linkage to human CLP and CPO. *Genomics* 34:299-303.

81. Hou YC, Richards JE, Bingham EL, Pawar H, Scott K, Segal M, Lunetta KL, **Boehnke M**, and Sieving PA (1996) Linkage study of Best's vitelliform macular dystrophy (*VMD2*) in a large North American family. *Human Heredity* 46:211-220.

82. Richards JE, Lichter PR, Herman S, Hauser ER, Hou YC, Johnson AT, and **Boehnke M** (1996) Probable exclusion of *GLC1A* as a candidate glaucoma gene in a family with middle-age-onset primary open-angle glaucoma. *Ophthalmology* 103:1035-1040.

83. Johnson AT, Richards JE, **Boehnke M**, Stringham HM, Herman SB, Wong DJ, and Lichter PR (1996) Clinical phenotype of juvenile-onset primary open-angle glaucoma linked to chromosome 1q. *Ophthalmology* 103:808-814.

84. Lunetta KL, **Boehnke M**, Lange K, and Cox DR (1996) Selected locus and multiple mapping panel models for radiation hybrid mapping. *American Journal of Human Genetics* 59:717-725.

85. Stringham HM and **Boehnke M** (1996) Identifying marker typing incompatibilities in linkage analysis. *American Journal of Human Genetics* 59:946-950.

86. Nichols WC, Antin JH, Lunetta KL, Terry VH, Hertel CE, Wheatley MA, Arnold ND, Siemieniak DR, **Boehnke M**, and Ginsburg D (1996) Polymorphism of adhesion molecule CD31 is not a significant risk factor for graft-versus-host disease. *Blood* 88:4429-4434.

87. Lichter PR, Richards JE, **Boehnke M**, Othman M, Cameron BD, Stringham HM, Downs CA, Lewis SB, and Boyd BF (1996) Juvenile glaucoma linked to *GLC1A* in a Panamanian family. *Transactions of the American Ophthalmology Society* 94:335-346.

88. Lichter PR, Richards JE, **Boehnke M**, Othman M, Cameron BD, Stringham HM, Downs CA, Lewis SB, and Boyd BF (1997) Juvenile glaucoma linked to the *GLC1A* gene on chromosome 1q in a Panamanian family. *American Journal of Ophthalmology* 123:413-416.

89. Ghosh S, Karanjawala ZE, Hauser ER, Ally D, Knapp JI, Rayman JB, Musick A, Tannenbaum J, Te C, Shapiro S, Eldridge W, Musick T, Martin C, Smith J, Carpten JD, Brownstein MJ, Powell JI, Whiten R, Chines P, Nylund SJ, Magnuson VL, **Boehnke M**, Collins FS, and the FUSION Study Group (1997) Methods for precise sizing, automated binning of alleles and reduction of error rates in large-scale genotyping using fluorescently-labeled dinucleotide markers. *Genome Research* 7:165-178.

90. **Boehnke M** and Cox NJ (1997) Accurate inference of relationships in sib-pair linkage studies. *American Journal of Human Genetics* 61:423-429.

91. Lichter PR, Richards JE, Downs CA, Stringham HM, **Boehnke M**, and Farley FA (1997) Cosegregation of open-angle glaucoma and the nail-patella syndrome. *American Journal of Ophthalmology* 124:506-515.

92. **Boehnke M** and Langefeld CD (1998) Genetic association mapping based on discordant sib pairs: the discordant alleles test (DAT). *American Journal of Human Genetics* 62:950-961.

93. Valle T, Tuomilehto J, Bergman RN, Ghosh S, Hauser ER, Eriksson J, Nylund SJ, Kohtamäki K, Toivanen L, Vidgren G, Tuomilehto-Wolf E, Ehnholm C, Blaschak J, Langefeld CD, Watanabe RM, Magnuson V, Ally DS, Hagopian WA, Ross E, Buchanan TA, Collins FS, and **Boehnke M** (1998) Mapping genes for NIDDM. Design of the Finland-United States Investigation of NIDDM Genetics (FUSION) Study. *Diabetes Care* 21:949-958.

94. Ghosh S, Hauser ER, Magnuson VL, Valle T, Ally DS, Karanjawala ZE, Rayman JB, Knapp JI, Musick A, Tannenbaum J, Te C, Eldridge W, Shapiro S, Musick T, Martin C, So A, Witt A, Blaschak-Harvan J, Watanabe RM, Hagopian W, Eriksson J, Nylund S, Kohtamäki K, Tuomilehto-Wolf E, Toivanen L, Vidgren G, Ehnholm C, Bergman R, Tuomilehto J, Collins FS, and **Boehnke M** (1998) A large sample of Finnish diabetic sib-pairs reveals no evidence for a non-insulin dependent diabetes mellitus susceptibility locus at 2qter. *Journal of Clinical Investigation* 102:704-709.

95. Othman MI, Sullivan SA, Skuta GL, Cockrell DA, Stringham HM, Downs CA, Fornes A, Mick A, **Boehnke M**, Vollrath D, and Richards JE (1998) Autosomal dominant nanophthalmos (NNO1) with high hyperopia and angle-closure glaucoma maps to chromosome 11. *American Journal of Human Genetics* 63:1411-1418.

96. Richards JE, Ritch R, Lichter PR, Rozsa FW, Stringham HM, Caronia RM, Johnson D, Abundo GP, Willcockson J, Downs CA, Thompson DA, Musarella MA, Gupta N, Othman MI, Torrez DM, Herman SB, Wong DJ, Higashi M, and **Boehnke M** (1998) Novel trabecular meshwork inducible glucocorticoid response mutation in an eight-generation juvenile-onset primary open-angle glaucoma pedigree. *Ophthalmology* 105:1698-1707.

97. Cerosaletti KM, Lange E, Stringham HM, Weemaes CM, Smeets D, Solder B, Belohradsky BH, Taylor AM, Karnes P, Elliott A, Komatsu K, Gatti RA, **Boehnke M**, and Concannon P (1998) Fine localization of the Nijmegen breakage syndrome gene to 8q21: evidence for a common founder haplotype. *American Journal of Human Genetics* 63:125-134.

98. Hauser ER and **Boehnke M** (1998) Genetic linkage analysis of complex genetic traits by using affected sibling pairs. *Biometrics* 54:1238-1246.

99. Ghosh S, Langefeld CD, Ally D, Watanabe RM, Hauser ER, Magnuson VL, Nylund SJ, Valle T, Eriksson J, Bergman RN, Tuomilehto J, Collins FS, and **Boehnke M** (1999) The W64R variant of the β3-adrenergic receptor is not associated with Type II diabetes or obesity in a large Finnish sample. *Diabetologia* 42:238-244.

100. Ghosh S, Watanabe RM, Hauser ER, Valle T, Magnuson VL, Erdos MR, Langefeld CD, Balow J Jr, Ally DS, Kohtamäki K, Chines P, Birznieks G, Kaleta H, Musick A, Te C, Tannenbaum J, Eldridge W, Shapiro S, Martin C, Witt A, So A, Chang J, Shurtleff B, Porter R, Kudelko K, Unni A, Segal L, Sharaf R, Blaschak-Harvan J, Eriksson J, Tenkula T, Vidgren G, Ehnholm C, Tuomilehto-Wolf E, Hagopian W, Buchanan TA, Tuomilehto J, Bergman RN, Collins FS, and **Boehnke M** (1999) Type 2 diabetes: evidence for linkage on chromosome 20 in 716 Finnish affected sib pairs. *Proceedings of the National Academy of Sciences USA* 96:2198-2203.

101. Hodge SE, **Boehnke M**, and Spence MA (1999) Loss of information due to ambiguous haplotyping of SNPs. *Nature Genetics* 21:360-361.

102. Watanabe RM, Valle T, Hauser ER, Ghosh S, Eriksson J, Kohtamäki K, Ehnholm C, Tuomilehto J, Collins FS, Bergman RN, and **Boehnke M** for the Finland-United States Investigation of NIDDM Genetics (FUSION) Study Investigators (1999) Familiality of

quantitative metabolic traits in Finnish families with non-insulin dependent diabetes mellitus. *Human Heredity* 49:159-168.

103. Stringham HM, **Boehnke M**, and Lange K (1999) Point and interval estimates of marker location in radiation hybrid mapping. *American Journal of Human Genetics* 65:545-553.

104. Douglas JA, **Boehnke M**, and Lange K (2000) A multipoint method for detecting genotyping errors and mutations in sibling-pair linkage data. *American Journal of Human Genetics* 66:1287-1297.

105. **Boehnke M** (2000) A look at linkage disequilibrium. *Nature Genetics* 25:246-247.

106. Ghosh S, Watanabe RM, Valle TT, Hauser ER, Magnuson VL, Langefeld CD, Ally DS, Mohlke KL, Silander K, Kohtamäki K, Chines P, Balow J, Birznieks G, Chang J, Eldridge W, Erdos MR, Karanjawala ZE, Knapp JI, Kudelko K, Martin C, Morales-Mena A, Musick A, Musick T, Pfahl C, Porter R, Rayman JB, Rha D, Segal L, Shapiro S, Sharaf R, Shurtleff B, So A, Tannenbaum J, Te C, Tover J, Unni A, Welch C, Whiten R, Witt A, Blaschak-Harvan J, Douglas JA, Duren WL, Epstein MP, Fingerlin TE, Kaleta HS, Lange EM, Li C, McEachin RC, Stringham HM, Trager E, White PP, Eriksson J, Toivanen L, Vidgren G, Nylund SJ, Tuomilehto-Wolf E, Ross EH, Demirchyan E, Hagopian WA, Buchanan TA, Tuomilehto J, Bergman RN, Collins FS, and **Boehnke M** (2000) The Finland-United States Investigation of Non-Insulin-Dependent Diabetes Mellitus Genetics (FUSION) study. I. An autosomal genome scan for genes that predispose to Type 2 diabetes. *American Journal of Human Genetics* 67:1174-1185.

107. Watanabe RM, Ghosh S, Langefeld CD, Valle TT, Hauser ER, Magnuson VL, Mohlke KL, Silander K, Ally DS, Chines P, Blaschak-Harvan J, Douglas JA, Duren WD, Epstein MP, Fingerlin TE, Kaleta HS, Lange EM, Li C, McEachin RC, Stringham HM, Trager E, White PP, Balow J, Birznieks G, Chang J, Eldridge W, Erdos MR, Karanjawala ZE, Knapp JI, Kudelko K, Martin C, Morales-Mena A, Musick A, Musick T, Pfahl C, Porter R, Rayman JB, Rha D, Segal L, Shapiro S, Sharaf R, Shurtleff B, So A, Tannenbaum J, Te C, Tovar J, Unni A, Welch C, Whiten R, Witt A, Kohtamäki K, Ehnholm C, Eriksson J, Toivanen L, Vidgren G, Nylund SJ, Tuomilehto-Wolf E, Ross EH, Demirchyan E, Hagopian WA, Buchanan TA, Tuomilehto J, Bergman RN, Collins FS, and **Boehnke M** (2000) The Finland-United States Investigation of Non-Insulin-Dependent Diabetes Mellitus Genetics (FUSION) study. II. An autosomal genome scan for diabetes-related quantitative-trait loci. *American Journal of Human Genetics* 67:1186-1200.

108. Epstein MP, Duren WL, and **Boehnke M** (2000) Improved inference of relationship for pairs of individuals. *American Journal of Human Genetics* 67:1219-1231.

109. Gillanders E, Douglas JA, Gruber SB, Yan H, Vogelstein B, Sood R, Carpten J, Dennis T, **Boehnke M**, and Trent JM (2001) Use of experimentally constructed haplotypes in gene mapping studies of hereditary cancers. *Nature Genetics* 27:87-88.

110. Mohlke KL, Lange EM, Valle TT, Ghosh S, Magnuson VL, Silander S, Watanabe RM, Chines PS, Bergman RN, Tuomilehto J, Collins FS, and **Boehnke M** (2001) Linkage disequilibrium between microsatellite markers extends beyond 1 cM on chromosome 20 in Finns. *Genome Research* 11:1221-1226.

111. Stringham HM and **Boehnke M** (2001) Lod scores for gene mapping in the presence of marker map uncertainty. *Genetic Epidemiology* 21:31-39.

112. Douglas JA, Erdos MR, Watanabe RM, Braun A, Johnston CL, Oeth P, Mohlke KL, Valle TT, Ehnholm C, Buchanan TA, Bergman RN, Collins FS, **Boehnke M**, and Tuomilehto J (2001) The peroxisome proliferator-activated receptor-gamma2 Pro12Ala variant: association with type 2 diabetes and trait differences. *Diabetes* 50:886-890.

113. Douglas JA, **Boehnke M**, Gillanders E, Trent JM, and Gruber SB (2001) Experimentally-derived haplotypes substantially increase the efficiency of linkage disequilibrium studies. *Nature Genetics* 28:361-364.

114. Tsuang DW, Skol AD, Faraone SV, Bingham S, Young KA, Prabhudesai S, Haverstock SL, Mena F, Menon AS, Bisset D, Pepple J, Sauter F, Baldwin C, Weiss D, Collins J, **Boehnke M**, Schellenberg GD, and Tsuang MT (2001) Examination of genetic linkage of chromosome 15 to schizophrenia in a large Veterans Affairs Cooperative Study sample. *American Journal of Medical Genetics* 105:662-668.

115. Douglas JA, Skol A, and **Boehnke M** (2002) Probability of detection of genotyping errors and mutations as inheritance inconsistencies in nuclear-family data. *American Journal of Human Genetics* 70:487-495.

116. Epstein MP, Lin X, and **Boehnke M** (2002) Ascertainment-adjusted parameter estimates revisited. *American Journal of Human Genetics* 70:886-895.

117. Fingerlin TE, Erdos MR, Watanabe RM, Wiles KR, Stringham HM, Mohlke KL, Silander K, Valle TT, Buchanan TA, Tuomilehto J, Bergman RN, **Boehnke M**, and Collins FS (2002) Variation in three single nucleotide polymorphisms in the calpain-10 gene not associated with type 2 diabetes in a large Finnish cohort. *Diabetes* 51:1644-1648.

118. Hanna GL, Veenstra-VanderWeele J, Cox NJ, **Boehnke M**, Himle JA, Curtis GC, Leventhal BL, and Cook EH Jr (2002) Genome-wide linkage analysis of families with obsessive-compulsive disorder ascertained through pediatric probands. *American Journal of Medical Genetics* 114:541-552.

119. Ayyagari R, Demirci FY, Liu JF, Bingham EL, Stringham H, Kakuk LE, **Boehnke M**, Gorin MB, Richards JE, and Sieving PA (2002) X-linked recessive atrophic macular degeneration from *RPGR* mutation. *Genomics* 80:166-171.

120. Faraone SV, Skol AD, Tsuang DW, Bingham S, Young KA, Prabhudesai S, Haverstock SL, Mena F, Menon AS, Bisset D, Pepple J, Sautter F, Baldwin C, Weiss D, Collins J, Keith T, **Boehnke M,** Tsuang MT, and Schellenberg GD (2002) Linkage of chromosome 13q32 to schizophrenia in a large Veterans Affairs Cooperative Study sample. *American Journal of Medical Genetics* 114:598-604.

121. Mohlke KL, Erdos MR, Scott LJ, Fingerlin TE, Jackson AU, Silander K, Hollstein P, **Boehnke M**, and Collins FS (2002) High-throughput screening for evidence of association using mass spectrometry genotyping on DNA pools. *Proceedings of the National Academy of Sciences USA* 99:16928-16933.

122. Epstein MP, Lin X, and **Boehnke M** (2003) A tobit variance-component method for linkage analysis of censored trait data. *American Journal of Human Genetics* 72:611-620.

123. Moroi SE, Gokhale PA, Schteingart MT, Sugar A, Downs CA, Shimizu S, Krafchak C, Fuse N, Elner SG, Elner VM, Flint A, Epstein MP, **Boehnke M,** and Richards JE (2003) Clinicopathologic correlation and genetic analysis in a case of Posterior Polymorphous Corneal Dystrophy. *American Journal of Ophthalmology* 135:461-470.

124. Skol AD, Young KA, Tsuang DW, Faraone SV, Haverstock SL, Bingham S, Prabhudesai S, Mena F, Menon AS, Yu CE, Rundell P, Pepple J, Sauter F, Baldwin C, Weiss D, Collins J, Keith T, **Boehnke M**, Schellenberg GD, and Tsuang MT (2003) Modest evidence for linkage and possible confirmation of association between *NOTCH4* and schizophrenia in a large Veterans Affairs Cooperative Study sample. *American Journal of Medical Genetics Part B* 118B:8-15.

125. Eriksson M, Brown TE, Gordon LB, Glynn MW, Singer J, Scott L, Erdos MR, Robbins CM, Moses TY, Berglund P, Dutra A, Pak E, Durkin S, Csoka AB, **Boehnke M**, Glover TW, and Collins FS (2003) Recurrent *de novo* point mutations in Lamin A cause Hutchinson-Gilford Progeria Syndrome. *Nature* 423:293-298.

126. Li C, Scott LJ, and **Boehnke M** (2004) Assessing whether an allele can account in part for a linkage signal: the genotype-IBD sharing test (GIST). *American Journal of Human Genetics* 74:418-431.

127. Fingerlin TE, **Boehnke M**, and Abacesis GR (2004) Increasing the power and efficiency of disease-marker case-control association studies through use of allele-sharing information. *American Journal of Human Genetics* 74:432-443.

128. Silander K, Scott LJ, Valle TT, Mohlke KL, Stringham HM, Wiles KR, Duren WL, Doheny KF, Pugh EW, Chines P, Narisu N, White PP, Fingerlin TE, Jackson AU, Li C, Ghosh S, Magnuson VL, Colby K, Erdos MR, Hill JE, Hollstein P, Humphreys KM, Kasad R, Lambert J, Lazaridis KN, Lin G, Morales-Mena A, Patzkowski K, Pfahl C, Porter R, Rha D, Segal L, Suh YD, Tovar J, Unni A, Welch C, Douglas JA, Epstein MP, Hauser ER, Hagopian W, Buchanan TA, Watanabe RM, Bergman RN, Tuomilehto J, Collins FS, and **Boehnke M** (2004) A large set of Finnish affected sibling pair families with type 2 diabetes suggests susceptibility loci on chromosomes 6, 11, and 14. *Diabetes* 53:821-829.

129. Silander K, Mohlke KL, Scott LJ, Peck EC, Hollstein P, Skol AD, Deloukas P, Hunt S, Stavrides G, Chines PS, Erdos MR, Narisu N, Li C, Fingerlin TE, Dhanjal SK, Valle TT, Bergman RN, Tuomilehto J, Watanabe RM, **Boehnke M**, and Collins FS (2004) Genetic variation near the Hepatocye Nuclear Factor-4 Alpha gene predicts susceptibility to type 2 diabetes. *Diabetes* 53:1141-1149.

130. Hauser ER, Watanabe RM, Duren WL, Bass MP, Langefeld CD, and **Boehnke M** (2004) Ordered subset analysis in genetic linkage mapping of complex traits. *Genetic Epidemiology* 27:53-63.

131. Lange EM and **Boehnke M** (2004) The haplotype runs test: I. The parent-parent-affected offspring trio design. *Genetic Epidemiology* 27:118-130.

132. Conneely KN, Silander K, Scott LJ, Mohlke KL, Lazaridis KN, Valle TT, Tuomilehto J, Bergman RN, Watanabe RM, Buchanan TA, Collins FS, and **Boehnke M** (2004) Variation in the resistin gene is associated with obesity and insulin-related phenotypes in Finnish subjects. *Diabetologia* 47:1782-1788.

133. Shimizu S, Krafchak C, Fuse N, Epstein MP, Schteingart MT, Sugar A, Eibschitz-Tsimhoni M, Downs CA, Rozsa F, Trager EH, Reed DM, **Boehnke M**, Moroi SE, and Richards JE (2004) A locus for posterior polymorphous corneal dystrophy (*PPCD3*) maps to chromosome 10. *American Journal of Medical Genetics* 130:372-377.

134. Mohlke KL and **Boehnke M** (2005) The role of *HNF4A* variants in the risk of type 2 diabetes. *Current Diabetes Reports* 5:149-156.

135. Mohlke KL, Skol AD, Scott LJ, Valle TT, Bergman RN, Tuomilehto J, **Boehnke M**, and Collins FS (2005) Evaluation of *SLC2A10* (*GLUT10*) as a candidate gene for type 2 diabetes and related traits in Finns. *Molecular Genetics and Metabolism* 85:323-327.

136. Li M, **Boehnke M**, and Abecasis GR (2005) Joint modeling of linkage and association: identifying SNPs responsible for a linkage signal. *American Journal of Human Genetics* 76:934-949.

137. Hanna G, Fingerlin TE, Himle JA, and **Boehnke M** (2005) Complex segregation analysis of obsessive-compulsive disorder in families with pediatric probands. *Human Heredity* 60:1–9.

138. Faraone SV, Skol AD, Tsuang DW, Young KA, Haverstock SL, Prabhudesai S, Mena F, Menon AS, Leong L, Sautter F, Baldwin C, Bingham S, Weiss D, Collins J, Keith T, vanden Eng JL, **Boehnke M**, Tsuang MT, and Schellenberg GD (2005) Genome scan of schizophrenia families in a large Veterans Affairs Cooperative Study Sample: evidence for linkage to 18p11.32 and for racial heterogeneity on chromosomes 6 and 14. *American Journal of Medical Genetics* 139:91-100.

139. Skol AD, Xiao R, and **Boehnke M** (2005) An algorithm to construct genetically similar subsets of families using self-reported ethnicity information. *American Journal of Human Genetics* 77:346-354.

140. Mohlke KL, Jackson AU, Scott LJ, Peck EC, Suh YD, Chines PS, Watanabe RM, Buchanan TA, Conneely KN, Erdos MR, Narisu N, Enloe S, Valle TT, Tuomilehto J, Bergman RN, **Boehnke M**, and Collins FS (2005) Mitochondrial polymorphisms and susceptibility to type 2 diabetes-related traits in Finns. *Human Genetics* 118:245-254.

141. Krafchak CM, Pawar H, Moroi SE, Sugar A., Lichter PR, Mackey DA, Mian S, Nairus T, Elner V, Schteingart MT, Downs CA, Kijek TG, Johnson JM, Trager EH, Rozsa FW, Mandal MNA, Epstein MP, Vollrath D, Ayyagari R, **Boehnke M**, and Richards JE (2005) Mutations in *TCF8* cause posterior polymorphous corneal dystrophy and ectopic expression of COL4A3 by corneal endothelial cells. *American Journal of Human Genetics* 77:694-708.

142. Skol AD, Scott LJ, Abecasis GR, and **Boehnke M** (2006) Joint analysis is more efficient than replication-based analysis for two-stage genome-wide association studies. *Nature Genetics* 38:209-213. Corrigenda. *Nature Genetics* 38:390. PMID: 16415888.

143. Willer CJ, Scott LJ, Bonnycastle LL, Jackson AU, Chines P, Pruim R, Bark CW, Tsai YY, Pugh EW, Doheny KF, Kinnunen L, Mohlke KL, Valle TT, Bergman RN, Tuomilehto J, Collins FS, and **Boehnke M** (2006) Tag SNP selection for Finnish individuals based on the CEPH Utah HapMap database. *Genetic Epidemiology* 30:180-190.

144. Li C and **Boehnke M** (2006) Haplotype association analysis for late onset diseases using nuclear family data. *Genetic Epidemiology* 30:220-230.

145. Woodroffe A, Krafchak CM, Fuse N, Lichter PR, Moroi SE, Schertzer R, Downs CA, Duren WL, **Boehnke M**, and Richards JE (2006) Ordered subset analysis supports a glaucoma locus at *GLC1I* on chromosome 15 in families with earlier adult age at diagnosis. *Experimental Eye Research* 82:1068-1074.

146. Li M, **Boehnke M**, and Abecasis GR (2006) Efficient study designs for test of genetic association using sibship data and unrelated cases and controls. *American Journal of Human Genetics* 78:778-792.

147. Li M, **Boehnke M**, Abecasis GR, and Song PXK (2006) Quantitative trait linkage analysis using Gaussian copulas. *Genetics* 173:2317-2327.

148. Fingerlin TE, Abecasis GR, and **Boehnke M** (2006) Using sex-averaged genetic maps in multipoint linkage analysis when identity-by-descent status is incompletely known. *Genetic Epidemiology* 30:384-396.

149. Tsuchiya T, Schwarz P, del Bosque-Plata L, Hayes MG, Dina C, Froguel P, Towers GW, Fischer S, Temelkova-Kurktschiev T, Rietzsch H, Graessler J, Vcelák J, Palyzová D, Selisko T, Bendlová B, Schulze J, Julius U, Hanefeld M, Weedon MN, Evans JC, Frayling TM, Hattersley AT, Orho-Melander M, Groop L, Malecki MT, Hansen T, Pedersen O, Fingerlin TE, **Boehnke M**, Hanis CL, Cox NJ, and Bell GI (2006) Association of the calpain-10 gene with type 2 diabetes in Europeans: results of pooled and meta-analyses. *Molecular Genetics and Metabolism* 89:174-184.

150. Bonnycastle LL, Willer CJ, Conneely KN, Jackson AU, Burrill CP, Watanabe RM, Chines PS, Narisu N, Scott LJ, Enloe ST, Swift AJ, Duren WL, Stringham HM, Erdos MR, Riebow NL, Buchanan TA, Valle TT, Tuomilehto J, Bergman RN, Mohlke KL, **Boehnke M**, and Collins FS (2006) Common variants in Maturity-Onset Diabetes of the Young genes contribute to risk of Type 2 Diabetes in Finns. *Diabetes* 55:2534-2540.

151. Scott LJ, Bonnycastle LL, Willer CJ, Sprau AG, Jackson AU, Narisu N, Duren WL, Chines PS, Stringham HM, Erdos MR, Valle TT, Tuomilehto J, Bergman RN, Mohlke KL, Collins FC, and **Boehnke M** (2006) Association of Transcription Factor 7-Like 2 (*TCF7L2*) variants with Type 2 Diabetes in a Finnish sample. *Diabetes* 55:2649-2653.

152. DeMets DL, Stormo G, **Boehnke M**, Louis TA, Taylor J, and Dixon D (2006) Training of the next generation of biostatisticians: A call to action in the U.S. *Statistics in Medicine* 25:3415-3429.

153. Huth C, Heid IM, Vollmert C, Gieger C, Grallert H, Wolford JK, Langer B, Thorand B, Klopp N, Hamid YH, Pedersen O, Hansen T, Lyssenko V, Groop L, Meisinger C, Döring A, Löwel H, Lieb W, Hengstenberg C, Rathmann W, Martin S, Stephens JW, Ireland H, Mather H, Miller GJ, Stringham HM, **Boehnke M**, Tuomilehto J, Boeing H, Möhlig M, Spranger J, Pfeiffer A, Wernstedt I, Niklason A, López-Bermejo A, Fernández-Real J, Hanson RL, Gallart L, Vendrell J, Tsiavou A, Hatziagelaki E, Humphries SE, Wichmann HE, Herder C, and Illig T (2006) *IL6* gene promoter polymorphisms and type 2 diabetes: joint analysis of individual participants' data from 21 studies. *Diabetes* 55:2915-2921.

154. Shtir C, Nagakawa IS, Duren WL, Conneely KN, Scott LJ, Silander K, Valle TT, Tuomilehto J, Buchanan TA, Bergman RN, Collins FS, **Boehnke M**, and Watanabe RM (2007) Subsets of Finns with high HDL to total cholesterol ratio show evidence for linkage to type 2 diabetes on chromosome 6q. *Human Heredity* 63:17-25. PMCID: PMC2923439.

155. Willer CJ, Bonnycastle LL, Conneely KN, Duren WL, Jackson AU, Scott LJ, Narisu N, Chines PS, Skol A, Stringham HM, Petrie J, Erdos MR, Swift AJ, Enloe ST, Sprau AG, Smith E, Tong M, Doheny KF, Pugh EW, Watanabe RM, Buchanan TA, Valle TT, Bergman RN, Tuomilehto J, Mohlke KL, Collins FS, and **Boehnke M** (2007) Screening of 134 SNPs previously associated with type 2 diabetes replicates association with twelve SNPs in nine genes. *Diabetes* 56:256-64.

156. Scott LJ, Mohlke KL, Bonnycastle LL, Willer CJ, Li Y, Duren WL, Erdos MR, Stringham HM, Chines PS, Jackson AU, Prokunina-Olsson L, Ding CJ, Swift AJ, Narisu N, Hu T, Pruim R, Xiao R, Li X-Y, Conneely KN, Riebow NL, Sprau AG, Tong M, White PP, Hetrick KN, Barnhart MW, Bark CW, Goldstein JL, Watkins L, Xiang F, Saramies J, Buchanan TA, Watanabe RM, Valle TT, Kinnunen L, Abecasis GR, Pugh EW, Doheny KF, Bergman RN, Tuomilehto J, Collins FS, and **Boehnke M** (2007) A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science* 316:1341-1345. PMCID: PMC3214617.

157. Chanock SJ, Manolio T, **Boehnke M**, Boerwinkle E, Hunter DJ, Thomas G, Hirschhorn JN, Abecasis G, Altshuler D, Bailey-Wilson JE, Brooks LD, Cardon LR, Daly M, Donnelly P, Fraumeni JF Jr, Freimer NB, Gerhard DS, Gunter C, Guttmacher AE, Guyer MS, Harris EL, Hoh J, Hoover R, Kong CA, Merikangas KR, Morton CC, Palmer LJ, Phimister EG, Rice JP, Roberts J, Rotimi C, Tucker MA, Vogan KJ, Wacholder S, Wijsman EM, Winn DM, and Collins FS (2007) Replicating genotype-phenotype associations. *Nature* 447:655-660.

158. Skol AD, Scott LJ, Abecasis GR, and **Boehnke M** (2007) Optimal designs for two-stage genome-wide association studies. *Genetic Epidemiology* 31**:**776-788. PMID: 17549752.

159. Conneely KN and **Boehnke M** (2007) So many correlated tests, so little time! Rapid adjustment of p-values for multiple correlated tests. *American Journal of Human Genetics* 81:1158-1168. PMCID: PMC2276357.

160. Saunders CL, Chiodini BD, Sham P, Lewis CM, Abkevich V, Adeyemo AA, de Andrade M, Arya R, Berenson GS, Blangero J, **Boehnke M**, Borecki IB, Chagnon YC, Chen W, Comuzzie AG, Deng HW, Duggirala R, Feitosa MF, Froguel P, Hanson RL, Hebebrand J, Huezo-Dias P, Kissebah AH, Li W, Luke A, Martin LJ, Nash M, Ohman M, Palmer LJ, Peltonen L, Perola M, Price RA, Redline S, Srinivasan SR, Stern MP, Stone S, Stringham H, Turner S, Wijmenga C, and Collier D (2007) Meta-analysis of genome-wide linkage studies in BMI and obesity. *Obesity* 15:2263-2275.

161. Willer CJ, Sanna S, Jackson AU, Scuteri A, Bonnycastle LL, Clarke R, Heath SC, Timpson NJ, Najjar SS, Stringham HM, Strait J, Duren WL, Maschio A, Busonero F, Mulas A, Albai G, Swift AJ, Morken MA, Narisu N, Bennett D, Parish S, Shen H, Galan P, Meneton P, Hercberg S, Zelenika D, Chen W-M, Li Y, Scott LJ, Scheet PA, Sundvall J, Watanabe RM, Nagaraja R, Ebrahim S, Lawlor DA, Ben-Shlomo Y, Davey-Smith G, Shuldiner AR, Collins R, Bergman RN, Uda M, Tuomilehto J, Cao A, Collins FS, Lakatta E, Lathrop GM, **Boehnke M**, Schlessinger D, Mohlke KL, and Abecasis GR (2008) Newly-identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics* 40:161-169. PMID: 18193043.

162. Sanna S, Jackson AU, Nagaraja R, Willer CJ, Chen W-M, Bonnycastle LL, Shen H, Timpson N, Lettre G, Usala G, Chines PS, Stringham HM, Scott LJ, Dei M, Lai S, Albai G, Crisponi L, Naitza S, Doheny KF, Pugh EW, Ben-Shlomo Y, Ebrahim S, Lawlor DA, Bergman RN, Watanabe RM, Uda M, Tuomilehto J, Coresh J, Hirschhorn JN, Shuldiner AR, Schlessinger D, Collins FS, Smith GD, Boerwinkle E, Cao A, **Boehnke M**, Abecasis GR, and Mohlke KL (2008) Common variants in the *GDF5-UQCC* region are associated with variation in human height. *Nature Genetics* 40:198-203. PMCID: PMC2914680.

163. Lettre G, Jackson AU, Gieger C, Schumacher FR, Berndt SI, Sanna S, Eyheramendy S, Voight BF, Butler JL, Guiducci C, Illig T, Hackett R, Heid IM, Jacobs KB, Lyssenko V, Uda M, Diabetes Genetics Initiative,FUSION, KORA, Prostate, Lung Colorectal and Ovarian Cancer Screening Trial, Nurses' Health Study, SardiNIA, **Boehnke M**, Chanock SJ, Groop LC, Hu FB, Isomaa B, Kraft P, Peltonen L, Salomaa V, Schlessinger D, Hunter DJ, Hayes RB, Abecasis GR, Wichmann HE, Mohlke KL, and Hirschhorn JN (2008) Identification of ten loci associated with height highlights new biological pathways in human growth. *Nature Genetics* 40:584-591. PMCID: PMC2687076.

164. Guan W, Pluzhnikov A, Cox NJ, and **Boehnke M** for the International Type 2 Diabetes Linkage Analysis Consortium (2008) Meta-analysis of 23 type 2 diabetes linkage studies from the International Type 2 Diabetes Linkage Analysis Consortium. *Human Heredity* 66:35-49. PMCID: PMC2855874.

165. Zeggini E, Scott LJ, Saxena R, Voight BF, Marchini JL, Hu T, de Bakker PI, Abecasis GR, Almgren P, Andersen G, Ardlie K, Boström KB, Bergman RN, Bonnycastle LL, Borch-Johnsen K, Burtt NP, Chen H, Chines PS, Daly MJ, Deodhar P, Ding CJ, Doney AS, Duren WL, Elliott KS, Erdos MR, Frayling TM, Freathy RM, Gianniny L, Grallert H, Grarup N, Groves CJ, Guiducci C, Hansen T, Herder C, Hitman GA, Hughes TE, Isomaa B, Jackson AU, Jørgensen T, Kong A, Kubalanza K, Kuruvilla FG, Kuusisto J, Langenberg C, Allen HL, Lauritzen T, Li Y, Lindgren CM, Lyssenko V, Marvelle AF, Meisinger C, Midthjell K, Mohlke KL, Morken MA, Morris AD, Narisu N, Nilsson P,

Owen KR, Palmer CN, Payne F, Perry JR, Pettersen E, Platou C, Prokopenko I, Qi L, Qin L, Rayner NW, Rees M, Roix JJ, Sandbaek A, Shields B, Sjögren M, Steinthorsdottir V, Stringham HM, Swift AJ, Thorleifsson G, Thorsteinsdottir U, Timpson NJ, Tuomi T, Tuomilehto J, Walker M, Watanabe RM, Weedon MN, Willer CJ, Wellcome Trust Case Control Consortium, Illig T, Hveem K, Hu FB, Laakso M, Stefansson K, Pedersen O, Wareham NJ, Barroso I, Hattersley AT, Collins FS, Groop L, McCarthy MI, **Boehnke M**, and Altshuler D (2008) Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics* 40:638-645. PMCID: PMC2672416.

166. Loos RJF, Lindgren CM, Li S, Wheeler E, Zhao JH, Prokopenko I, Inouye M, Freathy RM, Attwood AP, Beckmann JS, Berndt SI, The Prostate Lung Colorectal and Ovarian (PLCO) Cancer Screening Trial, Bergmann S, Bennett AJ, Bingham SA, Bochud M, Brown M, Cauchi S, Connell JM, Cooper C, Smith GD, Day I, Dina C, De S, Dermitzakis ET, Doney ASF, Elliott KS, Elliott P, Evans DM, Farooqi I Sadaf, Froguel P, Ghori J, Groves CJ, Gwilliam R, Hadley D, Hall AS, Hattersley AT, Hebebrand J, Heid IM, KORA, Herrera B, Hinney A, Hunt SE, Jarvelin M-R, Johnson T, Jolley JDM, Karpe F, Keniry A, Khaw K-T, Luben RN, Mangino M, Marchini J, McArdle WL, McGinnis R, Meyre D, Munroe PB, Morris AD, Ness AR, Neville MJ, Nica AC, Ong KK, O'Rahilly S, Owen KR, Palmer CNA, Papadakis K, Potter S, Pouta A, Qi L, Nurses' Health Study, Randall JC, Rayner NW, Ring SM, Sandhu MS, Scherag A, Sims MA, Song K, Soranzo N, Speliotes EK, Diabetes Genetics Initiative, Syddall HE, Teichman SA, Timpson NJ, Tobias JH, Uda M, The SardiNIA Study, Vogel CIG, Wallace C, Waterworth DM, Weedon MN, The Wellcome Trust Case Control Consortium, Willer CJ, FUSION (Jackson AU, Tuomilehto J, Collins FS, **Boehnke M**, Mohlke KL), Wraight VL, Yuan X, Zeggini E, Hirschhorn JN, Strachan DP, Ouwehand WH, Caulfield MJ, Samani NJ, Frayling TM, Vollenweider P, Waeber G, Mooser V, Deloukas P, McCarthy MI, Wareham NJ, and Barroso I (2008) Common variants near *MC4R* are associated with fat mass, weight and risk of obesity. *Nature Genetics* 40:768-775. PMCID: PMC2669167.

167. Gaulton KJ, Willer CJ, Li Y, Scott LJ, Conneely KN, Jackson AU, Duren WL, Chines PS, Narisu N, Bonnycastle LL, Luo J, Pugh EW, Doheny KF, Valle TT, Abecasis GR, Tuomilehto J, Bergman RN, Collins FS, **Boehnke M**, and Mohlke KL (2008) Comprehensive association study of type 2 diabetes and related quantitative traits with 222 candidate genes. *Diabetes* 57:3136-3144. PMCID: PMC2570412.

168. Chen W-M, Erdos MR, Jackson AU, Saxena R, Sanna S, Silver KD, Timpson NJ, Hansen T, Orrù M, Piras M, Bonnycastle LL, Willer CJ, Lyssenko V, Shen H, Kuusisto J, Ebrahim S, Sestu N, Duren WL, Spada MC, Stringham HM, Scott LJ, Olla N, Swift AJ, Najjar S, Mitchell BD, Lawlor DA, Davey Smith GD, Ben-Shlomo Y, Andersen G, Borch-Johnsen K, Jørgensen T, Saramies J, Valle TT, Buchanan TA, Shuldiner AR, Lakatta E, Bergman RN, Uda M, Tuomilehto J, Pedersen O, Cao A, Groop L, Mohlke KL, Laakso M, Schlessinger D, Collins FS, Altshuler D, Abecasis GR, **Boehnke M**, Scuteri A, and Watanabe RM (2008) Variations in the *G6PC2/ABCB11* genomic region are associated with fasting glucose levels. *Journal of Clinical Investigation* 118:2620-2628. PMCID: PMC2398737.

169. Mohlke KL, **Boehnke M**, and Abecasis GR (2008) Metabolic and cardiovascular traits: an abundance of recently identified common genetic variants. *Human Molecular Genetics* 17:R102-R108. PMCID: PMC2570060.

170. Keating BJ, Tischfield S, Murray SS, Bhangale T, Price TS, Glessner JT, Galver L, Barrett JC, Grant SF, Farlow DN, Chandrupatla HR, Hansen M, Ajmal S, Papanicolaou GJ, Guo Y, Li M, Derohannessian S, de Bakker PI, Bailey SD, Montpetit A, Edmondson AC, Taylor K, Gai X, Wang SS, Fornage M, Shaikh T, Groop L, **Boehnke M**, Hall AS, Hattersley AT, Frackelton E, Patterson N, Chiang CW, Kim CE, Fabsitz RR, Ouwehand W, Price AL, Munroe P, Caulfield M, Drake T, Boerwinkle E, Reich D, Whitehead AS, Cappola TP, Samani NJ, Lusis AJ, Schadt E, Wilson JG, Koenig W, McCarthy MI, Kathiresan S, Gabriel SB, Hakonarson H, Anand SS, Reilly M, Engert JC, Nickerson DA, Rader DJ, Hirschhorn JN, and Fitzgerald GA (2008) Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE* 3:e3583. PMCID: PMC2571995.

171. Huth C, Illig T, Herder C, Gieger C, Grallert H, Vollmert C, Rathmann W, Hamid YH, Pedersen O, Hansen T, Thorand B, Meisinger C, Döring A, Klopp N, Gohlke H, Lieb W, Hengstenberg C, Lyssenko V, Groop L, Ireland H, Stephens JW, Wernstedt AI, Jansson JO, Boeing H, Möhlig M, Stringham HM, **Boehnke M**, Tuomilehto J, Fernandez-Real JM, Lopez-Bermejo A, Gallart L, Vendrell J, Humphries SE, Kronenberg F, Wichmann HE, and Heid IM (2009) Joint analysis of individual participants' data from 17 studies on the association of the IL6 variant -174G>C with circulating glucose levels, interleukin-6 levels, and body-mass index. *Annals of Medicine* 41:128-138. PMCID: PMC3801210.

172. Kathiresan S, Willer CJ, Peloso GM, Demissie S, Musunuru K, Schadt E, Kaplan L, Bennett D, Li Y, Tanaka T, Voight BF, Bonnycastle LL, Jackson AU, Crawford G, Surti A, Guiducci C, Burtt NP, Parish S, Clarke R, Zelenika D, Kubalanza KA, Morken MA, Scott LJ, Stringham HM, Galan P, Swift AJ, Kuusisto J, Bergman RN, Sundvall J, Laakso M, Ferrucci L, Scheet P, Sanna S, Uda M, Yang Q, Lunetta KL , Dupuis J, deBakker PI, O'Donnell CJ, Chambers JC, Kooner JS, Hercberg S, Meneton P, Lakatta EG, Scuteri A, Schlessinger D, Tuomilehto J, Collins FS, Groop L, Altshuler D, Collins R, Lathrop GM, Melander O, Salomaa V, Peltonen L, Orho-Melander M, Ordovas M, **Boehnke M**, Abecasis GR, Mohlke KL, and Cupples LA (2009) Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics* 41:56-65. PMCID: PMC2881676.

173. Willer CJ, Speliotes EK, Loos RJ, Li S, Lindgren CM, Heid IM, Berndt SI, Elliott AL, Jackson AU, Lamina C, Lettre G, Lim N, Lyon HN, McCarroll SA, Papadakis K, Qi L, Randall JC, Roccasecca RM, Sanna S, Scheet P, Weedon MN, Wheeler E, Zhao JH, Jacobs LC, Prokopenko I, Soranzo N, Tanaka T, Timpson NJ, Almgren P, Bennett A, Bergman RN, Bingham SA, Bonnycastle LL, Brown M, Burtt NP, Chines P, Coin L, Collins FS, Connell JM, Cooper C, Davey-Smith G, Dennison EM, Deodhar P, Elliott P, Erdos MR, Estrada K, Evans DM, Gianniny L, Gieger C, Gillson CJ, Guiducci C, Hackett R, Hadley D, Hall AS, Havulinna AS, Hebebrand J, Hofman A, Isomaa B, Jacobs KB, Johnson T, Jousilahti P, Jovanovic Z, Khaw KT, Kraft P, Kuokkanen M, Kuusisto J, Laitinen J, Lakatta EG, Luan J, Luben RN, Mangino M, McArdle WL, Meitinger T, Mulas A, Munroe PB, Narisu N, Ness AR, Northstone K, O'Rahilly S,

Purmann C, Rees MG, Ridderstråle M, Ring SM, Rivadeneira F, Ruokonen A, Sandhu MS, Saramies J, Scott LJ, Scuteri A, Silander K, Sims MA, Song K, Stephens J, Stevens S, Stringham HM, Tung YC, Valle TT, Van Duijn CM, Vimaleswaran KS, Vollenweider P, Waeber G, Wallace C, Watanabe RM, Waterworth DM, Watkins N, The Wellcome Trust Case Control Consortium, Witteman JCM, Zeggini E, Zhai G, Zillikens MC, Altshuler D, Caulfield MJ, Chanock SJ, Farooqi IS, Ferrucci L, Guralnik JM, Hattersley AT, Hu FB, Jarvelin MR, Laakso M, Mooser V, Ong KK, Ouwehand WH, Salomaa V, Samani NJ, Spector TD, Tuomi T, Tuomilehto J, Uda M, Uitterlinden AG, Wareham NJ, Deloukas P, Frayling TM, Groop LC, Hayes RB, Hunter DJ, Mohlke KL, Peltonen L, Schlessinger D, Strachan DP, Wichmann HE, McCarthy MI, **Boehnke M**, Barroso I, Abecasis GR, and Hirschhorn JN for the GIANT consortium (2009) Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics* 41:25-34. PMCID: PMC2695662.

174. Lyssenko V, Nagorny CL, Erdos MR, Wierup N, Jonsson A, Spégel P, Bugliani M, Saxena R, Fex M, Pulizzi N, Isomaa B, Tuomi T, Nilsson P, Kuusisto J, Tuomilehto J, **Boehnke M**, Altshuler D, Sundler F, Eriksson JG, Jackson AU, Laakso M, Marchetti P, Watanabe RM, Mulder H, and Groop L (2009) Common variant in MTNR1B is associated with increased risk of future type 2 diabetes and impaired early insulin secretion. *Nature Genetics* 41:82-88. PMCID: PMC3725650.

175. Prokopenko I, Langenberg C, Florez JC, Saxena R, Soranzo N, Thorleifsson G, Loos RJ, Manning AK, Jackson AU, Aulchenko Y, Potter SC, Erdos MR, Sanna S, Hottenga JJ, Wheeler E, Kaakinen M, Lyssenko V, Chen W-M, Ahmadi K, Beckmann JS, Bergman RN, Bochud M, Bonnycastle LL, Buchanan TA, Cao A, Cervino A, Coin L, Collins FS, Crisponi L, de Geus EJ, Dehghan A, Deloukas P, Doney ASF, Elliott P, Freimer N, Gateva V, Herder C, Hofman A, Hughes TE, Hunt S, Illig T, Inouye M, Isomaa B, Johnson T, Kong A, Krestyaninova M, Kuusisto J, Laakso M, Lim N, Lindblad U, Lindgren CM, McCann OT, Mohlke KL, Morris AD, Naitza S, Orrù M, Palmer CNA, Pouta A, Randall J, Rathmann W, Saramies J, Scheet P, Scott LJ, Scuteri A, Sharp S, Sijbrands E, Smit JH, Song K, Steinthorsdottir V, Stringham HM, Tuomi T, Tuomilehto J, Uitterlinden AG, Voight BF, Waterworth D, Wichmann H-E, Willemsen G, Witteman JCM, Yuan X, Zhao JH, Zeggini E, Schlessinger D, Sandhu M, Boomsma DI, Uda M, Spector TD, Penninx BWJH, Altshuler D, Vollenweider P, Jarvelin MR, Lakatta E, Waeber G, Fox CS, Peltonen L, Groop LC, Mooser V, Cupples LA, Thorsteinsdottir U, **Boehnke M**, Barroso I, Van Duijn C, Dupuis J, Watanabe RM, Stefansson K, McCarthy MI, Wareham NJ, Meigs JB, and Abecasis GR (2009) Variants in MTNR1B influence fasting glucose levels. *Nature Genetics* 41:77-81. PMCID: PMC2682768.

176. Xiao R and **Boehnke M** (2009) Quantifying and correcting for the winner's curse in genetic association studies. *Genetic Epidemiology* 33:453-462. PMCID: PMC2706290.

177. Guan W, Liang L, **Boehnke M**, and Abecasis GR (2009) Genotype-based matching to correct for population stratification in large-scale case-control genetic association studies. *Genetic Epidemiology* 33:508-517. PMCID: PMC2732762.

178. Tsoi LC, **Boehnke M**, Klein RL, and Zheng WJ (2009) Evaluation of genome-wide association study results through development of ontology fingerprints. *Bioinformatics* 25:1314-1320. PMCID: PMC2732313.

179. Salanti G, Southam L, Altshuler D, Ardlie K, Barroso I, **Boehnke M**, Cornelis MC, Frayling TM, Grallert H, Grarup N, Groop L, Hansen T, Hattersley AT, Hu FB, Hveem K, Illig T, Kuusisto J, Laakso M, Langenberg C, Lyssenko V, McCarthy MI, Morris A, Morris AD, Palmer CN, Payne F, Platou CG, Scott LJ, Voight BF, Wareham NJ, Zeggini E, and Ioannidis JP (2009) Underlying genetic models of inheritance in established type 2 diabetes associations. *American Journal of Epidemiology* 170:537-545. PMCID: PMC2732984.

180. Lindgren CM, Heid IM, Randall JC, Lamina C, Steinthorsdottir V, Qi L, Speliotes EK, Thorleifsson G, Willer CJ, Herrera BM, Jackson AU, Lim N, Scheet P, Soranzo N, Amin N, Aulchenko YS, Chambers JC, Drong A, Luan J, Lyon HN, Rivadeneira F, Sanna S, Timpson NJ, Zillikens MC, Zhao JH, Almgren P, Bandinelli S, Bennett AJ, Bergman RN, Bonnycastle LL, Bumpstead SJ, Chanock SJ, Cherkas L, Chines P, Coin L, Cooper C, Crawford G, Doering A, Dominiczak A, Doney AS, Ebrahim S, Elliott P, Erdos MR, Estrada K, Ferrucci L, Fischer G, Forouhi NG, Gieger C, Grallert H, Groves CJ, Grundy S, Guiducci C, Hadley D, Hamsten A, Havulinna AS, Hofman A, Holle R, Holloway JW, Illig T, Isomaa B, Jacobs LC, Jameson K, Jousilahti P, Karpe F, Kuusisto J, Laitinen J, Lathrop GM, Lawlor DA, Mangino M, McArdle WL, Meitinger T, Morken MA, Morris AP, Munroe P, Narisu N, Nordström A, Nordström P, Oostra BA, Palmer CN, Payne F, Peden JF, Prokopenko I, Renström F, Ruokonen A, Salomaa V, Sandhu MS, Scott LJ, Scuteri A, Silander K, Song K, Yuan X, Stringham HM, Swift AJ, Tuomi T, Uda M, Vollenweider P, Waeber G, Wallace C, Walters GB, Weedon MN; Wellcome Trust Case Control Consortium, Witteman JC, Zhang C, Zhang W, Caulfield MJ, Collins FS, Davey Smith G, Day IN, Franks PW, Hattersley AT, Hu FB, Jarvelin MR, Kong A, Kooner JS, Laakso M, Lakatta E, Mooser V, Morris AD, Peltonen L, Samani NJ, Spector TD, Strachan DP, Tanaka T, Tuomilehto J, Uitterlinden AG, van Duijn CM, Wareham NJ, Hugh Watkins; Procardis Consortia, Waterworth DM, **Boehnke M**, Deloukas P, Groop L, Hunter DJ, Thorsteinsdottir U, Schlessinger D, Wichmann HE, Frayling TM, Abecasis GR, Hirschhorn JN, Loos RJ, Stefansson K, Mohlke KL, Barroso I, McCarthy MI, and the Giant Consortium (2009) Genome wide association scan meta-analysis identifies three loci influencing adiposity and fat distribution. *PLoS Genetics* 5:e1000508. PMCID: PMC2695778.

181. Scott LJ, Muglia P, Kong XQ, Guan W, Flickinger M, Upmanyu R, Tozzi F, Li JZ, Burmeister M, Absher D, Thompson RC, Francks C, Meng F, Antoniades A, Southwick AM, Schatzberg AF, Bunney WE, Barchas JD, Jones EG, Day R, Matthews K, McGuffin P, Strauss JS, Kennedy JL, Middleton L, Roses AD, Watson SJ, Vincent JB, Myers RM, Farmer AE, Akil H, Burns DK, and **Boehnke M** (2009) Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry. *Proceedings of the National Academy of Sciences USA* 106:7501-7506. PMCID: PMC2678639.

182. Prokunina-Olsson L, Welch C, Hansson O, Adhikari N, Scott LJ, Usher N, Tong M, Sprau A, Swift A, Bonnycastle LL, Erdos MR, He Z, Saxena R, Harmon B, Kotova O, Hoffman EP, Altshuler D, Groop L, **Boehnke M**, Collins FS, and Hall JL (2009) Tissue-

specific alternative splicing of *TCF7L2*. *Human Molecular Genetics* 18:3795-3804. PMCID: PMC2748888.

183. Stancáková A, Kuulasmaa T, Paananen J, Jackson AU, Bonnycastle LL, Collins FS, **Boehnke M**, Kuusisto J, and Laakso M (2009) Association of 18 confirmed susceptibility loci for type 2 diabetes with indices of insulin release, proinsulin conversion, and insulin sensitivity in 5,327 nondiabetic Finnish men. *Diabetes* 58:2129-2136. PMCID: PMC2731523.

184. Newton-Cheh C, Johnson T, Gateva V, Tobin MD, Bochud M, Coin L, Najjar SS, Zhao JH, Heath SC, Eyheramendy S, Papadakis K, Voight BF, Scott LJ, Zhang F, Farrall M, Tanaka T, Wallace C, Chambers JC, Khaw K-T, Nilsson P, van der Harst P, Polidoro S, Grobbee DE, Onland-Moret NC, Bots ML, Wain LV, Elliott KS, Teumer A, Luan J, Lucas G, Kuusisto J, Burton PR, Hadley D, McArdle WL, Wellcome Trust Case Control Consortium, Brown M, Dominiczak A, Newhouse SJ, Samani NJ, Webster J, Zeggini E, Beckmann JS, Bergmann S, Lim N, Song K, Vollenweider P, Waeber G, Waterworth DM, Yuan X, Groop L, Orho-Melander M, Allione A, Di Gregorio A, Guarrera S, Panico S, Ricceri F, Romanazzi V, Sacerdote C, Vineis P, Barroso I, Sandhu MS, Luben RN, Crawford GJ, Jousilahti P, Perola M, **Boehnke M**, Bonnycastle LL, Collins FS, Jackson AU, Mohlke KL, Stringham HM, Valle TT, Willer CJ, Bergman RN, Morken MA, Dring A, Gieger C, Illig T, Meitinger T, Org E, Pfeufer A, Wichmann HE, Kathiresan S, Marrugat J, O'Donnell CJ, Schwartz SM, Siscovick DS, Subirana I, Freimer NB, Hartikainen A-L, McCarthy MI, Oreilly PF, Peltonen L, Pouta A, de Jong PE, Snieder H, van Gilst WH, Clarke R, Goel A, Hamsten A, Peden JF, Seedorf U, Syvnen A-C, Tognoni G, Lakatta EG, Sanna S, Scheet P, Schlessinger D, Scuteri A, Dörr M, Ernst F, Felix SB, Homuth G, Lorbeer R, Reffelmann T, Rettig R, Vlker U, Galan P, Gut IG, Hercberg S, Lathrop GM, Zeleneka D, Deloukas P, Soranzo N, Williams FM, Zhai G, Salomaa V, Laakso M, Elosua R, Forouh NG, Vlzke H, Uiterwaa CS, van der Schouw YT, Numans ME, Matullo G, Navis G, Berglund G, Bingham SA, Kooner JS, Paterson AD, Connell JM, Bandinelli S, Ferrucci L, Watkins H, Spector TD, Tuomilehto J, Altshuler D, Strachan DP, Laan M, Meneton P, Wareham NJ, Uda M, Jarvelin M-R, Mooser V, Melander O, Loos RJF, Elliott P, Abecasis GR, Caulfield M, and Munroe PB (2009) Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics* 41:666-676. PMCID: PMC2891673.

185. Epstein MP, Hunter JE, Allen EG, Sherman SL, Lin X, and **Boehnke M** (2009) A variance-component framework for pedigree analysis of continuous and categorical outcomes. *Statistics in the Biosciences* 1:181-198. PMCID: PMC2860148.

186. Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorff LA, Hunter DJ, McCarthy MI, Ramos EM, Cardon LR, Chakravarti A, Cho JH, Guttmacher AE, Kong A, Kruglyak L, Mardis E, Rotimi CN, Slatkin M, Valle D, Whittemore AS, **Boehnke M**, Clark AG, Eichler EE, Gibson G, Haines JL, Mackay TF, McCarroll SA, and Visscher PM (2009) Finding the missing heritability of complex diseases. *Nature* 461:747-753. PMCID: PMC2831613.

187. Perry JR, Weedon MN, Langenberg C, Jackson AU, Lyssenko V, Sparsø T, Thorleifsson G, Grallert H, Ferrucci L, Maggio M, Paolisso G, Walker M, Palmer CN, Payne F,

Young E, Herder C, Narisu N, Morken MA, Bonnycastle LL, Owen KR, Shields B, Knight B, Bennett A, Groves CJ, Ruokonen A, Jarvelin MR, Pearson E, Pascoe L, Ferrannini E, Bornstein SR, Stringham HM, Scott LJ, Kuusisto J, Nilsson P, Neptin M, Gjesing AP, Pisinger C, Lauritzen T, Sandbaek A, Sampson M; MAGIC, Zeggini E, Lindgren CM, Steinthorsdottir V, Thorsteinsdottir U, Hansen T, Schwarz P, Illig T, Laakso M, Stefansson K, Morris AD, Groop L, Pedersen O, **Boehnke M**, Barroso I, Wareham NJ, Hattersley AT, McCarthy MI, and Frayling TM (2010) Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. *Human Molecular Genetics* 19:535-544. PMCID: PMC2798726.

188. Dupuis J, Langenberg C, Prokopenko I, Saxena R, Soranzo N, Jackson AU, Wheeler E, Glazer NL, Bouatia-Naji N, Gloyn AL, Lindgren CM, Mägi R, Morris AP, Randall J, Johnson T, Elliott P, Rybin D, Thorleifsson G, Steinthorsdottir V, Henneman P, Grallert H, Dehghan A, Hottenga JJ, Franklin CS, Navarro P, Song K, Goel A, Perry JR, Egan JM, Lajunen T, Grarup N, Sparsø T, Doney A, Voight BF, Stringham HM, Li M, Kanoni S, Shrader P, Cavalcanti-Proença C, Kumari M, Qi L, Timpson NJ, Gieger C, Zabena C, Rocheleau G, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Payne F, Roccasecca RM, Pattou F, Sethupathy P, Ardlie K, Ariyurek Y, Balkau B, Barter P, Beilby JP, Ben-Shlomo Y, Benediktsson R, Bennett AJ, Bergmann S, Bochud M, Boerwinkle E, Bonnefond A, Bonnycastle LL, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Charpentier G, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Cornelis M, Crawford G, Crisponi L, Day IN, de Geus EJ, Delplanque J, Dina C, Erdos MR, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Fox CS, Frants R, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Groves CJ, Grundy S, Gwilliam R, Gyllensten U, Hadjadj S, Hallmans G, Hammond N, Han X, Hartikainen AL, Hassanali N, Hayward C, Heath SC, Hercberg S, Herder C, Hicks AA, Hillman DR, Hingorani AD, Hofman A, Hui J, Hung J, Isomaa B, Johnson PR, Jørgensen T, Jula A, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Lyssenko V, Mahley R, Mangino M, Manning AK, Martínez-Larrad MT, McAteer JB, McCulloch LJ, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Morken MA, Mukherjee S, Naitza S, Narisu N, Neville MJ, Oostra BA, Orrù M, Pakyz R, Palmer CN, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Perola M, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Psaty BM, Rathmann W, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Roden M, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Scott LJ, Seedorf U, Sharp SJ, Shields B, Sigurðsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tanaka T, Thorand B, Tichet J, Tönjes A, Tuomi T, Uitterlinden AG, van Dijk KW, van Hoek M, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Walters GB, Ward KL, Watkins H, Weedon MN, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zeggini E, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global BPgen Consortium, Borecki IB, Loos RJ, Meneton P, Magnusson PK, Nathan DM, Williams GH, Hattersley AT, Silander K, Salomaa V, Smith GD, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Dedoussis GV, Serrano-Ríos M, Morris AD, Lind L, Palmer LJ, Hu FB, Franks PW, Ebrahim S, Marmot M, Kao WH, Pankow JS, Sampson MJ, Kuusisto J, Laakso M, Hansen T, Pedersen O, Pramstaller PP,

Wichmann HE, Illig T, Rudan I, Wright AF, Stumvoll M, Campbell H, Wilson JF; Hamsten A on behalf of Procardis Consortium; the MAGIC investigators, Bergman RN, Buchanan TA, Collins FS, Mohlke KL, Tuomilehto J, Valle TT, Altshuler D, Rotter JI, Siscovick DS, Penninx BW, Boomsma DI, Deloukas P, Spector TD, Frayling TM, Ferrucci L, Kong A, Thorsteinsdottir U, Stefansson K, van Duijn CM, Aulchenko YS, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Waterworth DM, Vollenweider P, Peltonen L, Mooser V, Abecasis GR, Wareham NJ, Sladek R, Froguel P, Watanabe RM, Meigs JB, Groop L, **Boehnke M**, McCarthy M, Florez JC and Barroso I for the MAGIC investigators (2010) New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics* 42:105-116. PMCID: PMC3018764.

189. Saxena R, Hivert MF, Langenberg C, Tanaka T, Pankow JS, Vollenweider P, Lyssenko V, Bouatia-Naji N, Dupuis J, Jackson AU, Kao WH, Li M, Glazer NL, Manning AK, Luan J, Stringham HM, Prokopenko I, Johnson T, Grarup N, Boesgaard TW, Lecoeur C, Shrader P, O'Connell J, Ingelsson E, Couper DJ, Rice K, Song K, Andreasen CH, Dina C, Köttgen A, Le Bacquer O, Pattou F, Taneera J, Steinthorsdottir V, Rybin D, Ardlie K, Sampson M, Qi L, van Hoek M, Weedon MN, Aulchenko YS, Voight BF, Grallert H, Balkau B, Bergman RN, Bielinski SJ, Bonnefond A, Bonnycastle LL, Borch-Johnsen K, Böttcher Y, Brunner E, Buchanan TA, Bumpstead SJ, Cavalcanti-Proença C, Charpentier G, Chen YD, Chines PS, Collins FS, Cornelis M, J Crawford G, Delplanque J, Doney A, Egan JM, Erdos MR, Firmann M, Forouhi NG, Fox CS, Goodarzi MO, Graessler J, Hingorani A, Isomaa B, Jørgensen T, Kivimaki M, Kovacs P, Krohn K, Kumari M, Lauritzen T, Lévy-Marchal C, Mayor V, McAteer JB, Meyre D, Mitchell BD, Mohlke KL, Morken MA, Narisu N, Palmer CN, Pakyz R, Pascoe L, Payne F, Pearson D, Rathmann W, Sandbaek A, Sayer AA, Scott LJ, Sharp SJ, Sijbrands E, Singleton A, Siscovick DS, Smith NL, Sparsø T, Swift AJ, Syddall H, Thorleifsson G, Tönjes A, Tuomi T, Tuomilehto J, Valle TT, Waeber G, Walley A, Waterworth DM, Zeggini E, Zhao JH; GIANT consortium; the MAGIC investigators, Illig T, Wichmann HE, Wilson JF, van Duijn C, Hu FB, Morris AD, Frayling TM, Hattersley AT, Thorsteinsdottir U, Stefansson K, Nilsson P, Syvänen AC, Shuldiner AR, Walker M, Bornstein SR, Schwarz P, Williams GH, Nathan DM, Kuusisto J, Laakso M, Cooper C, Marmot M, Ferrucci L, Mooser V, Stumvoll M, Loos RJ, Altshuler D, Psaty BM, Rotter JI, Boerwinkle E, Hansen T, Pedersen O, Florez JC, McCarthy MI, **Boehnke M**, Barroso I, Sladek R, Froguel P, Meigs JB, Groop L, Wareham NJ, and Watanabe RM (2010) Genetic variation in *GIPR* influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics* 42:142-148. PMCID: PMC2922003.

190. Conneely KN and **Boehnke M** (2010) Meta-analysis of genetic association studies and adjustment for multiple testing of correlated SNPs and traits. *Genetic Epidemiology* 34:739-746. PMCID: PMC3070606.

191. Stitzel ML, Sethupathy P, Pearson DS, Chines PS, Song L, Erdos MR, Welch R, Parker SC, Boyle AP, Scott LJ; NISC Comparative Sequencing Program,Margulies EH, **Boehnke M**, Furey TS, Crawford GE, and Collins FS (2010) Global epigenomic analysis of primary human pancreatic islets provides insights into type 2 diabetes susceptibility loci. *Cell Metabolism* 12:443-455. PMCID: PMC3026436.

192. Ingelsson E, Langenberg C, Hivert M-F, Prokopenko I, Lyssenko V, Dupuis J, Mägi R, Sharp S, Jackson AU, Assimes TL, Shrader P, Knowles JW, Zethelius B, Abbasi FA, Bergman RN, Bergmann A, Berne C, **Boehnke M**, Bonnycastle LL, Bornstein SR, Buchanan TA, Bumpstead SJ, Böttcher Y, Chines P, Collins FS, Cooper CC, Dennison EM, Erdos MR, Ferrannini E, Fox CS, Graessler J, Hao K, Isomaa B, Jameson KA, Kovacs P, Kuusisto J, Laakso M, Ladenvall C, Mohlke KL, Morken MA, Narisu N, Nathan DM, Pascoe L, Payne F, Petrie JR, Sayer AA, Schwarz P, Scott LJ, Stringham HM, Stumvoll M, Swift AJ, Syvänen A-C, Tuomi T, Tuomilehto J, Tönjes A, Valle TT, Williams GH, Lind L, Barroso I, Quertermous T, Walker M, Wareham NJ, Meigs JB, McCarthy MI, Groop L, Watanabe RM, and Florez JC on behalf of the MAGIC investigators (2010) Detailed physiologic characterization reveals diverse mechanisms for novel genetic loci regulating glucose and insulin metabolism in humans. *Diabetes* 59:1266-1275. PMCID: PMC2857908.

193. Boraska V, Jerončić A, Colonna V, Southam L, Nyholt DR, Rayner NW, Perry JR, Toniolo D, Albrecht E, Ang W, Bandinelli S, Barbalic M, Barroso I, Beckmann JS, Biffar R, Boomsma D, Campbell H, Corre T, Erdmann J, Esko T, Fischer K, Franceschini N, Frayling TM, Girotto G, Gonzalez JR, Harris TB, Heath AC, Heid IM, Hoffmann W, Hofman A, Horikoshi M, Zhao JH, Jackson AU, Hottenga JJ, Jula A, Kähönen M, Khaw KT, Kiemeney LA, Klopp N, Kutalik Z, Lagou V, Launer LJ, Lehtimäki T, Lemire M, Lokki ML, Loley C, Luan J, Mangino M, Mateo Leach I, Medland SE, Mihailov E, Montgomery GW, Navis G, Newnham J, Nieminen MS, Palotie A, Panoutsopoulou K, Peters A, Pirastu N, Polasek O, Rehnström K, Ripatti S, Ritchie GR, Rivadeneira F, Robino A, Samani NJ, Shin SY, Sinisalo J, Smit JH, Soranzo N, Stolk L, Swinkels DW, Tanaka T, Teumer A, Tönjes A, Traglia M, Tuomilehto J, Valsesia A, van Gilst WH, van Meurs JB, Smith AV, Viikari J, Vink JM, Waeber G, Warrington NM, Widen E, Willemsen G, Wright AF, Zanke BW, Zgaga L; Wellcome Trust Case Control Consortium, **Boehnke M**, d'Adamo AP, de Geus E, Demerath EW, den Heijer M, Eriksson JG, Ferrucci L, Gieger C, Gudnason V, Hayward C, Hengstenberg C, Hudson TJ, Järvelin MR, Kogevinas M, Loos RJ, Martin NG, Metspalu A, Pennell CE, Penninx BW, Perola M, Raitakari O, Salomaa V, Schreiber S, Schunkert H, Spector TD, Stumvoll M, Uitterlinden AG, Ulivi S, van der Harst P, Vollenweider P, Völzke H, Wareham NJ, Wichmann HE, Wilson JF, Rudan I, Xue Y, and Zeggini E E (2012) Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics* 21:4805-4815. PMCID: PMC3471397.

194. Guan W, **Boehnke M**, Pluzhnikov A, Cox NJ, and Scott JL (2012) Identifying plausible genetic models based on association and linkage results: application to type 2 diabetes. *Genetic Epidemiology* 36:820-828. PMCID: PMC3578091.

195. Voight BF, Scott LJ, Steinthorsdottir V, Morris AP, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Langenberg C, Hofmann OM, Dupuis J, Qi L, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Couper DJ, Crawford G, Doney ASF, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B,

Jackson AU, Johnson PRV, Jørgensen T, Kao WHL, Klopp N, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Perry JRB, Petersen A-K, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, The MAGIC investigators, The GIANT consortium, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter D, Hveem K, Laakso M, Mohlke KL, Morris AD, Palmer CAN, Pramstaller PP, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Wareham NJ, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Hu FB, Meigs JB, Pankow JS, Pedersen O, Wichmann H-E, Barroso I, Florez JC, Frayling TM, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, **Boehnke M**, and McCarthy MI (2010) Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics* 42:579–589. PMCID: PMC3080658.

196. Rosenberg NA, Huang L, Jewett EM, Szpiech ZA, Jankovic I, and **Boehnke M** (2010) Genome-wide association studies in diverse populations. *Nature Review Genetics* 11:356-366. PMCID: PMC3079573.

197. Tobacco and Genetics Consortium (including **Boehnke M**) (2010) Genome-wide meta-analyses identify multiple loci associated with smoking behavior. *Nature Genetics* 42:441-447. PMCID: PMC2914600.

198. Waterworth DM, Ricketts SL, Song K, Chen L, Zhao JH, Ripatti S, Aulchenko YS, Zhang W, Yuan X, Lim N, Luan J, Ashford S, Wheeler E, Hadley D, Thompson JR, Braund PS, Johnson T, Struchalin M, Lindqvist I, Luben R, Khaw K-T, Bingham SA, Loos RJF, Sims M, Inouye M, Deloukas P, Elliott P, Schlessinger D, Sanna S, Mohlke KL, Tuomilehto J, Roberts R, Stewart A, Kesäniemi YA, Mahley RW, Grundy SM, Wellcome Trust Case Control Consortium, McArdle W, Cardon L, Waeber G, Vollenweider P, Chambers JC, **Boehnke M**, Abecasis GR, Barroso I, Epstein SE, Rader DJ, Reilly MP, Witteman JCM, Samani NJ, Strachan DP, Barter P, van Duijn DM, Kooner JS, Peltonen L, Wareham NJ, McPherson R, Mooser V, and Sandhu MS (2010) Genetic variants influencing circulating lipid levels and risk of coronary artery disease. *Arteriosclerosis, Thrombosis and Vascular Biology* 30:2264-2276. PMCID: PMC3891568.

199. Teslovich TM, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Ripatti S, Chasman DI, Willer CJ, Johansen CT, Fouchier SW, Isaacs A, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Aulchenko YS, Thorleifsson G, Feitosa MF, Chambers J, Orho-Melander M, Melander O, Johnson T, Li X, Guo X, Li M, Cho YS, Go MJ, Kim YJ, Lee J-Y, Park T, Kim KJ, Sim X, Ong RT-H, Croteau-Chonka DC, Lange LA, Smith JD, Song K, Zhao JH, Yuan X, Luan J, Lamina C, CARDIoGRAM Consortium, ENGAGE Consortium, Candidate Gene Association Resource (CARe) Lipids Working Group, Ziegler A, Zhang W, Zee RYL, Wright AF, Witteman JCM,

Wilson JF, Willemsen G, Wichmann H-E, Whitfield JB, Waterworth DM, Wareham NJ, Waeber G, Vollenweider P, Voight BF, Vitart V, Uitterlinden AG, Uda M, Tuomilehto J, Thompson JR, Tanaka T, Surakka I, Stringham HM, Spector TD, Soranzo N, Smit JH, Sinisalo J, Silander K, Sijbrands EJG, Scuteri A, Scott J, Schlessinger D, Sanna S, Salomaa V, Saharinen J, Sabatti C, Ruokonen A, Rudan I, Rose LM, Roberts R, Rieder M, Psaty BM, PramstallerPP, Pichler I, Perola M, Penninx BWJH, Pedersen NL, Pattaro C, Parker AN, Pare G, Oostra BA, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, Meitinger T, McPherson R, McCarthy MI, McArdle W, Masson D, Martin NG, Marroni F, Mangino M, Magnusson P, Lucas G, Luben R, Loos RJF, Lokki M, Lettre G, Langenberg C, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, Kronenberg F, König IR, Khaw K-T, Kaprio J, Kaplan LM, Johansson A, Jarvelin M-R, Janssens ACJW, Ingelsson E, Igl W, Hovingh GK, Hottenga J-J, Hofman A, Hicks AA, Hengstenberg C, Heid IM, Hayward C, Havulinna AS, Hastie AD, Harris TB, Haritunians T, Hall AS, Gyllensten U, Guiducci C, Groop LC, Gonzalez E, Gieger C, Freimer NB, Ferrucci L, Erdmann J, Elliott P, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Geus EJC, de Faire U, Crawford G, Collins FS, Chen YI, Caulfield MJ, Campbell H, Burtt NP, Bonnycastle LL, Boomsma DI, Boekholdt SM, Bergman RN, Barroso I, Bandinelli S, Ballantyne CM, Assimes TL, Quertermous T, Altshuler D, Seielstad M, Wong TY, Tai E-S, Feranil AB, Kuzawa CW, Adair LS, Taylor HA, Borecki IB, Gabriel SB, Wilson JG, Stefansson K, Thorsteinsdottir U, Gudnason V, Krauss RM, Mohlke KL, Ordovas JM, Munroe PB, Kooner JC, Tall AR, Hegele RA, Kastelein JJP, Schadt EE, Rotter JI, Boerwinkle E, Strachan DP, Mooser V, Holm H, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, van Duijn CM, Peltonen L, Abecasis GR, **Boehnke M**, and Kathiresan S (2010) Biological, clinical, and population relevance of 95 loci for blood lipids. *Nature* 466:707-713. PMCID: PMC3039276.

200. Pruim RJ, Welch RP, Sanna S, Teslovich TM, Chines PS, Gliedt TP, **Boehnke M**, Abecasis GR, and Willer CJ (2010) LocusZoom: regional visualization of genome-wide association scan results. *Bioinformatics* 26:2336-2337. PMCID: PMC2935401.

201. Lango Allen H, Estrada K, Lettre G, Berndt SI, Weedon MN, Rivadeneira F, Willer CJ, Jackson AU, Vedantam S, Raychaudhuri S, Ferreira T, Wood AR, Weyant RJ, Segrè AV, Speliotes EK, Wheeler E, Soranzo N, Park JH, Yang J, Gudbjartsson D, Heard-Costa NL, Randall JC, Qi L, Vernon Smith A, Mägi R, Pastinen T,Liang L, Heid IM, Luan J, Thorleifsson G, Winkler TW, Goddard ME, Sin Lo K, Palmer C, Workalemahu T, Aulchenko YS, Johansson A, Zillikens MC, Feitosa MF, Esko T, Johnson T, Ketkar S, Kraft P, Mangino M, Prokopenko I, Absher D, Albrecht E, Ernst F, Glazer NL, Hayward C, Hottenga JJ, Jacobs KB, Knowles JW,Kutalik Z, Monda KL, Polasek O, Preuss M, Rayner NW, Robertson NR, Steinthorsdottir V, Tyrer JP, Voight BF, Wiklund F, Xu J, Zhao JH, Nyholt DR, Pellikka N,Perola M, Perry JR, Surakka I, Tammesoo ML, Altmaier EL, Amin N, Aspelund T, Bhangale T, Boucher G, Chasman DI, Chen C, Coin L, Cooper MN, Dixon AL,Gibson Q, Grundberg E, Hao K, Juhani Junttila M, Kaplan LM, Kettunen J, König IR, Kwan T, Lawrence RW, Levinson DF, Lorentzon M, McKnight B, Morris AP,Müller M, Suh Ngwa J, Purcell S, Rafelt S, Salem RM, Salvi E, Sanna S, Shi J, Sovio U, Thompson JR, Turchin MC, Vandenput L, Verlaan DJ, Vitart V, White CC,Ziegler A, Almgren

P, Balmforth AJ, Campbell H, Citterio L, De Grandi A, Dominiczak A, Duan J, Elliott P, Elosua R, Eriksson JG, Freimer NB, Geus EJ, Glorioso N, Haiqing S, Hartikainen AL, Havulinna AS, Hicks AA, Hui J, Igl W, Illig T, Jula A, Kajantie E, Kilpeläinen TO, Koiranen M, Kolcic I, Koskinen S, Kovacs P,Laitinen J, Liu J, Lokki ML, Marusic A, Maschio A, Meitinger T, Mulas A, Paré G, Parker AN, Peden JF, Petersmann A, Pichler I, Pietiläinen KH, Pouta A,Ridderstråle M, Rotter JI, Sambrook JG, Sanders AR, Schmidt CO, Sinisalo J, Smit JH, Stringham HM, Bragi Walters G, Widen E, Wild SH, Willemsen G,Zagato L, Zgaga L, Zitting P, Alavere H, Farrall M, McArdle WL, Nelis M, Peters MJ, Ripatti S, van Meurs JB, Aben KK, Ardlie KG, Beckmann JS, Beilby JP,Bergman RN, Bergmann S, Collins FS, Cusi D, den Heijer M, Eiriksdottir G, Gejman PV, Hall AS, Hamsten A, Huikuri HV, Iribarren C, Kähönen M, Kaprio J,Kathiresan S, Kiemeney L, Kocher T, Launer LJ, Lehtimäki T, Melander O, Mosley TH Jr, Musk AW, Nieminen MS, O'Donnell CJ, Ohlsson C, Oostra B, Palmer LJ, Raitakari O, Ridker PM, Rioux JD, Rissanen A, Rivolta C, Schunkert H, Shuldiner AR, Siscovick DS, Stumvoll M, Tönjes A, Tuomilehto J, van Ommen GJ,Viikari J, Heath AC, Martin NG, Montgomery GW, Province MA, Kayser M, Arnold AM, Atwood LD, Boerwinkle E, Chanock SJ, Deloukas P, Gieger C, Grönberg H,Hall P, Hattersley AT, Hengstenberg C, Hoffman W, Lathrop GM, Salomaa V, Schreiber S, Uda M, Waterworth D, Wright AF, Assimes TL, Barroso I, Hofman A,Mohlke KL, Boomsma DI, Caulfield MJ, Cupples LA, Erdmann J, Fox CS, Gudnason V, Gyllensten U, Harris TB, Hayes RB, Jarvelin MR, Mooser V, Munroe PB,Ouwehand WH, Penninx BW, Pramstaller PP, Quertermous T, Rudan I, Samani NJ, Spector TD, Völzke H, Watkins H, Wilson JF, Groop LC, Haritunians T, Hu FB, Kaplan RC, Metspalu A, North KE, Schlessinger D, Wareham NJ, Hunter DJ, O'Connell JR, Strachan DP, Wichmann HE, Borecki IB, van Duijn CM, Schadt EE, Thorsteinsdottir U, Peltonen L, Uitterlinden AG, Visscher PM, Chatterjee N, Loos RJ, **Boehnke M**, McCarthy MI, Ingelsson E, Lindgren CM, Abecasis GR,Stefansson K, Frayling TM, and Hirschhorn JN (2010) Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature* 467:832-838. PMCID: PMC2955183.

202. Speliotes EK, Willer CJ, Berndt SI, Monda KL, Thorleifsson G, Jackson AU, Lango Allen H, Lindgren CM, Luan J, Mägi R, Randall JC, Vedantam S, Winkler TW, Qi L, Workalemahu T, Heid IM, Steinthorsdottir V, Stringham HM, Weedon MN, Wheeler E, Wood AR, Ferreira T, Weyant RJ, Segrè AV, Estrada K, Liang L, Nemesh J, Park JH, Gustafsson S, Kilpeläinen TO, Yang J, Bouatia-Naji N, Esko T, Feitosa MF, Kutalik Z, Mangino M, Raychaudhuri S, Scherag A, Smith AV, Welch R, Zhao JH, Aben KK, Absher DM, Amin N, Dixon AL, Fisher E, Glazer NL, Goddard ME, Heard-Costa NL, Hoesel V, Hottenga JJ, Johansson A, Johnson T, Ketkar S, Lamina C, Li S, Moffatt MF, Myers RH, Narisu N, Perry JR, Peters MJ, Preuss M, Ripatti S, Rivadeneira F, Sandholt C, Scott LJ, Timpson NJ, Tyrer JP, van Wingerden S, Watanabe RM, White CC, Wiklund F, Barlassina C, Chasman DI, Cooper MN, Jansson JO, Lawrence RW, Pellikka N, Prokopenko I, Shi J, Thiering E, Alavere H, Alibrandi MT, Almgren P, Arnold AM, Aspelund T, Atwood LD, Balkau B, Balmforth AJ, Bennett AJ, Ben-Shlomo Y, Bergman RN, Bergmann S, Biebermann H, Blakemore AI, Boes T, Bonnycastle LL, Bornstein SR, Brown MJ, Buchanan TA, Busonero F, Campbell H, Cappuccio FP, Cavalcanti-Proença C, Chen YD, Chen CM, Chines PS, Clarke R, Coin L, Connell J, Day IN, den Heijer M, Duan J, Ebrahim S, Elliott P, Elosua R, Eiriksdottir G, Erdos MR, Eriksson JG, Facheris

MF, Felix SB, Fischer-Posovszky P, Folsom AR, Friedrich N, Freimer NB, Fu M, Gaget S, Gejman PV, Geus EJ, Gieger C, Gjesing AP, Goel A, Goyette P, Grallert H, Grässler J, Greenawalt DM, Groves CJ, Gudnason V, Guiducci C, Hartikainen AL, Hassanali N, Hall AS, Havulinna AS, Hayward C, Heath AC, Hengstenberg C, Hicks AA, Hinney A, Hofman A, Homuth G, Hui J, Igl W, Iribarren C, Isomaa B, Jacobs KB, Jarick I, Jewell E, John U, Jørgensen T, Jousilahti P, Jula A, Kaakinen M, Kajantie E, Kaplan LM, Kathiresan S, Kettunen J, Kinnunen L, Knowles JW, Kolcic I, König IR, Koskinen S, Kovacs P, Kuusisto J, Kraft P, Kvaløy K, Laitinen J, Lantieri O, Lanzani C, Launer LJ, Lecoeur C, Lehtimäki T, Lettre G, Liu J, Lokki ML, Lorentzon M, Luben RN, Ludwig B; MAGIC, Manunta P, Marek D, Marre M, Martin NG, McArdle WL, McCarthy A, McKnight B, Meitinger T, Melander O, Meyre D, Midthjell K, Montgomery GW, Morken MA, Morris AP, Mulic R, Ngwa JS, Nelis M, Neville MJ, Nyholt DR, O'Donnell CJ, O'Rahilly S, Ong KK, Oostra B, Paré G, Parker AN, Perola M, Pichler I, Pietiläinen KH, Platou CG, Polasek O, Pouta A, Rafelt S, Raitakari O, Rayner NW, Ridderstråle M, Rief W, Ruokonen A, Robertson NR, Rzehak P, Salomaa V, Sanders AR, Sandhu MS, Sanna S, Saramies J, Savolainen MJ, Scherag S, Schipf S, Schreiber S, Schunkert H, Silander K, Sinisalo J, Siscovick DS, Smit JH, Soranzo N, Sovio U, Stephens J, Surakka I, Swift AJ, Tammesoo ML, Tardif JC, Teder-Laving M, Teslovich TM, Thompson JR, Thomson B, Tönjes A, Tuomi T, van Meurs JB, van Ommen GJ, Vatin V, Viikari J, Visvikis-Siest S, Vitart V, Vogel CI, Voight BF, Waite LL, Wallaschofski H, Walters GB, Widen E, Wiegand S, Wild SH, Willemsen G, Witte DR, Witteman JC, Xu J, Zhang Q, Zgaga L, Ziegler A, Zitting P, Beilby JP, Farooqi IS, Hebebrand J, Huikuri HV, James AL, Kähönen M, Levinson DF, Macciardi F, Nieminen MS, Ohlsson C, Palmer LJ, Ridker PM, Stumvoll M, Beckmann JS, Boeing H, Boerwinkle E, Boomsma DI, Caulfield MJ, Chanock SJ, Collins FS, Cupples LA, Smith GD, Erdmann J, Froguel P, Grönberg H, Gyllensten U, Hall P, Hansen T, Harris TB, Hattersley AT, Hayes RB, Heinrich J, Hu FB, Hveem K, Illig T, Jarvelin MR, Kaprio J, Karpe F, Khaw KT, Kiemeney LA, Krude H, Laakso M, Lawlor DA, Metspalu A, Munroe PB, Ouwehand WH, Pedersen O, Penninx BW, Peters A, Pramstaller PP, Quertermous T, Reinehr T, Rissanen A, Rudan I, Samani NJ, Schwarz PE, Shuldiner AR, Spector TD, Tuomilehto J, Uda M, Uitterlinden A, Valle TT, Wabitsch M, Waeber G, Wareham NJ, Watkins H; Procardis Consortium, Wilson JF, Wright AF, Zillikens MC, Chatterjee N, McCarroll SA, Purcell S, Schadt EE, Visscher PM, Assimes TL, Borecki IB, Deloukas P, Fox CS, Groop LC, Haritunians T, Hunter DJ, Kaplan RC, Mohlke KL, O'Connell JR, Peltonen L, Schlessinger D, Strachan DP, van Duijn CM, Wichmann HE, Frayling TM, Thorsteinsdottir U, Abecasis GR, Barroso I, **Boehnke M**, Stefansson K, North KE, McCarthy MI, Hirschhorn JN, Ingelsson E, and Loos RJ (2010) Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics* 42:937-947. PMCID: PMC3014648.

203. Soranzo N, Sanna S, Wheeler E, Gieger C, Radke D, Dupuis J, Bouatia-Naji N, Langenberg C, Prokopenko I, Stolerman E, Sandhu MS, Heeney MM, Devaney JM, Reilly MP, Ricketts SL, Stewart AF, Voight BF, Willenborg C, Wright B, Altshuler D, Arking D, Balkau B, Barnes D, Boerwinkle E, Böhm B, Bonnefond A, Bonnycastle LL, Boomsma DI, Bornstein SR, Böttcher Y, Bumpstead S, Burnett-Miller MS, Campbell H, Cao A, Chambers J, Clark R, Collins FS, Coresh J, de Geus EJ, Dei M, Deloukas P, Döring A, Egan JM, Elosua R, Ferrucci L, Forouhi N, Fox CS, Franklin C, Franzosi MG,

Gallina S, Goel A, Graessler J, Grallert H, Greinacher A, Hadley D, Hall A, Hamsten A, Hayward C, Heath S, Herder C, Homuth G, Hottenga JJ, Hunter-Merrill R, Illig T, Jackson AU, Jula A, Kleber M, Knouff CW, Kong A, Kooner J, Köttgen A, Kovacs P, Krohn K, Kühnel B, Kuusisto J, Laakso M, Lathrop M, Lecoeur C, Li M, Li M, Loos RJ, Luan J, Lyssenko V, Mägi R, Magnusson PK, Mälarstig A, Mangino M, Martínez-Larrad MT, März W, McArdle WL, McPherson R, Meisinger C, Meitinger T, Melander O, Mohlke KL, Mooser VE, Morken MA, Narisu N, Nathan DM, Nauck M, O'Donnell C, Oexle K, Olla N, Pankow JS, Payne F, Peden JF, Pedersen NL, Peltonen L, Perola M, Polasek O, Porcu E, Rader DJ, Rathmann W, Ripatti S, Rocheleau G, Roden M, Rudan I, Salomaa V, Saxena R, Schlessinger D, Schunkert H, Schwarz P, Seedorf U, Selvin E, Serrano-Ríos M, Shrader P, Silveira A, Siscovick D, Song K, Spector TD, Stefansson K, Steinthorsdottir V, Strachan DP, Strawbridge R, Stumvoll M, Surakka I, Swift AJ, Tanaka T, Teumer A, Thorleifsson G, Thorsteinsdottir U, Tönjes A, Usala G, Vitart V, Völzke H, Wallaschofski H, Waterworth DM, Watkins H, Wichmann HE, Wild SH, Willemsen G, Williams GH, Wilson JF, Winkelmann J, Wright AF; WTCCC, Zabena C, Zhao JH, Epstein SE, Erdmann J, Hakonarson HH, Kathiresan S, Khaw KT, Roberts R, Samani NJ, Fleming MD, Sladek R, Abecasis G, **Boehnke M**, Froguel P, Groop L, McCarthy MI, Kao WH, Florez JC, Uda M, Wareham NJ, Barroso I, and Meigs JB (2010) Common variants at 10 genomic loci influence hemoglobin A1(C) levels via glycemic and nonglycemic pathways. *Diabetes* 59:3229-3239. PMCID: PMC2992787.

204. Jafar-Mohammadi B, Groves CJ, Gjesing AP, Herrera BM, Winckler W, Stringham HM, Morris AP, Lauritzen T, Doney AS, Morris AD, Weedon MN, Swift AJ, Kuusisto J, Laakso M, Altshuler D, Hattersley AT, Collins FS, **Boehnke M**, Hansen T, Pedersen O, Palmer CN, Frayling TM; DIAGRAM Consortium, Gloyn AL, and McCarthy MI (2011) A role for coding functional variants in HNF4A in type 2 diabetes susceptibility. *Diabetologia* 54:111-119. PMCID: PMC3119815.

205. Xiao R and **Boehnke M** (2011) Quantifying and correcting for the winner's curse in quantitative-trait association studies. *Genetic Epidemiology* 35:133-138. PMCID: PMC3500533.

206. Sim X, Ong RT-H, Suo C, Tay W-T, Liu J, Ng DPK, **Boehnke M**, Chia K-S, Wong T-Y, Seielstad M, and Teo Y-Y (2011) Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. *PloS Genetics* 7:e1001363. PMCID: PMC3072366.

207. Stancáková A, Paananen J, Soininen P, Kangas AJ, Bonnycastle LL, Morken MA, Collins FS, Jackson AU, **Boehnke M**, Kuusito J, Ala-Korpela M, and Laakso M (2011) Effects of 34 risk loci for type 2 diabetes or hyperglycemia on lipoprotein subclasses and their composition in 6,580 non-diabetic Finnish men. *Diabetes* 60:1608-1616. PMCID: PMC3292337.

208. Strawbridge RJ, Dupuis J, Prokopenko I, Barker A, Ahlqvist E, Rybin D, Petrie JR, Travers ME, Bouatia-Naji N, Dimas AS, Nica A, Wheeler E, Chen H, Voight BF, Taneera J, Kanoni S, Peden JF, Turrini F, Gustafsson S, Zabena C, Almgren P, Barker DJP, Barnes D, Dennison EM, Eriksson JG, Eriksson P, Eury E, Folkersen L, Fox CS, Frayling TM, Goel A, Gu HF, Horikoshi M, Isomaa B, Jackson AU, Jameson KA,

Kajantie E, Kerr-Conte J, Kuulasmaa T, Kuusisto J, Loos RJ, Luan J, Makrilakis K, Manning AK, Martínez-Larrad MT, Narisu N, Mannila MN, Öhrvik J, Osmond C, Pascoe L, Payne F, Sayer AA, Sennblad B, Silveira A, Stančáková A, Stirrups K, Swift AJ, Syvänen A-C, Tuomi T, van't Hooft FM, Walker M, Weedon MN, Xie W, Zethelius B, the DIAGRAM Consortium, the GIANT Consortium, the MuTHER Consortium, the CARDIoGRAM Consortium, the C4D Consortium, Ongen H, Mälarstig A, Hopewell JC, Saleheen D, Chambers J, Parish S, Danesh J, Kooner J, Östenson CG, Lind L, Cooper CC, Serrano-Ríos M, Ferrannini E, Forsen TJ, Clarke R, Franzosi MG, Seedorf U, Watkins H, Froguel P, Johnson P, Deloukas P, Collins FS, Laakso M, Dermitzakis ET, **Boehnke M**, McCarthy MI, Wareham NJ, Groop L, Pattou F, Gloyn AL, Dedoussis GV, Lyssenko V, Meigs JB, Barroso I, Watanabe RM, Ingelsson E, Langenberg C, Hamsten A, and Florez JC (2011) Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes* 60:2624-2634. PMCID: PMC3178302.

209. Wain LV, Verwoert GC, O'Reilly PF, Shi G, Johnson T, Johnson AD, Bochud M, Rice KM, Henneman P, Smith AV, Ehret GB, Amin N, Larson MG, Mooser V, Hadley D, Dörr M, Bis JC, Aspelund T, Esko T, Janssens ACJW, Zhao JH, Heath S, Laan M, Fu J, Pistis G, Luan J, Arora P, Lucas G, Pirastu N, Pichler I, Jackson AU, Webster RJ, Zhang F, Peden JF,Schmidt H, Tanaka T, Campbell H, Igl W, Milaneschi Y, Hottenga J-J, Vitart V, Chasman DI, Trompet S, Bragg-Gresham JL, Alizadeh BZ, Chambers JC, Guo X, Lehtimäki T, Kühnel B, Lopez LM, Polašek O, Boban M, Nelson CP, Morrison AC, Pihur V, Ganesh SK, Hofman A, Kundu S, Mattace-Raso FUS, Rivadeneira F, Sijbrands EJG, Uitterlinden AG, Hwang S-J, Vasan RS, Wang TJ, Bergmann S, Vollenweider P, Waeber G, Laitinen J, Pouta A, Zitting P, McArdle WL, Kroemer HK, Völker U, Völzke H, Glazer NL, Taylor KD, Harris TB, Alavere H, Haller T, Keis A, Tammesoo M-L, Aulchenko Y, Barroso I, Khaw K-T, Galan P, Hercberg S, Lathrop M, Eyheramendy S, Org E, Sõber S, Lu S, Nolte IM, Penninx BW, Corre T, Masciullo C, Sala C, Groop L, Voight BF, Melander O, O'Donnell CJ, Salomaa V, d'Adamo AP, Fabretto A, Faletra F, Ulivi S, Del Greco F, Facheris M, Collins FS, Bergman RN, Beilby JP, Hung J, Musk AW, Mangino M, Shin S-Y, Soranzo N, Watkins H, Goel A, Hamsten A, Gider P, Loitfelder M, Zeginigg M, Hernandez D, Najjar SS, Navarro P, Wild SH, Corsi AM, Singleton A, de Geus EJC, Willemsen G, Parker AN, Rose LM, Buckley B, Stott, D, Orru M, Uda M, LifeLines Cohort Study, van der Klauw MM, Zhang W, Li X, Scott J, Chen Y-DI, Burke GL, Kähönen M, Viikari J, Döring A, Meitinger T, Davies G, Starr JM, Emilsson V, Plump A, Lindeman JH, 't Hoen PAC, König IR, EchoGen Consortium, Felix JF, Clarke R, Hopewell JC, Ongen H, Breteler M, Debette S, DeStefano AL, Fornage M, AortaGen Consortium, Mitchell GF, CHARGE Consortium Heart Failure Working Group, Smith NL, KidneyGen Consortium, Holm H, Stefansson K, Thorleifsson G, Thorsteinsdottir U, CKDGen Consortium, Cardiogenics Consortium, CardioGram, Samani NJ, Preuss M, Rudan I, Hayward C, Deary IJ, Wichmann H-E, Raitakari OT, Palmas W, Kooner JS, Stolk RP, Jukema JW, Wright AF, Boomsma DI, Bandinelli S, Gyllensten UB, Wilson JF, Ferrucci L, Schmidt R, Farrall M, Spector TD, Palmer LJ, Tuomilehto J, Pfeufer A, Gasparini P, Siscovick D, Altshuler D, Loos RJF, Toniolo D, Snieder H, Gieger C, Meneton P, Wareham NJ, Oostra BA, Metspalu A, Launer L, Rettig R, Strachan DP, Beckmann JS, Witteman JCM, Erdmann J, van Dijk KW, Boerwinkle E, **Boehnke M**, Ridker PM, Jarvelin M-R, Chakravarti A, Abecasis

GR, Gudnason V, Newton-Cheh C, Levy D, Munroe PB, Psaty BM, Caulfield MJ, Rao DC, Tobin MD, Elliott P, and van Duijn CM (2011) Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics* 43:1005-1011. PMCID: PMC3445021.

210. International Consortium for Blood Pressure Genome-Wide Association Studies, Ehret GB, Munroe PM, Rice KM, Bochud M, Johnson AD, Chasman DI, Smith AV, Tobin MD, Verwoert GC, Hwang S-J, Pihurl V, Vollenweider P, O'Reilly PF, Amin N, Bragg-Gresham JL, Teumer A, Glazer NL, Launer L, Zhao JH, Aulchenko Y, Heath S, Sõber S, Parsa A, Luan J, Arora P, Dehghan A, Zhang F, Lucas G, Hicks AA, Jackson AU, Peden JF, Tanaka T, Wild SH, Rudan I, Igl W, Milaneschi Y, Parker AN, Fava C, Chambers JC, Fox ER, Kumari M, Go MJ, van der Harst P, Kao WHL, Sjögren M, Vinay DG, Alexander M, Tabara Y, Shaw-Hawkins S, Whincup PH, Liu Y, Shi G, Kuusisto J, Tayo B, Seielstad M, Sim X, Nguyen K-DH, Lehtimäki T, Matullo G, Wu Y, Gaunt TR, Onland-Moret NC, Cooper MN, Platou CGP, Org E, Hardy R, Dahgam S, Palmen J, Vitart V, Braund PS, Kuznetsova T, Uiterwaal CSPM, Adeyemo A, Palmas W, Campbell H, Ludwig B, Tomaszewski M, Tzoulaki I, Palmer ND, CARDIoGRAM Consortium, CKDGen Consortium, KidneyGen Consortium, EchoGen Consortium, CHARGE-HF Consortium, Aspelund T, Garcia M, Chang Y-PC, O'Connell JF, Steinle NI, Grobbee DE, Arking DE, Kardia SL, Morrison AC, Hernandez D, Najjar S, McArdle WL, Hadley D, Brown MJ, Connell JM, Hingorani AD, Day INM, Lawlor DA, Beilby JP, Lawrence RW, Clarke R, Hopewell JC, Ongen H, Dreisbach AW, Li Y, Young JH, Bis JC, Kähönen M, Viikari J, Adair LS, Lee NR, Chen M-H, Olden M, Pattaro, Bolton JAH, Köttgen A, Bergmann S, Mooser V, Chaturvedi N, Frayling TM, Islam M, Jafar TH, Erdmann J, Kulkarni SR, Bornstein SR, Grässler J, Groop L, Voight BF, Kettunen J, Howard P, Taylor A, Guarrera S, Ricceri F, Emilsson V, Plump A, Barroso I, Khaw K-T, Weder AB, Hunt SC, Sun YV, Bergman RN, Collins FS, Bonnycastle LL, Scott LJ, Stringham HM, Peltonen L, Perola M, Vartiainen E, Brand S-M, Staessen JA, Wang TJ, Burton PR, Artigas MS, Dong Y, Snieder H, Wang X, Zhu H, Lohman KK, Rudock ME, Heckbert SR, Smith NL, Wiggins KL, Doumatey A, Shriner D, Veldre G, Viigimaa M, Kinra S, Prabhakaran D, Tripathy V, Langefeld CD, Rosengren A, Thelle DS, Corsi AM, Singleton A, Forrester T, Hilton G, McKenzie CA, Salako T, Iwai N, Kita Y, Ogihara T, Ohkubo T, Okamura T, Ueshima H, Umemura S, Eyheramendy S, Meitinger T, Wichmann H-E, Cho YS, Kim H-L, Lee J-Y, Scott J, Sehmi JS, Zhang W, Hedblad B, Nilsson P, Smith GD, Wong A, Narisu N, Stančáková A, Raffel LJ, Yao J, Kathiresan S, O'Donnell C, Schwartz SM, Ikram MA, Longstreth WT Jr, Mosley TH, Seshadri S, Shrine NRG, Wain LV, Morken MA, Swift AJ, Laitinen J, Prokopenko I, Zitting P, Cooper JA, Humphries SE, Danesh J, Rasheed A, Goel A, Hamsten A, Watkins H, Bakker SJL, van Gilst WH, Janipalli CS, Mani KR, Yajnik CS, Hofman A, Mattace-Raso FUS, Oostra BA, Demirkan A, Isaacs A, Rivadeneira F, Lakatta EG, Orru M, Scuteri A, Ala-Korpela M, Kangas AJ, Lyytikäinen L-P, Soininen P, Tukiainen T, Würtz P, Ong RT-H, Marcus Dö rr M, Kroemer HK, Völker U, Völzke H, Galan P, Hercberg S, Lathrop M, Zelenika D, Deloukas P, Mangino M, Spector TD, Zhai G, Meschia JF, Nalls MA, Sharma P, Terzic J, Kumar MVK, Denniff M, Zukowska-Szczechowska E, Wagenknecht LE, Fowkes FGR, Charchar FJ, Schwarz PEH, Hayward C, Guo X, Rotimi C, Bots ML, Brand E, Samani NJ, Polasek O, Talmud PJ, Nyberg F, Kuh D, Laan M, Hveem K, Palmer LJ, van der Schouw YT, Casas JP, Mohlke KL, Vineis P, Raitakari O,

Ganesh SK, Wong TY, Tai ES, Cooper RS, Laakso M, Rao DC, Harris TB, Morris RW, Dominiczak AF, Kivimaki M, Marmot MG, Miki T, Saleheen D, Chandak GR, Coresh J, Navis G, Salomaa V, Han B-G, Zhu X, Kooner JS, Melander O, Ridker PM, Bandinelli S, Gyllensten Ub, Wright AF, Wilson JF, Ferrucci L, Farrall M, Tuomilehto J, Pramstaller PP, Elosua R, Soranzo N, Sijbrands EJG, Altshuler D, Loos RJF, Shuldiner AR, Gieger C, Meneton P, Uitterlinden AG, Wareham NJ, Gudnason V, Rotter JI, Rettig R, Uda M, Strachan DP, Witteman JCM, Hartikainen A-L, Beckmann JS, Boerwinkle E, Vasan RS, **Boehnke M**, Larson MG, Järvelin M-R, Psaty BM, Abecasis GR, Chakravarti A, Elliott P, van Duijn CM, Newton-Cheh C, Levy D, Caulfield MJ, and Johnson T (2011) Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* 478:103-109. PMCID: PMC3340926.

211. Kilpeläinen TO, Qi L, Brage S, Sharp SJ, Sonestedt E, Demerath E, Ahmad T, Mora S, Kaakinen M, Sandholt CH, Holzapfel C, Autenrieth CS, Hyppönen E, Cauchi S, He M, Kutalik Z, Kumari M, Stančáková A, Meidtner K, Balkau B, Tan JT, Mengino M, Timpson NJ, Song Y, Zillikens MC, Jablonski KA, Garcia ME, Johansson S, Bragg-Gresham JL, Wu Y, van Vliet-Ostaptchouk JV, Onland-Moret NC, Zimmermann E, Rivera NV, Tanaka T, Stringham HM, Silbernagel G, Kanoni S, Feitosa MF, Snitker S, Ruiz JR, Metter J, Larrad MTM, Atalay M, Hakanan M, Amin N, Cavalcanti-Proenca C, Grøntved A, Hallmans G, Jansson J-O, Kuusisto J, Kähönen M, Lutsey PL, Nolan JJ, Palla L, Pederson O, Pérusse L, Renström F, Scott RA, Shungin D, Sovio U, Tammelin TH, Rönnemaa T, Lakka TA, Uusitupa M, Rios MS, Ferrucci L, Bouchard C, Meirlaeghe A, Fu M, Walker M, Borecki IB, Dedoussis GV, Fritsche A, Ohlsson C, **Boehnke M**, Bandinelli S, van Duijn CM, Ebrahim S, Lawlor DA, Gudnason V, Harris TB, Sørensen TIA, Mohlke KL, Hofman A, Uitterlinden AG, Tuomilehto J, Lehtimäki T, Raitakari O, Isomaa B, Njølstad PR, Florez JC, Liu S, Ness A, Spector TD, Tai ES, Froguel P, Boeing H, Laakso M, Marmot M, Bergmann S, Power C, Khaw K-T, Chasman D, Ridker P, Hansen T, Monda KL, Illig T, Järvelin M-R, Wareham NJ, Hu FB, Groop LC, Orho-Melander M, Ekelund U, Franks PW, and Loos RJF (2011) Physical activity attenuates the influence of FTO variants on obesity risk: A meta-analysis of 218,166 adults and 19,268 children. *PloS Medicine* 8:e1001116. PMCID: PMC3206047.

212. Heid IM, Jackson AU, Randall JC, Winkler TW, Qi L, Steinthorsdottir V, Thorleifsson G, Zillikens MC, Speliotes EK, Mägi R, Workalemahu T, White CC, Bouatia-Naji N, Harris TB, Berndt SI, Ingelsson E, Willer CJ, Weedon MN, Luan J, Vedantam S, Esko T, Kilpeläinen TO, Kutalik Z, Li S, Monda KL, Dixon AL, Holmes CC, Kaplan LM, Liang L, Min JL, Moffatt MF, Molony C, Nicholson G, Schadt EE, Zondervan KT, Feitosa MF, Ferreira T, Allen HL, Weyant RJ, Wheeler E, Wood AR, Estrada K, Goddard ME, Lettre G, Mangino M, Nyholt DR, Purcell S, Vernon Smith A, Visscher PM, Yang J, McCarroll SA, Nemesh J, Voight BF, Absher D, Amin N, Aspelund T, Coin L, Glazer NL, Hayward C, Heard-Costa NL, Hottenga JJ, Johansson A, Johnson T, Kaakinen M, Kapur K, Ketkar S, Knowles JW, Kraft P, Kraja AT, Lamina C, Leitzmann MF, McKnight B, Morris AP, Ong KK, Perry JR, Peters MJ, Polasek O, Prokopenko I, Rayner NW, Ripatti S, Rivadeneira F, Robertson NR, Sanna S, Sovio U, Surakka I, Teumer A, van Wingerden S, Vitart V, Zhao JH, Cavalcanti-Proença C, Chines PS, Fisher E, Kulzer JR, Lecoeur C, Narisu N, Sandholt C, Scott LJ, Silander K, Stark K, Tammesoo ML, Teslovich TM, Timpson NJ, Watanabe RM, Welch R, Chasman DI, Cooper MN, Jansson JO, Kettunen

J, Lawrence RW, Pellikka N, Perola M, Vandenput L, Alavere H, Almgren P, Atwood LD, Bennett AJ, Biffar R, Bonnycastle LL, Bornstein SR, Buchanan TA, Campbell H, Day IN, Dei M, Dörr M, Elliott P, Erdos MR, Eriksson JG, Freimer NB, Fu M, Gaget S, Geus EJ, Gjesing AP, Grallert H, Gräßler J, Groves CJ, Guiducci C, Hartikainen AL, Hassanali N, Havulinna AS, Herzig KH, Hicks AA, Hui J, Igl W, Jousilahti P, Jula A, Kajantie E, Kinnunen L, Kolcic I, Koskinen S, Kovacs P, Kroemer HK, Krzelj V, Kuusisto J, Kvaloy K, Laitinen J, Lantieri O, Lathrop GM, Lokki ML, Luben RN, Ludwig B, McArdle WL, McCarthy A, Morken MA, Nelis M, Neville MJ, Paré G, Parker AN, Peden JF, Pichler I, Pietiläinen KH, Platou CG, Pouta A, Ridderstråle M, Samani NJ, Saramies J, Sinisalo J, Smit JH, Strawbridge RJ, Stringham HM, Swift AJ, Teder-Laving M, Thomson B, Usala G, van Meurs JB, van Ommen GJ, Vatin V, Volpato CB, Wallaschofski H, Walters GB, Widen E, Wild SH, Willemsen G, Witte DR, Zgaga L, Zitting P, Beilby JP, James AL, Kähönen M, Lehtimäki T, Nieminen MS, Ohlsson C, Palmer LJ, Raitakari O, Ridker PM, Stumvoll M, Tönjes A, Viikari J, Balkau B, Ben-Shlomo Y, Bergman RN, Boeing H, Smith GD, Ebrahim S, Froguel P, Hansen T, Hengstenberg C, Hveem K, Isomaa B, Jørgensen T, Karpe F, Khaw KT, Laakso M, Lawlor DA, Marre M, Meitinger T, Metspalu A, Midthjell K, Pedersen O, Salomaa V, Schwarz PE, Tuomi T, Tuomilehto J, Valle TT, Wareham NJ, Arnold AM, Beckmann JS, Bergmann S, Boerwinkle E, Boomsma DI, Caulfield MJ, Collins FS, Eiriksdottir G, Gudnason V, Gyllensten U, Hamsten A, Hattersley AT, Hofman A, Hu FB, Illig T, Iribarren C, Jarvelin MR, Kao WH, Kaprio J, Launer LJ, Munroe PB, Oostra B, Penninx BW, Pramstaller PP, Psaty BM, Quertermous T, Rissanen A, Rudan I, Shuldiner AR, Soranzo N, Spector TD, Syvanen AC, Uda M, Uitterlinden A, Völzke H, Vollenweider P, Wilson JF, Witteman JC, Wright AF, Abecasis GR, **Boehnke M**, Borecki IB, Deloukas P, Frayling TM, Groop LC, Haritunians T, Hunter DJ, Kaplan RC, North KE, O'Connell JR, Peltonen L, Schlessinger D, Strachan DP, Hirschhorn JN, Assimes TL, Wichmann HE, Thorsteinsdottir U, van Duijn CM, Stefansson K, Cupples LA, Loos RJ, Barroso I, McCarthy MI, Fox CS, Mohlke KL, and Lindgren CM (2011) Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics* 42:949-960. PMCID: PMC3000924.

213. Sklar P, Ripke S, Scott LJ, Andreassen OA, Cichon S, Craddock N, Edenberg HJ, Nurnberger JI Jr, Rietschel M, Blackwood D, Corvin A, Flickinger M, Guan W, Mattingsdal M, McQuillin A, Kwan P, Wienker TF, Daly M, Dudbridge F, Holmans PA, Lin D, Burmeister M, Greenwood TA, Hamshere ML, Muglia P, Smith EN, Zandi PP, Nievergelt CM, McKinney R, Shilling PD, Schork NJ, Bloss CS, Foroud T, Koller DL, Gershon ES, Liu C, Badner JA, Scheftner WA, Lawson WB, Nwulia EA, Hipolito M, Coryell W, Rice J, Byerley W, McMahon FJ, Schulze TG, Berrettini W, Lohoff FW, Potash JB, Mahon PB, McInnis MG, Zöllner S, Zhang P, Craig DW, Szelinger S, Barrett TB, Breuer R, Meier S, Strohmaier J, Witt SH, Tozzi F, Farmer A, McGuffin P, Strauss J, Xu W, Kennedy JL, Vincent JB, Matthews K, Day R, Ferreira MA, O'Dushlaine C, Perlis R, Raychaudhuri S, Ruderfer D, Hyoun PL, Smoller JW, Li J, Absher D, Thompson RC, Meng FG, Schatzberg AF, Bunney WE, Barchas JD, Jones EG, Watson SJ, Myers RM, Akil H, **Boehnke M**, Chambert K, Moran J, Scolnick E, Djurovic S, Melle I, Morken G, Gill M, Morris D, Quinn E, Mühleisen TW, Degenhardt FA, Mattheisen M, Schumacher J, Maier W, Steffens M, Propping P, Nöthen MM, Anjorin A, Bass N, Gurling H, Kandaswamy R, Lawrence J, McGhee K, McIntosh A, McLean AW,

Muir WJ, Pickard BS, Breen G, St Clair D, Caesar S, Gordon-Smith K, Jones L, Fraser C, Green EK, Grozeva D, Jones IR, Kirov G, Moskvina V, Nikolov I, O'Donovan MC, Owen MJ, Collier DA, Elkin A, Williamson R, Young AH, Ferrier IN, Stefansson K, Stefansson H, Thornorgeirsson T, Steinberg S, Gustafsson O, Bergen SE, 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, Sigur Sson E, Müller-Mysok B, Lucae S, Schwarz M, Schofield PR, Martin N, Montgomery GW, Lathrop M, Oskarsson H, Bauer M, Wright A, Mitchell PB, Hautzinger M, Reif A, Kelsoe JR, Purcell SM; and Psychiatric GWAS Consortium Bipolar Disorder Working Group (2011) Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. *Nature Genetics* 43:977-983. PMCID: PMC3637176.

214. Wu MC, Lee S, Cai T, Li Y, **Boehnke M**, and Lin X (2011) Rare-variant association testing for sequencing data with the sequence kernel association test. *American Journal of Human Genetics* 89:82-93. PMCID: PMC3135811.

215. Sanna S, Li B, Mulas A, Sidore C, Kang HM, Jackson AU, Piras MG, Usala G, Maninchedda G, Sassu A, Serra F, Palmas MA, Wood WH, Njøstad I, Laakso M, Hveem K, Tuomilehto J, Lakka TA, Rauramaa R, **Boehnke M**, Cucca F, Uda M, Schlessinger D, Nagaraja R, and Abecasis GR (2011) Fine mapping of five loci associated with low-density lipoprotein cholesterol detects variants that double the explained heritability. *PloS Genetics* 7:e1002198. PMCID: PMC3145627.

216. Chan Y, Holmen OL, Dauber A, Vatten L, Havulinna AS, Skorpen F, Kvaløy K, Silander K, Nguyen TT, Willer C, **Boehnke M**, Perola M, Palotie A, Salomaa V, Hveem K, Frayling TM, Hirschhorn JN, and Weedon MN (2011) Common variants show predicted polygenic effects on height in the tails of the distribution, except in extremely short individuals. *PloS Genetics* 7:e1002439. PMCID: PMC3248463.

217. Li Y, Sidore C, Kang HM, **Boehnke M**, and Abecasis GR (2011) Low-coverage sequencing: implications for design of complex trait association studies. *Genome Research* 21:940-951. PMCID: PMC3106327.

218. Reppell M, **Boehnke M**, and Zöllner S (2012) FTEC: a coalescent simulator for modeling faster than exponential growth. *Bioinformatics* 28:1282-1283. PMCID: PMC3338023.

219. Stefanovski D, Youn JH, Rees M, Watanabe RM, Ader M, Ionut V, Jackson AU, **Boehnke M**, Collins FS, and Bergman RN (2012) Estimating hepatic glucokinase activity using a simple model of lactate kinetics. *Diabetes Care* 35:1015-1020. PMCID: PMC3329822.

220. Scott RA, Chu AY, Grarup G, Manning AK, Hivert M-F, Shungin D, Tönjes A, Yesupriya A, Barnes D, Bouatia-Naji N, Glazer NL, Jackson AU, Kutalik Z, Lagou V, Marek D, Rasmussen-Torvik LJ, Stringham HM, Tanaka T, Aadahl M, Arking DE, Bergmann S, Boerwinkle E, Bonnycastle LL, Bornstein SR, Brunner E, Bumpstead SJ, Brage S, Carlson OD, Chen H, Chines PS, Collins FS, Couper DJ, Dennison EM, Dowling NF, Egan JS, Ekelund U, Erdos MR, Forouhi NF, Fox CS, Goodarzi MO,

Grässler J, Gustafsson S, Hallmans G, Hansen T, Hingorani A, Holloway JW, Hu FB, Isomaa B, Jameson KA, Johansson I, Jonsson A, Jørgensen T, Kivimaki M, Kovacs P, Kumari M, Kuusisto J, Laakso M, Lecoeur C, Lévy-Marchal C, Li G, Loos RJF, Lyssenko V, Marmot M, Marques-Vidal P, Morken MA, Müller G, North KE, Pankow JS, Payne F, Prokopenko I, Psaty BM, Renström F, Rice K, Rotter JI, Rybin D, Sandholt CH, Sayer AA, Shrader P, Schwarz PEH, Siscovick DS, Stančáková A, Stumvoll M, Teslovich TM, Waeber G, Williams GH, Witte DR, Wood AR, Xie W, **Boehnke M**, Cooper C, Ferrucci L, Froguel P, Groop L, Kao WHL, Vollenweider P, Walker M, Watanabe RM,l Pedersen O, Meigs JB, Ingelsson E, Barroso I, Florez JC, Franks PW, Dupuis J, Wareham NJ, and Langenberg C (2012) No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes* 61:1291-1296. PMCID: PMC3331745.

221. Conneely KN, Capell BC, Erdos MR, Sebastiani P, Solovieff N, Swift AJ, Baldwin CT, Budagov T, Barzalai N, Atzmon G, Puca AA, Perls TT, Geesaman BJ, **Boehnke M**, and Collins FS (2012) Human longevity and common variations in the LMNA gene: a meta-analysis. *Aging Cell* 11:475-481. PMCID: PMC3350595.

222. Stancáková A, Civelek M, Saleem NK, Soininen P, Kangas AJ, Cederberg H, Paananen J, Pihlajamäki J, Bonnycastle LL, Morken MA, **Boehnke M**, Pajukanta P, Lusis AJ, Collins FS, Kuusisto J, Ala-Korpela M, and Laakso M (2012) Hyperglycemia and a common variant of GCKR are associated with the levels of eight amino acids in 9,369 Finnish men. *Diabetes* 6:1895-1902. PMCID: PMC3379649.

223. Saxena R, Elbers CC, Guo Y, Peter I, Gaunt TR, Mega JL, Lanktree MB, Tare A, Castillo BA, Li YR, Johnson T, Bruinenberg M, Gilbert-Diamond D, Rajagopalan R, Voight BF, Balasubramanyam A, Barnard J, Bauer F, Baumert J, Bhangale T, Böhm BO, Braund PS, Burton PR, Chandrupatla HR, Clarke R, Cooper-DeHoff RM, Crook ED, Davey-Smith G, Day IN, de Boer A, de Groot MC, Drenos F, Ferguson J, Fox CS, Furlong CE, Gibson Q, Gieger C, Gilhuijs-Pederson LA,Glessner JT, Goel A, Gong Y, Grant SF, Grobbee DE, Hastie C, Humphries SE, Kim CE, Kivimaki M, Kleber M, Meisinger C, Kumari M, Langaee TY, Lawlor DA,Li M, Lobmeyer MT, Maitland-van der Zee AH, Meijs MF, Molony CM, Morrow DA, Murugesan G, Musani SK, Nelson CP, Newhouse SJ, O'Connell JR,Padmanabhan S, Palmen J, Patel SR, Pepine CJ, Pettinger M, Price TS, Rafelt S, Ranchalis J, Rasheed A, Rosenthal E, Ruczinski I, Shah S, Shen H,Silbernagel G, Smith EN, Spijkerman AW, Stanton A, Steffes MW, Thorand B, Trip M, van der Harst P, van der A DL, van Iperen EP, van Setten J, van Vliet-Ostaptchouk JV, Verweij N, Wolffenbuttel BH, Young T, Zafarmand MH, Zmuda JM; Look AHEAD Research Group; DIAGRAM consortium, **Boehnke M**, Altshuler D, McCarthy M, Kao WH, Pankow JS, Cappola TP, Sever P, Poulter N, Caulfield M, Dominiczak A, Shields DC, Bhatt DL, Zhang L, Curtis SP, Danesh J, Casas JP, van der Schouw YT, Onland-Moret NC, Doevendans PA, Dorn GW 2nd, Farrall M, FitzGerald GA, Hamsten A, Hegele R, Hingorani AD, Hofker MH, Huggins GS, Illig T, Jarvik GP, Johnson JA, Klungel OH, Knowler WC, Koenig W, März W, Meigs JB, Melander O, Munroe PB, Mitchell BD, Bielinski SJ, Rader DJ, Reilly MP, Rich SS, Rotter JI, Saleheen D, Samani NJ, Schadt EE, Shuldiner AR, Silverstein R, Kottke-Marchant K, Talmud PJ, Watkins H, Asselbergs FW, de Bakker PI, McCaffery J, Wijmenga C, Sabatine MS, Wilson JG, Reiner A, Bowden

DW, Hakonarson H, Siscovick DS, and Keating BJ (2012) Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics* 90:410-425. PMCID: PMC3309185.

224. IL6R Genetics Consortium Emerging Rick Factors Collaboration, Sarwar N, Butterworth AS, Freitag DF, Gregson J, Willeit P, Gorman DN, Gao P, Saleheen D,Rendon A, Nelson CP, Braund PS, Hall AS, Chasman DI, Tybjærg-Hansen A, Chambers JC, Benjamin EJ, Franks PW, Clarke R, Wilde AA, Trip MD, Steri M,Witteman JC, Qi L, van der Schoot CE, de Faire U, Erdmann J, Stringham HM, Koenig W, Rader DJ, Melzer D, Reich D, Psaty BM, Kleber ME, Panagiotakos DB,Willeit J, Wennberg P, Woodward M, Adamovic S, Rimm EB, Meade TW, Gillum RF, Shaffer JA, Hofman A, Onat A, Sundström J, Wassertheil-Smoller S,Mellström D, Gallacher J, Cushman M, Tracy RP, Kauhanen J, Karlsson M, Salonen JT, Wilhelmsen L, Amouyel P, Cantin B, Best LG, Ben-Shlomo Y, Manson JE, Davey-Smith G, de Bakker PI, O'Donnell CJ, Wilson JF, Wilson AG, Assimes TL, Jansson JO, Ohlsson C, Tivesten Å, Ljunggren Ö, Reilly MP, Hamsten A,Ingelsson E, Cambien F, Hung J, Thomas GN, **Boehnke M**, Schunkert H, Asselbergs FW, Kastelein JJ, Gudnason V, Salomaa V, Harris TB, Kooner JS, Allin KH, Nordestgaard BG, Hopewell JC, Goodall AH, Ridker PM, Hólm H, Watkins H, Ouwehand WH, Samani NJ, Kaptoge S, Di Angelantonio E, Harari O, and Danesh J (2012) Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet* 379:1205-1213. PMCID: PMC3316940.

225. Voight B, Peloso G, Orho-Melander M, Frikke-Schmidt R, Barbalic M, Jensen M, Hindy G, Hólm H, Ding E, Johnson T, Schunkert H, Samani N, Clarke R, Hopewell J, Thompson J, Li M, Thorleifsson G, Newton-Cheh C, Musunuru K, Pirruccello J, Salaheen D, Chen L, Stewart A, Schillert A, Thorsteinsdottir U, Thorgeirsson G, Anand S, Engert J, Morgan T, Spertus J, Stoll M, Berger K, Martinelli N, Girelli D, McKeown P, Patterson C, Epstein S, Devaney J, Burnett M-S, Mooser V, Ripatti S, Surakka I, Nieminen M, Sinisalo J, Lokki M-L, Perola M, Havulinna A, de Faire U, Gigante B, Ingelsson E, Zeller T, Wild P, deBakker P, Klungel O, Maitland-van der Zee A-H, Peters B, de Boer A, Grobbee D, Kamphuisen P, Deneer V, Elbers C, Onland-Moret NC, Hofker M, Wijmenga C, Verschuren WM, Boer J, van der Schouw Y, Rasheed A, Frossard P, Demissie S, Willer C, Do R, Ordovas J, Abecasis G, **Boehnke M**, Mohlke K, Daly M, Guiducci C, Burtt N, Surti A, Gonzalez E, Purcell S, Gabriel S, Marrugat J, Peden J, Erdmann J, Linsel-Nitschke P, Willenborg C, Konig I, Fischer M, Hengstenberg C, Ziegler A, Buysschaert I, Lambrechts D, Van de Werf F, Fox K, El Mokhtari NE, Rubin D, Schrezenmeir J, Schreiber S, Schäfer A, Danesh J, Blankenberg S, Roberts R, McPherson R, Watkins H, Hall A, Overvad K, Rimm E, Boerwinkle E, Tybjaerg-Hansen A, Cupples LA, Reilly M, Melander O, Mannucci P, Ardissino D, Siscovick D, Elosua R, Stefansson K, O'Donnell C, Salomaa V, Radar D, Peltonen L, Schwartz S, Altshuler D, and Kathiresan S (2012) Plasma HDL cholesterol and risk of myocardial infraction: a Mendelian randomization. *Lancet* 380:572-580. PMCID: PMC3419820.

226. Manning AK, Hivert M-F, Scott RA, Grimsby JL, Bouatia-Naji N, Chen H, Rybin D, Liu C-T, Bielak LF, Prokopenko I, Amin N, Barnes D, Cadby G, Hottenga JJ, Ingelsson E, Jackson AU, Johnson T, Kanoni S, Ladenvall C, Lagou V, Lahti J, Lecoeur C, Liu Y, Martinez-Larrad MT, Montasser ME, Navarro P, Perry JRB, Rasmussen-Torvik LJ, Salo P, Sattar N, Shungin D, Strawbridge RJ, Tanaka T, van Duijn CM, An P, de Andrade M,

Andrews JS, Aspelund T, Atalay M, Aulchenko Y, Balkau B, Bandinelli S, Beckmann JS, Beilby JP, Bellis C, Bergman RN, Blangero J, Roban M, **Boehnke M**, Boerwinkle E, Bonnycastle LL, Boomsma DI, Borecki IB, Böttcher Y, Bouchard C, Brunner E, Budimir D, Campbell H, Carlson O, Chines PS, Clarke R, Collins FS, Corbatón-Anchuelo A, Couper D, de Faire U, Dedoussis GV, Deloukas P, Dimitriou M, Egan JM, Eiriksdottir G, Erdos MR, Eriksson JG, Eury E, Ferrucci L, Ford I, Forouhi NG, Fox CS, Fox CS, Franzosi MG, Franks PW, Frayling TM, Froguel P, Galan P, de Geus E, Gigante B, Glazer NL, Goel A, Groop L, Gudnason V, Hallmans G, Hamsten A, Hansson O, Harris TB, Hayward C, Heath S, Hercberg S, Hicks AA, Hingorani A, Hofman A, Hui J, Hung J, Jarvelin MR, Jhun MA, Johnson PCD, Jukema JW, Jula A, Kao WH, Kaprio J, Kardia SLR, Keinanen-Kiukaanniemi S, Kivimaki M, Kolcic I, Kovacs P, Kumari M, Kuusisto J, Kyvik KO, Laakso M, Lakka T, Lannfelt L, Lathrop GM, Launer LJ, Leander K, Li G, Lind L, Lindstrom J, Lobbens S, Loos RJF, Luan J, Lyssenko V, Mägi R, Magnusson PKE, Marmot M, Meneton P, Mohlke KL, Mooser V, Morken MA, Miljkovic I, Narisu N, O'Connell J, Ong KK, Oostra BA, Palmer LJ, Palotie A, Pankow JS, Peden JF, Pedersen NL, Pehlic M, Peltonen L, Penninx B, Pericic M, Perola M, Perusse L, Peyser PA, Polasek O, Pramstaller PP, Province MA, Räikkönen K, Rauramaa R, Rehnberg E, Rice K, Rotter JI, Rudan I, Ruokonen A, Saaristo T, Sabater-Lleal M, Salomaa V, Savage DB, Saxena R, Schwarz P, Seedorf U, Sennblad B, Serrano-Rios M, Shuldiner AR, Sijbrands EJG, Siscovick DS, Smit JH, Small KS, Smith NL, Smith AV, Stančáková A, Stirrups K, Stumvoll M, Sun YV, Swift AJ, Tönjes A, Tuomilehto J, Trompet S, Uitterlinden AG, Uusitupa M, Vikström M, Vitart V, Vohl M-C, Voight BF, Vollenweider P, Waeber G, Waterworth DM, Watkins H, Wheeler E, Widen E, Wild SH, Willems SM, Willemsen G, Wilson JF, Witteman JCM, Wright AF, Yaghootkar H, Zelenika D, Zemunik T, Zgaga L, DIAGRAM Consortium, The MUTHER Consortium, Wareham NJ , McCarthy MI, Barroso I, Watanabe RM, Florez JC, Dupuis J, Meigs JB, and Langenberg C (2012) A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics* 44:659-669. PMCID: PMC3613127.

227. Perry JRB, Voight BF, Yengo L, Amin N, Dupuis J, Ganser M, Grallert H, Navarro P, Li M, Qi L, Steinthorsdottir V, Scott RA, Almgren P, Arking DE, Aulchenko Y, Balkau B, Benediktsson R, Bergman RN, Boerwinkle E, Bonnycastle L, Burtt NP, Campbell H, Charpentier G, Collins FS, Gieger C, Green T, Hadjadj S, Hattersley AT, Herder C, Hofman A, Johnson AD, Kottgen A, Kraft P, Labrune Y, Langenberg C, Manning AK, Mohlke KL, Morris AP, Oostra B, Pankow J, Petersen A-K, Pramstaller PP, Prokopenko I, Rathmann W, Rayner W, Roden M, Rudan I, Rybin D, Scott LJ, Sigurdsson G, Sladek R, Thorleifsson G, Thorsteinsdottir U, Tuomilehto J, Uitterlinden AG, Vivequin S, Weedon MN, Wright AF, MAGIC, DIAGRAM Consortium, GIANT Consortium, Hu FB, Illig T, Kao L, Meigs JB, Wilson JF, Stefansson K, van Duijn C, Altschuler D, Morris AD, **Boehnke M**, McCarthy MI, Froguel P, Palmer CAN, Wareham NJ, Groop L, Frayling TM, and Cauchi S (2012) Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PloS Genetics* 8:e1002741. PMCID: PMC3364960.

228. Scott RA, Lagou V, Welch RP, Wheeler E, Montasser ME, Luan J, Mägi R, Strawbridge RJ, Rehnberg E, Gustafsson S, Kanoni S, Rasmussen-Torvik LJ, Yengo L, Leceour C,

Shungin D, Sanna S, Sidore C, Johnson PCD, Jukema JW, Johnson T, Mahajan A, Verweij N, Thorleifsson G, Hottenga JJ, Shah S, Smith AV, Sennblad B, Gieger C, Salo P, Perola M, Timpson NJ, Evans DM, St. Pourcain B, Wu Y, Andrews JS, Hui J, Bielak LF, Zhao W, Horikoshi M, Navarro P, Isaacs AM, O'Connell JR, Stirrups K, Vitart V, Hayward C, Esko T, Mihailov E, Fraser RM, Fall T, Voight BF, Raychaudhuri S, Chen H, Lindgren CM, Morris AP, Rayner NW, Robertson N, Rybin D, Liu C-T, Beckmann JS, Willems SM, Chines PS, Jackson AU, Kang HM, Stringham HM, Song K, Tanaka T, Peden JF, Goel A, Hicks AA, An P, Müller-Nurasyid M, Franco-Cereceda A, Folkersen L, Marullo L,l Jansen H, Oldehinkel AJ, Bruinenberg M, Pankow JS, North KE, Forouhi NG, Loos RJF, Edkins S, Varga TV, Hallmans G, Oksa H, Antonella M, Nagaraja R, Trompet S, Ford I,l Bakker SJL, Kong A, Kumari M, Gigante B, Herder C, Munroe PB, Caulfield M, Antti J, Mangino M, Small K, Miljkovic I, Liu Y, Atalay M, Kiess W, James AL, Rivadeneira R, Uitterlinden AG, Palmer CAN, Doney A, Willemsen G, Smit JH, Campbell S, Polasek O, Bonnycastle LL, Hercberg S, Dimitriou M, Bolton JL,l Fowkes GR, Kovacs P, Lindström J, Zemunik T, Bandinelli S, Wild SH, Basart HV, Rathmann W, Grallert H, DIAGRAM Consortium, Maerz W, Kleber ME, Boehm BO, Peters A, Pramstaller PP, Province MA, Borecki IB, Hastie ND, Rudan I, Campbell H, Watkins H, Farrall, M, Stumvoll M, Ferrucci L, Waterworth DM, Bergman RN, Collins FS, Tuomilehto J, Watanabe RM, de Geus EJC, Penninx BW, Hofman A, Oostra BA, Psaty BM, Vollenweider P, Wilson JF, Wright AF, Hovingh GK, Metspalu A, Uusitupa M, Magnusson PKE, Kyvik KO, Kaprio J, Price JF, Dedousis GV, Deloukas P, Meneton P, Lind L, **Boehnke M**, Shuldiner AR, van Duijn CM, Morris AD, Toenjes A, Peyser PA, Beilby JP, Körner A, Kuusisto J, Laakso M, Bornstein SR, Schwarz PEH, Lakka TA, Rauramaa R, Adair LS, Smith GD, Spector TD, Illig T, de Faire U, Hamsten A, Gudnason V, Kivimaki M, Hingorani A, Keinanen-Kiukaanniemi SM, Saaristo TE, Boomsma DI, Stefansson K, van der Harst P, Dupuis J, Pedersen NL, Sattar N, Harris TB, Cucca F, Ripatti S, Salomaa V, Mohlke KL, Balkau B, Froguel P, Pouta A, Jarvelin M-R, Wareham NJ, Bouatia-Naji N, McCarthy MI, Franks PW, Meigs JB, Teslovich TM, Florez JC, Langenberg C, Ingelsson E, Prokopenko I, and Barroso I, for the MAGIC Investigators (2012) Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics* 44:991-1005. PMCID: PMC3433394.

229. Voight BF, Kang HM, Ding J, Palmer CD, Sidore C, Chines PS, Burtt NP, Fuchsberger C, Li Y, Erdmann J, Frayling TM, Heid IM, Jackson AU, Johnson T, Kilpeläinen TO, Lindgren C, Morris AP, Prokopenko I, Randall JC, Saxena R, Soranzo N, Speliotes EK, Teslovich TM, Wheeler E, Maguire J, Parkin M, Potter S, Rayner NW, Robertson N, Stirrups K, Winckler W, Sanna S, Mulas A, Nagaraja R, Cucca F, Barroso I, Deloukas P, Loos RJF, Kathiresan S, Munroe PB, Newton-Cheh C, Pfeufer A, Samani NJ, Schunkert H, Hirschhorn JN, Altshuler D, McCarthy MI, Abecasis GR, and **Boehnke M** (2012) The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PloS Genetics* 8: e1002793. PMCID: PMC3410907.

230. Boraska V, Jerončić A, Colonna V, Southam L, Nyholt DR, Rayner NW, Perry JRB, Toniolo D, Albrecht E, Ang W, Bandinelli S, Barbalic M, Barroso I, Beckmann JS, Biffar R, Boomsma D, Campbell H, Corre T, Erdmann J, Esko T, Fischer K, Franceschini N, Frayling TM, Girotto G, Gonzalez JR, Harris TB, Heath AC, Heid IM,

Hoffmann W, Hofman A, Horikoshi M, Zhao JH, Jackson AU, Hottenga J-J, Jula A, Kähönen M, Khaw K-T, Kiemeney LA, Klopp N, Kutalik Z, Lagou V, Launer LJ, Lehtimäki T, Lemire M, Lokki M-L, Loley C, Luan J, Mangino M, Leach IM, Medland SE, Mihailov E, Montgomery GW, Navis G, Newnham J, Nieminen MS, Palotie A, Panoutsopoulou K, Peters A, Pirastu N, Polašek O, Rehnström K, Ripatti S, Ritchie GRS, Rivadeneira F, Robino A, Samani NJ, Shin S-Y, Sinisalo J, Smit J, Soranzo N, Stolk L, Swinkels DW, Tanaka T, Teumer A, Töonjes A, Traglia M, Tuomilehto J, Valsesia A, van Gilst WH, van Meurs JBJ, Smith AV, Viikari J, Vink JM, Waeber G, Warrington NM, Widen E, Willemsen G, Wright AF, Zanke BW, Zgaga L, Wellcome Trust Case Control Consortium (WTCCC), **Boehnke M**, d'Adamo AP, de Geus E, Demerath EW, den Heijer M, Eriksson JG, Ferrucci L, Gieger C, Gudnason V, Hayward C, Hengstenberg C, Hudson TJ, Järvelin M-R, Kogevinas M, Loos RJF, Martin NG, Metspalu A, Pennell CE, Penninx BW, Perola M, Raitakari O, Salomaa V, Schreiber S, Schunkert H, Spector TD, Stumvoll M, Uitterlinden AG, Ulivi S, van der Harst P, Vollenweider P, Völzke H, Wareham NJ, Wichmann H-E, Wilson JF, Rudan I, Xue Y, and Zeggini E (2012) Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics* 21:4805-4815. PMCID: PMC3471397.

231. Jun G, Flickinger M, Hetrick KN, Romm JM, Doheny KF, Abecasis GR, **Boehnke M**, and Kang HM (2012) Detecting and estimating contamination of human DNA samples in sequencing and array-based genotype data. *American Journal of Human Genetics* 91:839-848. PMCID: PMC3487130.

232. Yang J, Loos RJ, Powell JE, Medland SE, Speliotes EK, Chasman DI, Rose LM, Thorleifsson G, Steinthorsdottir V, Mägi R, Waite L, Smith AV, Yerges-Armstrong LM, Monda KL, Hadley D, Mahajan A, Li G, Kapur K, Vitart V, Huffman JE, Wang SR, Palmer C, Esko T, Fischer K, Zhao JH, Demirkan A, Isaacs A, Feitosa MF, Luan J, Heard-Costa NL, White C, Jackson AU, Preuss M, Ziegler A, Eriksson J, Kutalik Z, Frau F, Nolte IM, Van Vliet-Ostaptchouk JV, Hottenga JJ, Jacobs KB, Verweij N, Goel A, Medina-Gomez C, Estrada K, Bragg-Gresham JL, Sanna S, Sidore C, Tyrer J, Teumer A, Prokopenko I, Mangino M, Lindgren CM, Assimes TL, Shuldiner AR, Hui J, Beilby JP, McArdle WL, Hall P, Haritunians T, Zgaga L, Kolcic I, Polasek O, Zemunik T, Oostra BA, Junttila MJ, Grönberg H, Schreiber S, Peters A, Hicks AA, Stephens J, Foad NS, Laitinen J, Pouta A, Kaakinen M, Willemsen G, Vink JM, Wild SH, Navis G, Asselbergs FW, Homuth G, John U, Iribarren C, Harris T, Launer L, Gudnason V, O'Connell JR, Boerwinkle E, Cadby G, Palmer LJ, James AL, Musk AW, Ingelsson E, Psaty BM, Beckmann JS, Waeber G, Vollenweider P, Hayward C, Wright AF, Rudan I, Groop LC, Metspalu A, Khaw KT, van Duijn CM, Borecki IB, Province MA, Wareham NJ, Tardif JC, Huikuri HV, Cupples LA, Atwood LD, Fox CS, **Boehnke M**, Collins FS, Mohlke KL, Erdmann J, Schunkert H, Hengstenberg C, Stark K, Lorentzon M, Ohlsson C, Cusi D, Staessen JA, Van der Klauw MM, Pramstaller PP, Kathiresan S, Jolley JD, Ripatti S, Jarvelin MR, de Geus EJ, Boomsma DI, Penninx B, Wilson JF, Campbell H, Chanock SJ, van der Harst P, Hamsten A, Watkins H, Hofman A, Witteman JC, Zillikens MC, Uitterlinden AG, Rivadeneira F, Zillikens MC, Kiemeney LA, Vermeulen SH, Abecasis GR, Schlessinger D, Schipf S, Stumvoll M, Tönjes A, Spector TD, North KE, Lettre G, McCarthy MI, Berndt SI, Heath AC, Madden PA, Nyholt DR, Montgomery GW, Martin

NG, McKnight B, Strachan DP, Hill WG, Snieder H, Ridker PM, Thorsteinsdottir U, Stefansson K, Frayling TM, Hirschhorn JN, Goddard ME, and Visscher PM (2012) FTO genotype is associated with phenotypic variability of body mass index. *Nature* 490:267-272. PMCID: PMC3564953.

233. Morris AP, Voight BF, Teslovich TM, Ferreira T, Segrè AV, Steinthorsdottir V, Strawbridge RJ, Khan H, Grallert H, Mahajan A, Prokopenko I, Kang HM, Dina C, Esko T, Fraser RM, Kanoni S, Kumar A, Lagou V, Langenberg C, Luan J, Lindgren CM, Müller-Nurasyid M, Pechlivanis S, Rayner NW, Scott LJ, Wiltshire S, Yengo L, Kinnunen L, Rossin EJ, Raychaudhuri S, Johnson AD, Dimas AS, Loos RJ, Vedantam S, Chen H, Florez JC, Fox C, Liu CT, Rybin D, Couper DJ, Kao WH, Li M, Cornelis MC, Kraft P, Sun Q, van Dam RM, Stringham HM, Chines PS, Fischer K, Fontanillas P, Holmen OL, Hunt SE, Jackson AU, Kong A, Lawrence R, Meyer J, Perry JR, Platou CG, Potter S, Rehnberg E, Robertson N, Sivapalaratnam S, Stančáková A, Stirrups K, Thorleifsson G, Tikkanen E, Wood AR, Almgren P, Atalay M, Benediktsson R, Bonnycastle LL, Burtt N, Carey J, Charpentier G, Crenshaw AT, Doney AS, Dorkhan M, Edkins S, Emilsson V, Eury E, Forsen T, Gertow K, Gigante B, Grant GB, Groves CJ, Guiducci C, Herder C, Hreidarsson AB, Hui J, James A, Jonsson A, Rathmann W, Klopp N, Kravic J, Krjutškov K, Langford C, Leander K, Lindholm E, Lobbens S, Männistö S, Mirza G, Mühleisen TW, Musk B, Parkin M, Rallidis L, Saramies J, Sennblad B, Shah S, Sigurðsson G, Silveira A, Steinbach G, Thorand B, Trakalo J, Veglia F, Wennauer R, Winckler W, Zabaneh D, Campbell H, van Duijn C, Uitterlinden AG, Hofman A, Sijbrands E, Abecasis GR, Owen KR, Zeggini E, Trip MD, Forouhi NG, Syvänen AC, Eriksson JG, Peltonen L, Nöthen MM, Balkau B, Palmer CN, Lyssenko V, Tuomi T, Isomaa B, Hunter DJ, Qi L; Wellcome Trust Case Control Consortium; Meta-Analyses of Glucose and Insulin-related traits Consortium (MAGIC) Investigators; Genetic Investigation of ANthropometric Traits (GIANT) Consortium; Asian Genetic Epidemiology Network–Type 2 Diabetes (AGEN-T2D) Consortium; South Asian Type 2 Diabetes (SAT2D) Consortium, Shuldiner AR, Roden M, Barroso I, Wilsgaard T, Beilby J, Hovingh K, Price JF, Wilson JF, Rauramaa R, Lakka TA, Lind L, Dedoussis G, Njølstad I, Pedersen NL, Khaw KT, Wareham NJ, Keinanen-Kiukaanniemi SM, Saaristo TE, Korpi-Hyövälti E, Saltevo J, Laakso M, Kuusisto J, Metspalu A, Collins FS, Mohlke KL, Bergman RN, Tuomilehto J, Boehm BO, Gieger C, Hveem K, Cauchi S, Froguel P, Baldassarre D, Tremoli E, Humphries SE, Saleheen D, Danesh J, Ingelsson E, Ripatti S, Salomaa V, Erbel R, Jöckel KH, Moebus S, Peters A, Illig T, de Faire U, Hamsten A, Morris AD, Donnelly PJ, Frayling TM, Hattersley AT, Boerwinkle E, Melander O, Kathiresan S, Nilsson PM, Deloukas P, Thorsteinsdottir U, Groop LC, Stefansson K, Hu F, Pankow JS, Dupuis J, Meigs JB, Altshuler D, **Boehnke M**, McCarthy MI, and DIAGRAM Consortium (2012) Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics* 44:981-990. PMCID: PMC3442244.

234. Dastani Z, Hivert MF, Timpson N, Perry JR, Yuan X, Scott RA, Henneman P, Heid IM, Kizer JR, Lyytikäinen LP, Fuchsberger C, Tanaka T, Morris AP, Small K, Isaacs A, Beekman M, Coassin S, Lohman K, Qi L, Kanoni S, Pankow JS, Uh HW, Wu Y, Bidulescu A, Rasmussen-Torvik LJ, Greenwood CM, Ladouceur M, Grimsby J, Manning AK, Liu CT, Kooner J, Mooser VE, Vollenweider P, Kapur KA, Chambers J, Wareham

NJ, Langenberg C, Frants R, Willems-Vandijk K, Oostra BA, Willems SM, Lamina C, Winkler TW, Psaty BM, Tracy RP, Brody J, Chen I, Viikari J, Kähönen M, Pramstaller PP, Evans DM, St Pourcain B, Sattar N, Wood AR, Bandinelli S, Carlson OD, Egan JM, Böhringer S, van Heemst D, Kedenko L, Kristiansson K, Nuotio ML, Loo BM, Harris T, Garcia M, Kanaya A, Haun M, Klopp N, Wichmann HE, Deloukas P, Katsareli E, Couper DJ, Duncan BB, Kloppenburg M, Adair LS, Borja JB; DIAGRAM+ Consortium; MAGIC Consortium; GLGC Investigators; MuTHER Consortium, Wilson JG, Musani S, Guo X, Johnson T, Semple R, Teslovich TM, Allison MA, Redline S, Buxbaum SG, Mohlke KL, Meulenbelt I, Ballantyne CM, Dedoussis GV, Hu FB, Liu Y, Paulweber B, Spector TD, Slagboom PE, Ferrucci L, Jula A, Perola M, Raitakari O, Florez JC, Salomaa V, Eriksson JG, Frayling TM, Hicks AA, Lehtimäki T, Smith GD, Siscovick DS, Kronenberg F, van Duijn C, Loos RJ, Waterworth DM, Meigs JB, Dupuis J, Richards JB, Voight BF, Scott LJ, Steinthorsdottir V, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Hofmann OM, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Morris AD, Palmer CN, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Pedersen O, Barroso I, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, **Boehnke M**, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Elliott P, Rybin D, Dehghan A, Hottenga JJ, Song K, Goel A, Lajunen T, Doney A, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hillman DR, Hingorani AD, Hui J, Hung J, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Orrù M, Pakyz R,

Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sigurðsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global B Pgen Consortium, Borecki IB, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Serrano-Ríos M, Lind L, Palmer LJ, Hu FB 1st, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A; Procardis Consortium, Buchanan TA, Valle TT, Rotter JI, Penninx BW, Boomsma DI, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Peltonen L, Mooser V, Sladek R; MAGIC investigators; GLGC Consortium, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Chasman DI, Johansen CT, Fouchier SW, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Feitosa MF, Orho-Melander M, Melander O, Li X, Li M, Cho YS, Go MJ, Kim YJ, Lee JY, Park T, Kim K, Sim X, Ong RT, Croteau-Chonka DC, Lange LA, Smith JD, Ziegler A, Zhang W, Zee RY, Whitfield JB, Thompson JR, Surakka I, Spector TD, Smit JH, Sinisalo J, Scott J, Saharinen J, Sabatti C, Rose LM, Roberts R, Rieder M, Parker AN, Pare G, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, McArdle W, Masson D, Martin NG, Marroni F, Lucas G, Luben R, Lokki ML, Lettre G, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, König IR, Khaw KT, Kaplan LM, Johansson Å, Janssens AC, Igl W, Hovingh GK, Hengstenberg C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Groop LC, Gonzalez E, Freimer NB, Erdmann J, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Faire U, Crawford G, Chen YD, Caulfield MJ, Boekholdt SM, Assimes TL, Quertermous T, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Taylor HA Jr, Gabriel SB, Holm H, Gudnason V, Krauss RM, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Strachan DP, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, and Kathiresan S (2012) Novel loci for adiponectin levels and their influence on type 2 dibetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics* 8:e1002607. PMCID: PMC3315470.

235. Palmer ND, McDonough CW, Hicks PJ, Roh BH, Wing MR, An SS, Hester JM, Cooke JN, Bostrom MA, Rudock ME, Talbert ME, Lewis JP; DIAGRAM Consortium; MAGIC Investigators, Ferrara A, Lu L, Ziegler JT, Sale MM, Divers J, Shriner D, Adeyemo A, Rotimi CN, Ng MC, Langefeld CD, Freedman BI, Bowden DW, Voight BF, Scott LJ, Steinthorsdottir V, Morris AP, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Langenberg C, Hofmann OM, Dupuis J, Qi L, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Couper DJ, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T,

Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Klopp N, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Perry JR, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Mohlke KL, Morris AD, Palmer CN, Pramstaller PP, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Wareham NJ, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Hu FB, Meigs JB, Pankow JS, Pedersen O, Wichmann HE, Barroso I, Florez JC, Frayling TM, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, **Boehnke M**, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Johnson T, Elliott P, Rybin D, Henneman P, Dehghan A, Hottenga JJ, Song K, Goel A, Egan JM, Lajunen T, Doney A, Kanoni S, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Frants R, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hicks AA, Hillman DR, Hingorani AD, Hui J, Hung J, Jula A, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Manning AK, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Oostra BA, Orrù M, Pakyz R, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Perola M, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Psaty BM, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tanaka T, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC, Borecki IB, Loos RJ, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Salomaa V, Smith GD, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Dedoussis GV, Serrano-Ríos M, Lind L, Palmer LJ, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A, Buchanan TA, Valle TT, Rotter JI, Siscovick DS, Penninx BW, Boomsma DI, Deloukas P, Spector TD, Ferrucci L, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Waterworth DM, Vollenweider P, Peltonen L, Mooser V, and Sladek R (2012) A

genome-wide association search for type 2 diabetes genes in African Americans. *PLoS One* 7:e29202. PMCID: PMC3251563.

236. Minelli C, De Grandi A, Weichenberger CX, Gögele M, Modenese M, Attia J, Barrett JH, **Boehnke M**, Borsani G, Casari G, Fox CS, Freina T, Hicks AA, Marroni F, Parmigiani G, Pastore A, Pattaro C, Pfeufer A, Ruggeri F, Schwienbacher C, Taliun D, Pramstaller PP, Domingues FS, and Thompson JR (2013) Importance of different types of prior knowledge in selecting genome-wide findings for follow-up. *Genetic Epidemiology* 37:205-213. PMCID: PMC3725558.

237. Deloukas P, Kanoni S, Willenborg C, Farrall M, Assimes TL, Thompson JR, Ingelsson E, Salaheen D, Erdmann J, Goldstein BA, Stirrups K, König IR, Cazier J-B, Johansson A, Hall AS, Lee J-Y, Willer CJ, Chambers JC, Esko T, Foldersen L, Goel A, Grundberg E, Havulinna AS, Ho WK, Hopewell JC, Eriksson N, Kleber ME, Kristiansson K, Lundmark P, Lyytikäinen L-P, Rafelt S, Shungin D, Strawbridge RJ, Thorleifsson G, Tikkanen E, Van Zuydam N, Voight BF, Waite LL, Zhang W, Zeigler A, Absher D, Altshuler D, Balmforth AJ, Barroso I, Braund PS, Burgdorf C, Claudi-Boehm S, Cox D, Dimitriou M, Do R, DIAGRAM Consortium, CARDIOGENICS Consortium, Doney ASF, El Mokhtari N, Eriksson P, Fischer K, Fontanillas P, Franco-Cereceda A, Gigante B, Groop L, Gustafsson S, Hager J, Hallmans G, Han B-G, Hunt SE, Kang HM, Illig T, Kessler T, Knowles JW, Kolovou G, Kuusisto J, Langenberg C, Langford C, Leander K, Lokki M-L, Lundmark A, McCarthy Mim, Meisinger C, Melander O, Mihailov E, Maouche S, Morris AD, Müller-Nurasyid M, MuTHER Consortium, Nikus K, Peden JF, Rayner NW, Rasheed A, Rosinger S, Rubin D, Rumpf MP, Schäfer A, Sivananthan M, Song C, Stewart AFR, Tan S-T, Thorgeirsson G, van der Schoot CE, Wagner PJ, Wellcome Trust Case Control Consortium, Wells GA, Wild PS, Yang T-P, Anouyel P, Arveiler D, Basart H, **Boehnke M**, Boerwinkle E, Brambilla P, Cambien F, Cupples AL, de Faire U, Dehghan A, Diemert P, Epstein SE, Evans A, Ferrario MM, Ferrières J, Gauguier D, Go AS, Goodall AH, Gudnason V, Hazan SL, Holm H, Iribarren C, Jang Y, Kähönen M, Kee F, Kim H-S, Klopp N, Koenig W, Kratzer W, Kuulasmaa K, Laakso M, Laaksonen R, Lee J-Y, Lind L, Ouwehand WH, Parish S, Park JE, Pedersen NL, Peters A, Quertermous T, Rader DJ, Salomaa V, Schadt E, Shah SH, Sinisalo J, Stark K, Stefansson K, Trégouët D-A, Virtamo J, Wallentin L, Wareham N, Zimmermann ME, Nieminen MS, Hengstenberg C, Sandhu MS, Pastinen T, Syvänen A-C, Hovingh GK, Dedoussis G, Franks PW, Lehtimäki T, Metspalu A, Zalloua PA, Siegbahn A, Schreiber S, Ripatti S, Blankenberg SS, Perola M, Clarke R, Boehm BO, O'Donnell C, Reilly MP, März W, Collins R, Kathiresan S, Hamsten A, Kooner JS, Thorsteinsdottir U, Danesh J, Palmer CAN, Roberts R, Watkins H, Schunkert H, and Samani NJ (2013) Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics* 45:25-33. PMCID: PMC3679547

238. Huyghe JR, Jackson AU, Fogarty MP, Buchkovich ML, Stančákova A, Stringham HM, Sim X, Yang L, Fuchsberger C, Cederberg H, Chines PS, Teslovich TM, Romm JM, Ling H, McMullen I, Ingersoll R, Pugh EW, Doheny KF, Neale BM, Daly MJ, Kuusisto J, Scott LJ, Kang HM, Collins FS, Abecasis GR, Watanabe RM, **Boehnke M**, Laakso M, and Mohlke K (2013) Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. *Nature Genetics* 45:197-201. PMCID: PMC3727235.

239. Mahendran Y, Vangipurapu J, Cederberg H, Stancáková A, Pihlajamäki J, Soininen P, Kangas AJ, Paananen J, Civelek M, Saleem NK, Pajukanta P, Lusis AJ, Bonnycastle LL, Morken MA, Collins FS, Mohlke KL, **Boehnke M**, Ala-Korpela M, Kuusisto J, and Laakso M (2013) Association of ketone body levels with hyperglycemia and type 2 diabetes in 9,398 Finnish men. *Diabetes* 62:3618-3626. PMCID: PMC3781437.

240. Wu Y, Waite LL, Jackson AU, Sheu WH, Buyske S, Absher D, Arnett DK, Boerwinkle E, Bonnycastle LL, Carty CL, Cheng I, Cochran B, Croteau-Chonka DC, Dumitrescu L, Eaton CB, Franceschini N, Guo X, Henderson BE, Hindorff LA, Kim E, Kinnunen L, Komulainen P, Lee WJ, Le Marchand L, Lin Y, Lindström J, Lingaas-Holmen O, Mitchell SL, Narisu N, Robinson JG, Schumacher F, Stančáková A, Sundvall J, Sung YJ, Swift AJ, Wang WC, Wilkens L, Wilsgaard T, Young AM, Adair LS, Ballantyne CM, Bůžková P, Chakravarti A, Collins FS, Duggan D, Feranil AB, Ho LT, Hung YJ, Hunt SC, Hveem K, Juang JM, Kesäniemi AY, Kuusisto J, Laakso M, Lakka TA, Lee IT, Leppert MF, Matise TC, Moilanen L, Njølstad I, Peters U, Quertermous T, Rauramaa R, Rotter JI, Saramies J, Tuomilehto J, Uusitupa M, Wang TD, **Boehnke M**, Haiman CA, Chen YD, Kooperberg C, Assimes TL, Crawford DC, Hsiung CA, North KE, and Mohlke KL (2013) Trans-ethnic fine-maping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PloS Genetics* 9:e1003379. PMCID: PMC3605054.

241. Thompson JR, Gögele M, Weichenberger CX, Modenese M, Attia J, Barrett JH, **Boehnke M**, De Grandi A, Domingues FS, Hicks AA, Marroni F, Pattaro C, Ruggeri F, Borsani G, Casari G, Parmigiani G, Pastore A, Pfeufer A, Schwienbacher C, Taliun D, Consortium C, Fox CS, Pramstaller PP, and Minelli C (2013) SNP prioritization using a Bayesian probability of association. *Genetic Epidemiology* 37:214-221. PMCID: PMC3725584.

242. Lee S, Teslovich TM, **Boehnke M**, and Lin X (2013) General framework for meta-analysis of rare variants in sequencing association studies. *American Journal of Human Genetics* 93:42-53. PMCID: PMC3710762.

243. Ma C, Blackwell T, **Boehnke M**, and Scott LJ (2013) Recommended joint and meta-analysis strategies for case-control association testing of single low-count variants. *Genetic Epidemiology* 37:539-559. PMCID: PMC4049324.

244. Cross-Disorder Group of the Psychiatric Genomics Consortium, Lee SH, Ripke S, Neale BM, Faraone SV, Purcell SM, Perlis RH, Mowry BJ, Thapar A, Goddard MD, Witte JS, Absher D, Agartz I, Akil H, Amin F, Andreassen OA, Anjorin A, Anney R, Anttila V, Arking DE, Asherson P, Azevedo MH, Backlund L, Badner JA, Bailey AJ, Banaschewski T, Barchas JD, Barnes MR, Barrett TB, Bass N, Battaglia A, Bauer M, Bayés M, Bellivier F, Bergen SE, Berrettini W, Betancur C, Bettecken T, Biederman J, Binder EB, Black DW, Blackwood DHR, Bloss CS, **Boehnke M**, Boomsma DI, Breen G, Breuer R, Bruggeman R, Cormican P, Buccola NG, Buitelaar JK, Bunney WE, Buxbaum JD, Byerley WF, Byrne EM, Caesar S, Cahn W, Mcantor R, Casas M, Chakravarti A, Chambert K, Choudhury K, Cichon S, Cloninger CR, Collier DA, Cook EH, Coon H, Cormand B, Corvi A, Coryell WH, Craig DW, Craig IW, Crosbie J, Cuccaro ML, Curtis D, Czamara D, Datta S, Dawson G, Day R, De Geus EJ, Degenhardt F, Djurovic S,

Donohoe GJ, Doyle AE, Duan J, Dudbridge F, Duketis E, Ebstein RP, Edenberg HJ, Elia J, Ennis S, Etain B, Fanous A, Farmer AE, Ferrier IN, Flickinger M, Fombonne E, Foroud T, Frank J, Franke B, Fraser C, Freedman R, Freimer NB, Freitag CM, Friedl M, Frisén L, Gallagher L, Gejman PV, Georgieva L, Gershon ES, Geschwind DH, Giegling I, Gill M, Gordon SD, Gordon-Smith K, Green EK, Greenwood TA, Grice DE, Gross M, Grozeva D, Guan W, Gurling H, De Haan L, Haines JL, Hakonarson H, Hallmayer J, Hamilton SP, Hamshere ML, Hansen TF, Hartmann AM, Hautzinger M, Heath AC, Henders AK, Herms S, Hickie IB, Hipolito M, Hoefels S, Holmans PA, Holsboer F, Hoogendijk WJ, Hottenga J-J, Hultman CM, Hus V, Ingason A, Ising M, Jamain S, Jones EG, Jones I, Jones L, Tzeng J-Y, Kähler AK, Kahn RS, Kandaswamy R, Keller MC, Kennedy JK, Kenny E, Kent L, Kim Y, Kirov GK, Klauck SM, Klei L, Knowles JA, Kohli MA, Koller DL, Konte B, Korszun A, Krabbendam L, Krasucki R, Kuntsi J, Kwan P, Landén M, Långström N, Lathrop M, Lawrence J, Lawson WB, Leboyer M, Ledbetter DH, Lee PH, Lencz T, Lesch K-P, Levinson DF, Lewis CM, Li J, Lichtenstein P, Lieberman JA, Lin D-Y, Linszen DH, Liu C, Lohoff FW, Loo SK, Lord C, Lowe JK, Lucae S, MacIntyre DJ, Madden PAF, Maestrini E, Magnusson PKE, Mahon PB, Maier W, Malhotra AK, Mane SM, Martin CL, Martin NG, Mattheisen M, Matthews K, Mattingsdal M, McCarroll SA, McGhee KA, McGough JJ, McGrath PJ, McGuffin P, McInnis MG, McIntosh A, McKinney R, McLean AW, McMahon FJ, McMahon WM, McQuillin A, Medeiros H, Medland SE, Meier S, Melle I, Meng F, Meyer J, Middeldorp CM, Middleton L, Milanova V, Miranda A, Monaco AP, Montgomery GW, Moran JL, Moreno-De-Luca D, Morken G, Morriw DW, Morrow EM, Moskvina V, Muglia P, Mühleisen TW, Muir WJ, Müller-Myhsok B, Murtha M, Myers RM, Myin-Germeys I, Neale MC, Nelson SF, Nievergelt CM, Nikolov I, Nimgaonkar V, Nolen WA, Nöthen MM, Nurnberger JI, Nwulia EA, Nyholt DR, O'Dushlaine C, Oades RD, Olincy A, Oliveira G, Olsen L, Ophoff FA, Osby U, Owen MJ, Palotie A, Parr JR, PatersonAD, Pato CN, Pato MT, Penninx BW, Pergadia ML, Pericak-Vance MA, Pickard BS, Pimm J, Piven J, Posthuma D, Potash JB, Poustka F, Propping P, Puri V, Quested DJ, Mquinn E, Ramos-Quiroga JA, Rasmussen HB, Raychaudhuri S, Rehnström K, Reif A, Ribasés M, Rice JP, Rietschel M, Roeder K, Roeyers H, Rossin L, Rothenberger A, Rouleau G, Ruderfer D, Rujescu D, Sanders AR, Sanders SJ, Santangelo SL, Sergeant JA, Schachar R, Schalling M, Schatzberg AF, Scheftner WA, Schellenberg GD, Scherer SW, Schork NJ, Schulze TG, Schumacher J, Schwarz M, Scolnick E, Scott LJ, Shi J, Shilling PD, Shyn SI, Silverman JM, Slager SL, Smalley SL, Smit JH, Smith EN, Sonuga-Barke ES, St. Clair D, State M, Steffens M, Steinhausen H-C, Strauss JS, Strohmaier J, Stroup TS, Sutcliffe JS, Szatmari P, Szelinger S, Thirumalai S, Thompson RC, Todorov AA, Tozzi F, Treutlein J, Uhr M, van den Oord EJCG, Van Grootheest G, Os JV, Vicente AM, Vieland VJ, Vincent JB, Visscher PM, Walsh CA, Wassink TH, Watson SJ, Weissman MM, Werge T, Wienker TF, Wijsman EM, Willemsen G, Williams N, Willsey AJ, Witt SH, Xu W, Young AH, Yu TW, Zammit S, Zandi PP, Zhang P, Zitman FG, Zöllner S, International Inflammatory Bowel Disease Genetics Consortium (IIBDGC), Devlin B, Kelsoe JR, Sklar P, Daly MJ, O'Donovan MC, Craddock N, Sullivan PF, Smoller JW, Kendler KS, and Wray NR (2013) Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics* 45:984-994. PMCID: PMC3800159 .

245. Global Lipids Genetics Consortium, Willer CJ, Schmidt EM, Sengupta S, Peloso GM, Gustafsson S, Kanoni S, Ganna A, Chen J, Buchkovich ML, Mora S, Beckmann JS, Bragg-Gresham JL, Chang HY, Demirkan A, Den Hertog HM, Do R, Donnelly LA, Ehret GB, Esko T, Feitosa MF, Ferreira T, Fischer K, Fontanillas P, Fraser RM, Freitag DF, Gurdasani D, Heikkilä K, Hyppönen E, Isaacs A, Jackson AU, Johansson A, Johnson T, Kaakinen M, Kettunen J, Kleber ME, Li X, Luan J, Lyytikäinen LP, Magnusson PK, Mangino M, Mihailov E, Montasser ME, Müller-Nurasyid M, Nolte IM, O'Connell JR, Palmer CD, Perola M, Petersen AK, Sanna S, Saxena R, Service SK, Shah S, Shungin D, Sidore C, Song C, Strawbridge RJ, Surakka I, Tanaka T, Teslovich TM, Thorleifsson G, Van den Herik EG, Voight BF, Volcik KA, Waite LL, Wong A, Wu Y, Zhang W, Absher D, Asiki G, Barroso I, Been LF, Bolton JL, Bonnycastle LL, Brambilla P, Burnett MS, Cesana G, Dimitriou M, Doney AS, Döring A, Elliott P, Epstein SE, Eyjolfsson GI, Gigante B, Goodarzi MO, Grallert H, Gravito ML, Groves CJ, Hallmans G, Hartikainen AL, Hayward C, Hernandez D, Hicks AA, Holm H, Hung YJ, Illig T, Jones MR, Kaleebu P, Kastelein JJ, Khaw KT, Kim E, Klopp N, Komulainen P, Kumari M, Langenberg C, Lehtimäki T, Lin SY, Lindström J, Loos RJ, Mach F, McArdle WL, Meisinger C, Mitchell BD, Müller G, Nagaraja R, Narisu N, Nieminen TV, Nsubuga RN, Olafsson I, Ong KK, Palotie A, Papamarkou T, Pomilla C, Pouta A, Rader DJ, Reilly MP, Ridker PM, Rivadeneira F, Rudan I, Ruokonen A, Samani N, Scharnagl H, Seeley J, Silander K, Stancáková A, Stirrups K, Swift AJ, Tiret L, Uitterlinden AG, van Pelt LJ, Vedantam S, Wainwright N, Wijmenga C, Wild SH, Willemsen G, Wilsgaard T, Wilson JF, Young EH, Zhao JH, Adair LS, Arveiler D, Assimes TL, Bandinelli S, Bennett F, Bochud M, Boehm BO, Boomsma DI, Borecki IB, Bornstein SR, Bovet P, Burnier M, Campbell H, Chakravarti A, Chambers JC, Chen YD, Collins FS, Cooper RS, Danesh J, Dedoussis G, de Faire U, Feranil AB, Ferrières J, Ferrucci L, Freimer NB, Gieger C, Groop LC, Gudnason V, Gyllensten U, Hamsten A, Harris TB, Hingorani A, Hirschhorn JN, Hofman A, Hovingh GK, Hsiung CA, Humphries SE, Hunt SC, Hveem K, Iribarren C, Järvelin MR, Jula A, Kähönen M, Kaprio J, Kesäniemi A, Kivimaki M, Kooner JS, Koudstaal PJ, Krauss RM, Kuh D, Kuusisto J, Kyvik KO, Laakso M, Lakka TA, Lind L, Lindgren CM, Martin NG, März W, McCarthy MI, McKenzie CA, Meneton P, Metspalu A, Moilanen L, Morris AD, Munroe PB, Njølstad I, Pedersen NL, Power C, Pramstaller PP, Price JF, Psaty BM, Quertermous T, Rauramaa R, Saleheen D, Salomaa V, Sanghera DK, Saramies J, Schwarz PE, Sheu WH, Shuldiner AR, Siegbahn A, Spector TD, Stefansson K, Strachan DP, Tayo BO, Tremoli E, Tuomilehto J, Uusitupa M, van Duijn CM, Vollenweider P, Wallentin L, Wareham NJ, Whitfield JB, Wolffenbuttel BH, Ordovas JM, Boerwinkle E, Palmer CN, Thorsteinsdottir U, Chasman DI, Rotter JI, Franks PW, Ripatti S, Cupples LA, Sandhu MS, Rich SS, **Boehnke M**, Deloukas P, Kathiresan S, Mohlke KL, Ingelsson E, and Abecasis GR (2013) Discovery and refinement of loci associated with lipid levels. *Nature Genetics* 45:1274-1283. PMCID: PMC3838666.

246. Do R, Willer CJ, Schmidt EM, Sengupta S, Gao C, Peloso GM, Gustafsson S, Kanoni S, Ganna A, Chen J, Buchkovich ML, Mora S, Beckmann JS, Bragg-Gresham JL, Chang HY, Demirkan A, Den Hertog HM, Donnelly LA, Ehret GB, Esko T, Feitosa MF, Ferreira T, Fischer K, Fontanillas P, Fraser RM, Freitag DF, Gurdasani D, Heikkilä K, Hyppönen E, Isaacs A, Jackson AU, Johansson A, Johnson T, Kaakinen M, Kettunen J, Kleber ME, Li X, Luan J, Lyytikäinen LP, Magnusson PK, Mangino M, Mihailov E,

Montasser ME, Müller-Nurasyid M, Nolte IM, O'Connell JR, Palmer CD, Perola M, Petersen AK, Sanna S, Saxena R, Service SK, Shah S, Shungin D, Sidore C, Song C, Strawbridge RJ, Surakka I, Tanaka T, Teslovich TM, Thorleifsson G, Van den Herik EG, Voight BF, Volcik KA, Waite LL, Wong A, Wu Y, Zhang W, Absher D, Asiki G, Barroso I, Been LF, Bolton JL, Bonnycastle LL, Brambilla P, Burnett MS, Cesana G, Dimitriou M, Doney AS, Döring A, Elliott P, Epstein SE, Eyjolfsson GI, Gigante B, Goodarzi MO, Grallert H, Gravito ML, Groves CJ, Hallmans G, Hartikainen AL, Hayward C, Hernandez D, Hicks AA, Holm H, Hung YJ, Illig T, Jones MR, Kaleebu P, Kastelein JJ, Khaw KT, Kim E, Klopp N, Komulainen P, Kumari M, Langenberg C, Lehtimäki T, Lin SY, Lindström J, Loos RJ, Mach F, McArdle WL, Meisinger C, Mitchell BD, Müller G, Nagaraja R, Narisu N, Nieminen TV, Nsubuga RN, Olafsson I, Ong KK, Palotie A, Papamarkou T, Pomilla C, Pouta A, Rader DJ, Reilly MP, Ridker PM, Rivadeneira F, Rudan I, Ruokonen A, Samani N, Scharnagl H, Seeley J, Silander K, Stančáková A, Stirrups K, Swift AJ, Tiret L, Uitterlinden AG, van Pelt LJ, Vedantam S, Wainwright N, Wijmenga C, Wild SH, Willemsen G, Wilsgaard T, Wilson JF, Young EH, Zhao JH, Adair LS, Arveiler D, Assimes TL, Bandinelli S, Bennett F, Bochud M, Boehm BO, Boomsma DI, Borecki IB, Bornstein SR, Bovet P, Burnier M, Campbell H, Chakravarti A, Chambers JC, Chen YD, Collins FS, Cooper RS, Danesh J, Dedoussis G, de Faire U, Feranil AB, Ferrières J, Ferrucci L, Freimer NB, Gieger C, Groop LC, Gudnason V, Gyllensten U, Hamsten A, Harris TB, Hingorani A, Hirschhorn JN, Hofman A, Hovingh GK, Hsiung CA, Humphries SE, Hunt SC, Hveem K, Iribarren C, Järvelin MR, Jula A, Kähönen M, Kaprio J, Kesäniemi A, Kivimaki M, Kooner JS, Koudstaal PJ, Krauss RM, Kuh D, Kuusisto J, Kyvik KO, Laakso M, Lakka TA, Lind L, Lindgren CM, Martin NG, März W, McCarthy MI, McKenzie CA, Meneton P, Metspalu A, Moilanen L, Morris AD, Munroe PB, Njølstad I, Pedersen NL, Power C, Pramstaller PP, Price JF, Psaty BM, Quertermous T, Rauramaa R, Saleheen D, Salomaa V, Sanghera DK, Saramies J, Schwarz PE, Sheu WH, Shuldiner AR, Siegbahn A, Spector TD, Stefansson K, Strachan DP, Tayo BO, Tremoli E, Tuomilehto J, Uusitupa M, van Duijn CM, Vollenweider P, Wallentin L, Wareham NJ, Whitfield JB, Wolffenbuttel BH, Altshuler D, Ordovas JM, Boerwinkle E, Palmer CN, Thorsteinsdottir U, Chasman DI, Rotter JI, Franks PW, Ripatti S, Cupples LA, Sandhu MS, Rich SS, **Boehnke M**, Deloukas P, Mohlke KL, Ingelsson E, Abecasis GR, Daly MJ, Neale BM, and Kathiresan S (2013) Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics* 45:1345-1352. PMCID: PMC3904346.

247. Ahmad S, Rukh G, Varga TV, Ali A, Kurbasic A, Shungin D, Ericson U, Koivula RW, Chu AY, Rose LM, Ganna A, Qi Q, Stančáková A, Sandholt CH, Elks CE, Curhan G, Jensen MK, Tamimi RM, Allin KH, Jørgensen T, Brage S, Langenberg C, Aadahl M, Grarup N, Linneberg A, Paré G; InterAct Consortium; DIRECT Consortium, Magnusson PK, Pedersen NL, **Boehnke M**, Hamsten A, Mohlke KL, Pasquale LT, Pedersen O, Scott RA, Ridker PM, Ingelsson E, Laakso M, Hansen T, Qi L, Wareham NJ, Chasman DI, Hallmans G, Hu FB, Renström F, Orho-Melander M, and Franks PW (2013) Gene × physical activity interactions in obesity: combined analysis of 111,421 individuals of European ancestry. *PLoS Genetics* 9:e1003607. PMCID: PMC3723486.

248. Bonnycastle LL, Chines PS, Hara T, Huyghe JR, Swift AJ, Heikinheimo P, Mahadevan J, Peltonen S, Huopio H, Nuutila P, Narisu N, Goldfeder RL, Stitzel ML, Lu S, **Boehnke**

M, Urano F, Collins FS, and Laakso M (2013) Autosomal dominant diabetes arising from a wolfram syndrome 1 mutation. *Diabetes* 62:3943-3950. PMCID: PMC3806620.

249. Hu Y-J, Berndt SI, Gustafsson S, Mägi R, Ganna A, Wheeler E, Feitosa MF, Justice AE, Monda KL, Croteau-Chonka DC, Day FR, Esko T, Fall T, Ferreira T,Gentilini D, Jackson AU, Luan J, Randall JC, Vedantam S, Willer CJ, Winkler TW, Wood AR, Workalemahu T, Hu YJ, Lee SH, Liang L, Lin DY, Min JL, Neale BM, Thorleifsson G, Yang J, Albrecht E, Amin N, Bragg-Gresham JL, Cadby G, den Heijer M, Eklund N, Fischer K, Goel A, Hottenga JJ,Huffman JE, Jarick I, Johansson A, Johnson T, Kanoni S, Kleber ME, König IR, Kristiansson K, Kutalik Z, Lamina C, Lecoeur C, Li G, Mangino M, McArdle WL, Medina-Gomez C, Müller-Nurasyid M, Ngwa JS, Nolte IM, Paternoster L, Pechlivanis S, Perola M, Peters MJ, Preuss M, Rose LM, Shi J, Shungin D, Smith AV, Strawbridge RJ, Surakka I, Teumer A, Trip MD, Tyrer J, Van Vliet-Ostaptchouk JV, Vandenput L, Waite LL, Zhao JH, Absher D, Asselbergs FW, Atalay M, Attwood AP, Balmforth AJ, Basart H, Beilby J, Bonnycastle LL, Brambilla P, Bruinenberg M, Campbell H, Chasman DI,Chines PS, Collins FS, Connell JM, Cookson W, de Faire U, de Vegt F, Dei M, Dimitriou M, Edkins S, Estrada K, Evans DM, Farrall M, Ferrario MM,Ferrières J, Franke L, Frau F, Gejman PV, Grallert H, Grönberg H, Gudnason V, Hall AS, Hall P, Hartikainen AL, Hayward C, Heard-Costa NL, Heath AC, Hebebrand J, Homuth G, Hu FB, Hunt SE, Hyppönen E, Iribarren C, Jacobs KB, Jansson JO, Jula A, Kähönen M, Kathiresan S, Kee F, Khaw KT, Kivimaki M, Koenig W, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Laitinen JH, Lakka TA, Langenberg C, Launer LJ, Lind L, Lindström J, Liu J, Liuzzi A, Lokki ML, Lorentzon M, Madden PA, Magnusson PK, Manunta P, Marek D, März W, Mateo Leach I, McKnight B, Medland SE, Mihailov E, Milani L, Montgomery GW, Mooser V, Mühleisen TW, Munroe PB, Musk AW, Narisu N, Navis G, Nicholson G, Nohr EA, Ong KK, Oostra BA,Palmer CN, Palotie A, Peden JF, Pedersen N, Peters A, Polasek O, Pouta A, Pramstaller PP, Prokopenko I, Pütter C, Radhakrishnan A, Raitakari O, Rendon A, Rivadeneira F, Rudan I, Saaristo TE, Sambrook JG, Sanders AR, Sanna S, Saramies J, Schipf S, Schreiber S, Schunkert H, Shin SY,Signorini S, Sinisalo J, Skrobek B, Soranzo N, Stančáková A, Stark K, Stephens JC, Stirrups K, Stolk RP, Stumvoll M, Swift AJ, Theodoraki EV,Thorand B, Tregouet DA, Tremoli E, Van der Klauw MM, van Meurs JB, Vermeulen SH, Viikari J, Virtamo J, Vitart V, Waeber G, Wang Z, Widén E,Wild SH, Willemsen G, Winkelmann BR, Witteman JC, Wolffenbuttel BH, Wong A, Wright AF, Zillikens MC, Amouyel P, Boehm BO, Boerwinkle E,Boomsma DI, Caulfield MJ, Chanock SJ, Cupples LA, Cusi D, Dedoussis GV, Erdmann J, Eriksson JG, Franks PW, Froguel P, Gieger C, Gyllensten U, Hamsten A, Harris TB, Hengstenberg C, Hicks AA, Hingorani A, Hinney A, Hofman A, Hovingh KG, Hveem K, Illig T, Jarvelin MR, Jöckel KH,Keinanen-Kiukaanniemi SM, Kiemeney LA, Kuh D, Laakso M, Lehtimäki T, Levinson DF, Martin NG, Metspalu A, Morris AD, Nieminen MS, Njølstad I, Ohlsson C, Oldehinkel AJ, Ouwehand WH, Palmer LJ, Penninx B, Power C, Province MA, Psaty BM, Qi L, Rauramaa R, Ridker PM, Ripatti S,Salomaa V, Samani NJ, Snieder H, Sørensen TI, Spector TD, Stefansson K, Tönjes A, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P,Vollenweider P, Wallaschofski H, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Abecasis GR, Assimes TL, Barroso I, **Boehnke M**, Borecki IB, Deloukas P, Fox CS, Frayling T, Groop LC, Haritunian T, Heid IM, Hunter D, Kaplan RC, Karpe

F, Moffatt M, Mohlke KL, O'Connell JR, Pawitan Y, Schadt EE, Schlessinger D, Steinthorsdottir V, Strachan DP, Thorsteinsdottir U, van Duijn CM, Visscher PM, Di Blasio AM, Hirschhorn JN, Lindgren CM, Morris AP, Meyre D, Scherag A, McCarthy MI, Speliotes EK, North KE, Loos RJ, and Ingelsson E (2013) Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics* 93:236-248. PMCID: PMC3738834.

250. Yaghootkar H, Lamina C, Scott RA, Dastani Z, Hivert MF, Warren LL, Stancáková A, Buxbaum SG, Lyytikäinen LP, Henneman P, Wu Y, Cheung CY, Pankow JS, Jackson AU, Gustafsson S, Zhao JH, Ballantyne CM, Xie W, Bergman RN, **Boehnke** M, el Bouazzaoui F, Collins FS, Dunn SH, Dupuis J, Forouhi NG, Gillson C, Hattersley AT, Hong J, Kähönen M, Kuusisto J, Kedenko L, Kronenberg F, Doria A, Assimes TL, Ferrannini E, Hansen T, Hao K, Häring H, Knowles JW, Lindgren CM, Nolan JJ, Paananen J, Pedersen O, Quertermous T, Smith U; GENESIS Consortium; RISC Consortium, Lehtimäki T, Liu CT, Loos RJ, McCarthy MI, Morris AD, Vasan RS, Spector TD, Teslovich TM, Tuomilehto J, van Dijk KW, Viikari JS, Zhu N, Langenberg C, Ingelsson E, Semple RK, Sinaiko AR, Palmer CN, Walker M, Lam KS, Paulweber B, Mohlke KL, van Duijn C, Raitakari OT, Bidulescu A, Wareham NJ, Laakso M, Waterworth DM, Lawlor DA, Meigs JB, Richards JB, and Frayling TM (2013) Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. *Diabetes* 62:3589-3598. PMCID: PMC3781444.

251. Randall JC, Winkler TW, Kutalik Z, Berndt SI, Jackson AU, Monda KL, Kilpeläinen TO, Esko T, Mägi R, Li S, Workalemahu T, Feitosa MF, Croteau-Chonka DC, Day FR, Fall T, Ferreira T, Gustafsson S, Locke AE, Mathieson I, Scherag A, Vedantam S, Wood AR, Liang L, Steinthorsdottir V, Thorleifsson G, Dermitzakis ET, Dimas AS, Karpe F, Min JL, Nicholson G, Clegg DJ, Person T, Krohn JP, Bauer S, Buechler C, Eisinger K; DIAGRAM Consortium, Bonnefond A, Froguel P; MAGIC Investigators, Hottenga JJ, Prokopenko I, Waite LL, Harris TB, Smith AV, Shuldiner AR, McArdle WL, Caulfield MJ, Munroe PB, Grönberg H, Chen YD, Li G, Beckmann JS, Johnson T, Thorsteinsdottir U, Teder-Laving M, Khaw KT, Wareham NJ, Zhao JH, Amin N, Oostra BA, Kraja AT, Province MA, Cupples LA, Heard-Costa NL, Kaprio J, Ripatti S, Surakka I, Collins FS, Saramies J, Tuomilehto J, Jula A, Salomaa V, Erdmann J, Hengstenberg C, Loley C, Schunkert H, Lamina C, Wichmann HE, Albrecht E, Gieger C, Hicks AA, Johansson A, Pramstaller PP, Kathiresan S, Speliotes EK, Penninx B, Hartikainen AL, Jarvelin MR, Gyllensten U, Boomsma DI, Campbell H, Wilson JF, Chanock SJ, Farrall M, Goel A, Medina-Gomez C, Rivadeneira F, Estrada K, Uitterlinden AG, Hofman A, Zillikens MC, den Heijer M, Kiemeney LA, Maschio A, Hall P, Tyrer J, Teumer A, Völzke H, Kovacs P, Tönjes A, Mangino M, Spector TD, Hayward C, Rudan I, Hall AS, Samani NJ, Attwood AP, Sambrook JG, Hung J, Palmer LJ, Lokki ML, Sinisalo J, Boucher G, Huikuri H, Lorentzon M, Ohlsson C, Eklund N, Eriksson JG, Barlassina C, Rivolta C, Nolte IM, Snieder H, Van der Klauw MM, Van Vliet-Ostaptchouk JV, Gejman PV, Shi J, Jacobs KB, Wang Z, Bakker SJ, Mateo Leach I, Navis G, van der Harst P, Martin NG, Medland SE, Montgomery GW, Yang J, Chasman DI, Ridker PM, Rose LM, Lehtimäki T, Raitakari O, Absher D, Iribarren C, Basart H, Hovingh KG, Hyppönen E, Power C, Anderson D, Beilby JP, Hui J, Jolley J, Sager H, Bornstein SR, Schwarz PE, Kristiansson

K, Perola M, Lindström J, Swift AJ, Uusitupa M, Atalay M, Lakka TA, Rauramaa R, Bolton JL, Fowkes G, Fraser RM, Price JF, Fischer K, Krjutå Kov K, Metspalu A, Mihailov E, Langenberg C, Luan J, Ong KK, Chines PS, Keinanen-Kiukaanniemi SM, Saaristo TE, Edkins S, Franks PW, Hallmans G, Shungin D, Morris AD, Palmer CN, Erbel R, Moebus S, Nöthen MM, Pechlivanis S, Hveem K, Narisu N, Hamsten A, Humphries SE, Strawbridge RJ, Tremoli E, Grallert H, Thorand B, Illig T, Koenig W, Müller-Nurasyid M, Peters A, Boehm BO, Kleber ME, März W, Winkelmann BR, Kuusisto J, Laakso M, Arveiler D, Cesana G, Kuulasmaa K, Virtamo J, Yarnell JW, Kuh D, Wong A, Lind L, de Faire U, Gigante B, Magnusson PK, Pedersen NL, Dedoussis G, Dimitriou M, Kolovou G, Kanoni S, Stirrups K, Bonnycastle LL, Njølstad I, Wilsgaard T, Ganna A, Rehnberg E, Hingorani A, Kivimaki M, Kumari M, Assimes TL, Barroso I, **Boehnke** M, Borecki IB, Deloukas P, Fox CS, Frayling T, Groop LC, Haritunians T, Hunter D, Ingelsson E, Kaplan R, Mohlke KL, O'Connell JR, Schlessinger D, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, McCarthy MI, Hirschhorn JN, Qi L, Loos RJ, Lindgren CM, North KE, and Heid IM (2013) Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics* 9:e1003500. PMCID: PMC3674993.

252. den Hoed M, Eijgelsheim M, Esko T, Brundel BJ, Peal DS, Evans DM, Nolte IM, Segrè AV, Holm H, Handsaker RE, Westra HJ, Johnson T, Isaacs A, Yang J, Lundby A, Zhao JH, Kim YJ, Go MJ, Almgren P, Bochud M, Boucher G, Cornelis MC, Gudbjartsson D, Hadley D, van der Harst P, Hayward C, den Heijer M, Igl W, Jackson AU, Kutalik Z, Luan J, Kemp JP, Kristiansson K, Ladenvall C, Lorentzon M, Montasser ME, Njajou OT, O'Reilly PF, Padmanabhan S, St Pourcain B, Rankinen T, Salo P, Tanaka T, Timpson NJ, Vitart V, Waite L, Wheeler W, Zhang W, Draisma HH, Feitosa MF, Kerr KF, Lind PA, Mihailov E, Onland-Moret NC, Song C, Weedon MN, Xie W, Yengo L, Absher D, Albert CM, Alonso A, Arking DE, de Bakker PI, Balkau B, Barlassina C, Benaglio P, Bis JC, Bouatia-Naji N, Brage S, Chanock SJ, Chines PS, Chung M, Darbar D, Dina C, Dörr M, Elliott P, Felix SB, Fischer K, Fuchsberger C, de Geus EJ, Goyette P, Gudnason V, Harris TB, Hartikainen AL, Havulinna AS, Heckbert SR, Hicks AA, Hofman A, Holewijn S, Hoogstra-Berends F, Hottenga JJ, Jensen MK, Johansson A, Junttila J, Kääb S, Kanon B, Ketkar S, Khaw KT, Knowles JW, Kooner AS, Kors JA, Kumari M, Milani L, Laiho P, Lakatta EG, Langenberg C, Leusink M, Liu Y, Luben RN, Lunetta KL, Lynch SN, Markus MR, Marques-Vidal P, Mateo Leach I, McArdle WL, McCarroll SA, Medland SE, Miller KA, Montgomery GW, Morrison AC, Müller-Nurasyid M, Navarro P, Nelis M, O'Connell JR, O'Donnell CJ, Ong KK, Newman AB, Peters A, Polasek O, Pouta A, Pramstaller PP, Psaty BM, Rao DC, Ring SM, Rossin EJ, Rudan D, Sanna S, Scott RA, Sehmi JS, Sharp S, Shin JT, Singleton AB, Smith AV, Soranzo N, Spector TD, Stewart C, Stringham HM, Tarasov KV, Uitterlinden AG, Vandenput L, Hwang SJ, Whitfield JB, Wijmenga C, Wild SH, Willemsen G, Wilson JF, Witteman JC, Wong A, Wong Q, Jamshidi Y, Zitting P, Boer JM, Boomsma DI, Borecki IB, van Duijn CM, Ekelund U, Forouhi NG, Froguel P, Hingorani A, Ingelsson E, Kivimaki M, Kronmal RA, Kuh D, Lind L, Martin NG, Oostra BA, Pedersen NL, Quertermous T, Rotter JI, van der Schouw YT, Verschuren WM, Walker M, Albanes D, Arnar DO, Assimes TL, Bandinelli S, **Boehnke** M, de Boer RA, Bouchard C, Caulfield WL, Chambers JC, Curhan G, Cusi D, Eriksson J, Ferrucci L, van Gilst WH, Glorioso N, de Graaf J, Groop L, Gyllensten U, Hsueh WC, Hu FB, Huikuri HV, Hunter DJ, Iribarren C, Isomaa B,

Jarvelin MR, Jula A, Kähönen M, Kiemeney LA, van der Klauw MM, Kooner JS, Kraft P, Iacoviello L, Lehtimäki T, Lokki ML, Mitchell BD, Navis G, Nieminen MS, Ohlsson C, Poulter NR, Qi L, Raitakari OT, Rimm EB, Rioux JD, Rizzi F, Rudan I, Salomaa V, Sever PS, Shields DC, Shuldiner AR, Sinisalo J, Stanton AV, Stolk RP, Strachan DP, Tardif JC, Thorsteinsdottir U, Tuomilehto J, van Veldhuisen DJ, Virtamo J, Viikari J, Vollenweider P, Waeber G, Widen E, Cho YS, Olsen JV, Visscher PM, Willer C, Franke L; Global BPgen Consortium; CARDIoGRAM Consortium, Erdmann J, Thompson JR; PR GWAS Consortium, Pfeufer A; QRS GWAS Consortium, Sotoodehnia N; QT-IGC Consortium, Newton-Cheh C; CHARGE-AF Consortium, Ellinor PT, Stricker BH, Metspalu A, Perola M, Beckmann JS, Smith GD, Stefansson K, Wareham NJ, Munroe PB, Sibon OC, Milan DJ, Snieder H, Samani NJ, and Loos RJ (2013) Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics* 45:621-631. PMCID: PMC3696959.

253. Berndt SI, Gustafsson S, Mägi R, Ganna A, Wheeler E, Feitosa MF, Justice AE, Monda KL, Croteau-Chonka DC, Day FR, Esko T, Fall T, Ferreira T, Gentilini D, Jackson AU, Luan J, Randall JC, Vedantam S, Willer CJ, Winkler TW, Wood AR, Workalemahu T, Hu YJ, Lee SH, Liang L, Lin DY, Min JL, Neale BM, Thorleifsson G, Yang J, Albrecht E, Amin N, Bragg-Gresham JL, Cadby G, den Heijer M, Eklund N, Fischer K, Goel A, Hottenga JJ, Huffman JE, Jarick I, Johansson Å, Johnson T, Kanoni S, Kleber ME, König IR, Kristiansson K, Kutalik Z, Lamina C, Lecoeur C, Li G, Mangino M, McArdle WL, Medina-Gomez C, Müller-Nurasyid M, Ngwa JS, Nolte IM, Paternoster L, Pechlivanis S, Perola M, Peters MJ, Preuss M, Rose LM, Shi J, Shungin D, Smith AV, Strawbridge RJ, Surakka I, Teumer A, Trip MD, Tyrer J, Van Vliet-Ostaptchouk JV, Vandenput L, Waite LL, Zhao JH, Absher D, Asselbergs FW, Atalay M, Attwood AP, Balmforth AJ, Basart H, Beilby J, Bonnycastle LL, Brambilla P, Bruinenberg M, Campbell H, Chasman DI, Chines PS, Collins FS, Connell JM, Cookson WO, de Faire U, de Vegt F, Dei M, Dimitriou M, Edkins S, Estrada K, Evans DM, Farrall M, Ferrario MM, Ferrières J, Franke L, Frau F, Gejman PV, Grallert H, Grönberg H, Gudnason V, Hall AS, Hall P, Hartikainen AL, Hayward C, Heard-Costa NL, Heath AC, Hebebrand J, Homuth G, Hu FB, Hunt SE, Hyppönen E, Iribarren C, Jacobs KB, Jansson JO, Jula A, Kähönen M, Kathiresan S, Kee F, Khaw KT, Kivimäki M, Koenig W, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Laitinen JH, Lakka TA, Langenberg C, Launer LJ, Lind L, Lindström J, Liu J, Liuzzi A, Lokki ML, Lorentzon M, Madden PA, Magnusson PK, Manunta P, Marek D, März W, Mateo Leach I, McKnight B, Medland SE, Mihailov E, Milani L, Montgomery GW, Mooser V, Mühleisen TW, Munroe PB, Musk AW, Narisu N, Navis G, Nicholson G, Nohr EA, Ong KK, Oostra BA, Palmer CN, Palotie A, Peden JF, Pedersen N, Peters A, Polasek O, Pouta A, Pramstaller PP, Prokopenko I, Pütter C, Radhakrishnan A, Raitakari O, Rendon A, Rivadeneira F, Rudan I, Saaristo TE, Sambrook JG, Sanders AR, Sanna S, Saramies J, Schipf S, Schreiber S, Schunkert H, Shin SY, Signorini S, Sinisalo J, Skrobek B, Soranzo N, Stančáková A, Stark K, Stephens JC, Stirrups K, Stolk RP, Stumvoll M, Swift AJ, Theodoraki EV, Thorand B, Tregouet DA, Tremoli E, Van der Klauw MM, van Meurs JB, Vermeulen SH, Viikari J, Virtamo J, Vitart V, Waeber G, Wang Z, Widén E, Wild SH, Willemsen G, Winkelmann BR, Witteman JC, Wolffenbuttel BH, Wong A, Wright AF, Zillikens MC, Amouyel P, Boehm BO, Boerwinkle E, Boomsma DI, Caulfield MJ, Chanock SJ, Cupples LA, Cusi D, Dedoussis GV, Erdmann J, Eriksson JG, Franks PW, Froguel P, Gieger C, Gyllensten

U, Hamsten A, Harris TB, Hengstenberg C, Hicks AA, Hingorani A, Hinney A, Hofman A, Hovingh KG, Hveem K, Illig T, Jarvelin MR, Jöckel KH, Keinanen-Kiukaanniemi SM, Kiemeney LA, Kuh D, Laakso M, Lehtimäki T, Levinson DF, Martin NG, Metspalu A, Morris AD, Nieminen MS, Njølstad I, Ohlsson C, Oldehinkel AJ, Ouwehand WH, Palmer LJ, Penninx B, Power C, Province MA, Psaty BM, Qi L, Rauramaa R, Ridker PM, Ripatti S, Salomaa V, Samani NJ, Snieder H, Sørensen TI, Spector TD, Stefansson K, Tönjes A, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Vollenweider P, Wallaschofski H, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Abecasis GR, Assimes TL, Barroso I, **Boehnke M**, Borecki IB, Deloukas P, Fox CS, Frayling T, Groop LC, Haritunian T, Heid IM, Hunter D, Kaplan RC, Karpe F, Moffatt MF, Mohlke KL, O'Connell JR, Pawitan Y, Schadt EE, Schlessinger D, Steinthorsdottir V, Strachan DP, Thorsteinsdottir U, van Duijn CM, Visscher PM, Di Blasio AM, Hirschhorn JN, Lindgren CM, Morris AP, Meyre D, Scherag A, McCarthy MI, Speliotes EK, North KE, Loos RJ, and Ingelsson E (2013) Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics* 45:501-512. PMCID: PMC3973018.

254. Dimas AS, Lagou V, Barker A, Knowles JW, Mägi R, Hivert MF, Benazzo A, Rybin D, Jackson AU, Stringham HM, Song C, Fischer-Rosinski A, Boesgaard TW, Grarup N, Abbasi FA, Assimes TL, Hao K, Hang X, Lecoeur C, Barroso I, Bonnycastle LL, Böttcher Y, Bumpstead S, Chines PS, Erdos MR, Graessler J, Kovacs P, Morken MA, Narisu N, Payne F, Stancakova A, Swift AJ, Tönies A, Bornstein SR, Cauchi S, Froguel P, Meyre D, Schwarz PE, Häring HU, Smith U, **Boehnke M**, Bergman RN, Collins FS, Mohlke KL, Tuomilehto J, Quertemous T, Lind L, Hansen T, Pedersen O, Walker M, Pfeiffer AF, Spranger J, Stumvoll M, Meigs JB, Wareham NJ, Kuusisto J, Laakso M, Langenberg C, Dupuis J, Watanabe RM, Florez JC, Ingelsson E, McCarthy MI, and Prokopenko I, on behalf of the MAGIC investigators (2014) Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes* 63:2158-2171. PMCID: PMC4030103.

255. Service SK, Teslovich TM, Fuchsberger C, Ramensky V, Yajnik P, Koboldt DC, Larson DE, Zhang Q, Lin L, Welch R, Ding L, McLellan MD, O'Laughlin M, Fronick C, Fulton LL, Magrini V, Swift A, Elliott P, Jarvelin M-R, Kaakinen M, McCarthy MI, Peltonen L, Pouta A, Bonnycastle LL, Collins FS, Narisu N, Stringham HM, Tuomilehto J, Ripatti S, Fulton FS, Sabatti C, Wilson RK, **Boehnke M**, and Freimer NB (2014) Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. *PLoS Genetics* 10:e1004147. PMCID: PMC3907339.

256. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, Tang Z-Z, Bizon C, Lange EM, Smith JD, Turner EH, Jun G, Kang HM, Peloso G, Auer P, Li K, Flannick J, Zhang J, Fuchsberger C, Gaulton K, Lindgren C, Locke A, Manning A, Sim X, Rivas MA, Holmen OL, Gottesman O, Lu Y, Ruderfer D, Stahl EA, Duan Q, Li Y, Durda P, Jiao S, Isaacs A, Hofman A, Bis JC, Correa A, Griswold ME, Jakobsdottir J, Smith AV, Schreiner PJ, Feitosa MF, Zhang Q, Huffman JE, Crosby J, Wassel CL, Do R, Franceschini N, Martin LW, Robinson JG, Assimes TL, Crosslin DR, Rosenthal EA, Tsai M, Rieder MJ, Farlow DN, Folsom AR, Lumley T, Fox ER, Carlson CS, Peters U, Jackson RD, van Duijn CM, Uitterlinden AG, Levy D, Rotter JI, Taylor HA, Gudnason V, Siscovick DS, Fornage M, Borecki IB, Hayward C, Rudan I, Chen YE, Bottinger EP,

Loos RJF, Saetrom P, Hveen K, **Boehnke M**, Groop L, McCarthy M, Meitinger T, Ballantyne CM, Gabriel SB, O'Donnell CJ, Post WS, North KE, Reiner AP, Boerwinkle E, Psaty BM, Altshuler D, Kathiresan S, Lin D-Y, Jarvik GP, Cupples LA, Kooperberg C, Wilson JG, Nickerson DA, Abecasis GR, Rich SS, Tracy RP, Willer CJ, and the NHLBI Opportunity Exome Sequencing Project (2014) Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics* 94:233-245. PMCID: PMC3928660.

257. Flannick J, Thorleifsson G, Beer NL, Jacobs SBR, Grarup N, Burtt NP, Mahajan A, Fuchsberger C, Atzmon G, Benekidtsson R, Blangero J, Bowden DW, Brandslund I, Brosnan J, Burslem F, Chambers J, Cho YS, Christensen C, Douglas DA, Duggirala R, Dymek Z, Farjoun Y, Fennell T, Fontanillas P, Forsén T, Gabriel S, Glaser B, Gudbjartsson DF, Hanis C, Hansen T, Hreidarsson AB, Hveen K, Ingelsson E, Isomaa B, Johansson S, Jørgensen T, Jørgensen ME, Kathiresan S, Kong A, Kooner J, Kravic J, Laakso M, Lee J-Y, Lind L, Lindgren CM, Linneberg A, Masson G, Meitinger T, Mohlke KL, Molven A, Morris AP, Potluri S, Rauramaa R, Ribel-Madsen R, Richard A-M, Rolph T, Salomaa V, Segrè AV, Skärstrand H, Steinthorsdottir V, Stringham HM, Sulem P, Tai ES, Teo YY, Teslovich T, Thorsteinsdottir U, Trimmer JK, Tuomi T, Tuomilehto J, Vaziri-Sani F, Voight BF, Wilson JG, **Boehnke M**, McCarthy MI, Njølstad PR, Pedersen O, Go-T2D Consortium, T2D-GENES Consortium, Groop L, Cox DR, Stefansson K, and Altshuler D (2014) Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics* 46:357-363. PMCID: PMC4051628.

258. DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium; Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium; South Asian Type 2 Diabetes (SAT2D) Consortium; Mexican American Type 2 Diabetes (MAT2D) Consortium; Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic , Samples (T2D-GENES) Consortium, Mahajan A, Go MJ, Zhang W, Below JE, Gaulton KJ, Ferreira T, Horikoshi M, Johnson AD, Ng MC, Prokopenko I, Saleheen D, Wang X, Zeggini E, Abecasis GR, Adair LS, Almgren P, Atalay M, Aung T, Baldassarre D, Balkau B, Bao Y, Barnett AH, Barroso I, Basit A, Been LF, Beilby J, Bell GI, Benediktsson R, Bergman RN, Boehm BO, Boerwinkle E, Bonnycastle LL, Burtt N, Cai Q, Campbell H, Carey J, Cauchi S, Caulfield M, Chan JC, Chang LC, Chang TJ, Chang YC, Charpentier G, Chen CH, Chen H, Chen YT, Chia KS, Chidambaram M, Chines PS, Cho NH, Cho YM, Chuang LM, Collins FS, Cornelis MC, Couper DJ, Crenshaw AT, van Dam RM, Danesh J, Das D, de Faire U, Dedoussis G, Deloukas P, Dimas AS, Dina C, Doney AS, Donnelly PJ, Dorkhan M, van Duijn C, Dupuis J, Edkins S, Elliott P, Emilsson V, Erbel R, Eriksson JG, Escobedo J, Esko T, Eury E, Florez JC, Fontanillas P, Forouhi NG, Forsen T, Fox C, Fraser RM, Frayling TM, Froguel P, Frossard P, Gao Y, Gertow K, Gieger C, Gigante B, Grallert H, Grant GB, Grrop LC, Groves CJ, Grundberg E, Guiducci C, Hamsten A, Han BG, Hara K, Hassanali N, Hattersley AT, Hayward C, Hedman AK, Herder C, Hofman A, Holmen OL, Hovingh K, Hreidarsson AB, Hu C, Hu FB, Hui J, Humphries SE, Hunt SE, Hunter DJ, Hveem K, Hydrie ZI, Ikegami H, Illig T, Ingelsson E, Islam M, Isomaa B, Jackson AU, Jafar T, James A, Jia W, Jockel KH, Jonsson A, Jowett JB, Kadowaki T, Kang HM, Kanoni S, Kao WH, Kathiresan S, Kato N, Katulanda P, Keinanen-Kiukaanniemi KM, Kelly AM, Khan H, Khaw KT, Khor CC, Kim HL, Kim S, Kim YJ, Kinnunen L, Klopp N, Kong A,

Korpi-Hyovalti E, Kowlessur S, Kraft P, Kravic J, Kristensen MM, Krithika S, Kumar A, Kumate J, Kuusisto J, Kwak SH, Laakso M, Lagou V, Lakka TA, Langenberg C, Langford C, Lawrence R, Leander K, Lee JM, Lee NR, Li M, Li X, Li Y, Liang J, Liju S, Lim WY, Lind L, Lindgren CM, Lindholm E, Liu CT, Liu JJ, Lobbens S, Long J, Loos RJ, Lu W, Luan J, Lyssenko V, Ma RC, Maeda S, Magi R, Mannisto S, Matthews DR, Meigs JB, Melander O, Metspalu A, Meyer J, Mirza G, Mihailov E, Moebus S, Mohan V, Mohlke KL, Morris AD, Muhleisen TW, Muller-Nurasyid M, Musk B, Nakamura J, Nakashima E, Navarro P, Ng PK, Nica AC, Nilsson PM, Njolstad I, Nothen MM, Ohnaka K, Ong TH, Owen KR, Palmer CN, Pankow JS, Park KS, Parkin M, Pechlivanis S, Pedersen NL, Peltonen L, Perry JR, Peters A, Pinidiyapathirage JM, Platou CG, Potter S, Price JF, Qi L, Radha V, Rallidis L, Rasheed A, Rathman W, Rauramaa R, Raychaudhuri S, Rayner NW, Rees SD, Rehnberg E, Ripatti S, Robertson N, Roden M, Rossin EJ, Rudan I, Rybin D, Saaristo TE, Salomaa V, Saltevo J, Samuel M, Sanghera DK, Saramies J, Scott J, Scott LJ, Scott RA, Segre AV, Sehmi J, Sennblad B, Shah N, Shah S, Shera AS, Shu XO, Shuldiner AR, Sigurdsson G, Sijbrands E, Silveira A, Sim X, Sivapalaratnam S, Small KS, So WY, Stancáková A, Stefansson K, Steinbach G, Steinthorsdottir V, Stirrups K, Strawbridge RJ, Stringham HM, Sun Q, Suo C, Syvanen AC, Takayanagi R, Takeuchi F, Tay WT, Teslovich TM, Thorand B, Thorleifsson G, Thorsteinsdottir U, Tikkanen E, Trakalo J, Tremoli E, Trip MD, Tsai FJ, Tuomi T, Tuomilehto J, Uitterlinden AG, Valladares-Salgado A, Vedantam S, Veglia F, Voight BF, Wang C, Wareham NJ, Wennauer R, Wickremasinghe AR, Wilsgaard T, Wilson JF, Wiltshire S, Winckler W, Wong TY, Wood AR, Wu JY, Wu Y, Yamamoto K, Yamauchi T, Yang M, Yengo L, Yokota M, Young R, Zabaneh D, Zhang F, Zhang R, Zheng W, Zimmet PZ, Altshuler D, Bowden DW, Cho YS, Cox NJ, Cruz M, Hanis CL, Kooner J, Lee JY, Seielstad M, Teo YY, **Boehnke M**, Parra EJ, Chambers JC, Tai ES, McCarthy MI, and Morris AP (2014) Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics* 46:234-244. PMCID: PMC3969612.

259. Holmen OL, Zhang H, Fan Y, Hovelson DH, Schmidt EM, Zhou W, Guo Y, Zhang J, Langhammer A, Løchen ML, Ganesh SK, Vatten L, Skorpen F, Dalen H, Zhang J, Pennathur S, Chen J, Platou C, Mathiesen EB, Wilsgaard T, Njølstad I, **Boehnke M,** Chen YE, Abecasis GR, Hveem K, and Willer CJ (2014) Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. *Nature Genetics* 46:345-351. PMCID: PMC41269222.

260. Holmen OL, Zhang H, Zhou W, Schmidt E, Hovelson DH, Langhammer A, Løchen ML, Ganesh SK, Mathiesen EB, Vatten L, Platou C, Wilsgaard T, Chen J, Skorpen F, Dalen H, **Boehnke M**, Abecasis GR, Njølstad I, Hveem K, and Willer CJ (2014) No large-effect low-frequency coding variation found for myocardial infarction. *Human Molucular Genetics* 94:223-232. PMCID: PMC4119412.

261. Reppell M, **Boehnke M**, and Zöllner S (2014) The impact of accelerating faster than exponential population growth on genetic variation. *Genetics* 196:819-828. PMCID: PMC3948808.

262. Lim ET, Würtz P, Havulinna AS, Palta P, Tukiainen T, Rehnström K, Esko T, Mägi R, Inouye M, Lappalainen T, Chan Y, Salem RM, Lek M, Flannick J, Sim X, Manning A,

Ladenvall C, Bumpstead S, Hämäläinen E, Aalto K, Maksimow M, Salmi M, Blankenberg S, Ardissino D, Shah S, Horne B, McPherson R, Hovingh GK, Reilly MP, Watkins H, Goel A, Farrall M, Girelli D, Reiner AP, Stitziel NO, Kathiresan S, Gabriel S, Barrett JC, Lehtimäki T, Laakso M, Groop L, Kaprio J, Perola M, McCarthy MI, **Boehnke M**, Altshuler DM, Lindgren CM, Hirschhorn JN, Metspalu A, Freimer NB, Zeller T, Jalkanen S, Koskinen S, Raitakari O, Durbin R, MacArthur DG, Salomaa V, Ripatti S, Daly MJ, Palotie A; Sequencing Initiative Suomi (SISu) Project (2014) Distribution and medical impace of loss-of-function variants in the Finnish founder population. *PLoS Genetics* 10:e1044494. PMCID: PMC4117444.

263. Lee S, Abecasis GR, **Boehnke M**, and Lin X (2014) Rare-variant association analysis: study designs and statistical tests. *American Journal of Human Genetics* 95:5-23. PMCID: PMC4085641.

264. SIGMA Type 2 Diabetes Consortium, Estrada K, Aukrust I, Bjørkhaug L, Burtt NP, Mercader JM, García-Ortiz H, Huerta-Chagoya A, Moreno-Macías H, Walford G, Flannick J, Williams AL, Gómez-Vázquez MJ, Fernandez-Lopez JC, Martínez-Hernández A, Centeno-Cruz F, Mendoza-Caamal E, Revilla-Monsalve C, Islas-Andrade S, Córdova EJ, Soberón X, González-Villalpando ME, Henderson E, Wilkens LR, Le Marchand L, Arellano-Campos O, Ordóñez-Sánchez ML, Rodríguez-Torres M, Rodríguez-Guillén R, Riba L, Najmi LA, Jacobs SB, Fennell T, Gabriel S, Fontanillas P, Hanis CL, Lehman DM, Jenkinson CP, Abboud HE, Bell GI, Cortes ML, **Boehnke M**, González-Villalpando C, Orozco L, Haiman CA, Tusié-Luna T, Aguilar-Salinas CA, Altshuler D, Njølstad PR, Florez JC, and MacArthur DG (2014) Association of a low-frequency variant in HNF1A with type 2 diabetes in a Latino population. *Journal of the American Medical Association* 311:2305-2314. PMCID: PMC4425850.

265. Wang SR, Agarwala V, Flannick J, Chiang CW, Altshuler D; GoT2D Consortium, Hirschhorn JN, Flannick J, Manning A, Hartl C, Fontanillas P, Green T, Banks E, Depristo M, Poplin R, Shakir K, Fennell T, Murphy J, Burtt N, Gabriel S, Altshuler D, Fuchsberger C, Kang HM, Sim X, Ma C, Locke A, Blackwell T, Jackson A, Teslovich T, Stringham H, Chines P, Kwan P, Huyghe J, Tan A, Jun G, Stitzel M, Bergman RN, Bonnycastle L, Tuomilehto J, Collins FS, Scott L, Mohlke K, Abecasis G, **Boehnke M**, Strom T, Gieger C, Müller-Nurasyid M, Grallert H, Kriebel J, Ried J, Hrabé de Angelis M, Huth C, Meisinger C, Peters A, Rathmann W, Strauch K, Meitinger T, Kravic J, Ladenvall C, Toumi T, Isomaa B, Groop L, Gaulton K, Moutsianas L, Rivas M, Pearson R, Mahajan A, Prokopenko I, Kumar A, Perry J, Chen J, Howie B, van de Bunt M, Small K, Lindgren C, Lunter G, Robertson N, Rayner W, Morris A, Buck D, Hattersley A, Spector T, McVean G, Frayling T, Donnelly P, and McCarthy M (2014) Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. *American Journal of Human Genetics* 94:710-720. PMCID: PMC4067550.

266. Kulzer JR, Stitzel ML, Morken MA, Huyghe JR, Fuchsberger C, Kuusisto J, Laakso M, **Boehnke M**, Collins FS, and Mohlke KL (2014) A common functional regulatory variant at a type 2 diabetes locus upregulates ARAP1 expression in the pancreatic beta cell. *American Journal of Human Genetics* 94:186-197. PMCID: PMC3928648.

267. Li S, Mukherjee B, Taylor JM, Rice KM, Wen X, Rice JD, Stringham HM,and **Boehnke M** (2014) The role of environmental heterogeneity in meta-analysis of gene-environment interactions with quantitative traits. *Genetic Epidemiology* doi: 10.1002 /gepi.21810. PMCID: PMC4108593.

268. Garnai SJ, Huyghe JR, Reed DM, Scott KM, Liebmann JM, **Boehnke M**, Richards JE, Ritch R, and Pawar H (2014) Congenital cataracts: de novo gene conversion event in CRYBB2. *Molecular Vision* 20:1579-1593. PMCID: PMC4225141.

269. Jaiswal S, Fontanillas P, Flannick J, Manning A, Grauman PV, Mar BG, Lindsley RC, Mermel CH, Burtt N, Chavez A, Higgins JM, Moltchanov V, Kuo FC, Kluk MJ, Henderson B, Kinnunen L, Koistinen HA, Ladenvall C, Getz G, Correa A, Banahan BF, Gabriel S, Kathiresan S, Stringham HM, McCarthy MI, **Boehnke M**, Tuomilehto J, Haiman C, Groop L, Atzmon G, Wilson JG, Neuberg D, Altshuler D, and Ebert BL (2014) Age-related clonal hematopoiesis associated with adverse outcomes. *New England Journal of Medicine* 372:2488-2498. PMCID: PMC4306669.

270. Wood AR, Esko T, Yang J, Vedantam S, Pers TH, Gustafsson S, Chu AY, Estrada K, Luan J, Kutalik Z, Amin N, Buchkovich ML, Croteau-Chonka DC, Day FR, Duan Y, Fall T, Fehrmann R, Ferreira T, Jackson AU, Karjalainen J, Lo KS, Locke AE, Mägi R, Mihailov E, Porcu E, Randall JC, Scherag A, Vinkhuyzen AA, Westra HJ, Winkler TW, Workalemahu T, Zhao JH, Absher D, Albrecht E, Anderson D, Baron J, Beekman M, Demirkan A, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Fraser RM, Goel A, Gong J, Justice AE, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Lui JC, Mangino M, Mateo Leach I, Medina-Gomez C, Nalls MA, Nyholt DR, Palmer CD, Pasko D, Pechlivanis S, Prokopenko I, Ried JS, Ripke S, Shungin D, Stancáková A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Afzal U, Arnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Bolton JL, Böttcher Y, Boyd HA, Bruinenberg M, Buckley BM, Buyske S, Caspersen IH, Chines PS, Clarke R, Claudi-Boehm S, Cooper M, Daw EW, De Jong PA, Deelen J, Delgado G, Denny JC, Dhonukshe-Rutten R, Dimitriou M, Doney AS, Dörr M, Eklund N, Eury E, Folkersen L, Garcia ME, Geller F, Giedraitis V, Go AS, Grallert H, Grammer TB, Gräßler J, Grönberg H, de Groot LC, Groves CJ, Haessler J, Hall P, Haller T, Hallmans G, Hannemann A, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hemani G, Henders AK, Hillege HL, Hlatky MA, Hoffmann W, Hoffmann P, Holmen O, Houwing-Duistermaat JJ, Illig T, Isaacs A, James AL, Jeff J, Johansen B, Johansson Å, Jolley J, Juliusdottir T, Junttila J, Kho AN, Kinnunen L, Klopp N, Kocher T, Kratzer W, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Lu Y, Lyssenko V, Magnusson PK, Mahajan A, Maillard M, McArdle WL, McKenzie CA, McLachlan S, McLaren PJ, Menni C, Merger S, Milani L, Moayyeri A, Monda KL, Morken MA, Müller G, Müller-Nurasyid M, Musk AW, Narisu N, Nauck M, Nolte IM, Nöthen MM, Oozageer L, Pilz S, Rayner NW, Renstrom F, Robertson NR, Rose LM, Roussel R, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Schunkert H, Scott RA, Sehmi J, Seufferlein T, Shi J, Silventoinen K, Smit JH, Smith AV, Smolonska J, Stanton AV, Stirrups K, Stott DJ, Stringham HM, Sundström J, Swertz MA, Syvänen AC, Tayo BO, Thorleifsson G, Tyrer JP, van Dijk S, van Schoor NM, van der Velde N, van Heemst D, van Oort FV, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Waldenberger M, Wennauer R, Wilkens

LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Bergmann S, Biffar R, Blangero J, Boomsma DI, Bornstein SR, Bovet P, Brambilla P, Brown MJ, Campbell H, Caulfield MJ, Chakravarti A, Collins R, Collins FS, Crawford DC, Cupples LA, Danesh J, de Faire U, den Ruijter HM, Erbel R, Erdmann J, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Gansevoort RT, Gejman PV, Gieger C, Golay A, Gottesman O, Gudnason V, Gyllensten U, Haas DW, Hall AS, Harris TB, Hattersley AT, Heath AC, Hengstenberg C, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Hovingh GK, Humphries SE, Hunt SC, Hypponen E, Jacobs KB, Jarvelin MR, Jousilahti P, Jula AM, Kaprio J, Kastelein JJ, Kayser M, Kee F, Keinanen-Kiukaanniemi SM, Kiemeney LA, Kooner JS, Kooperberg C, Koskinen S, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lupoli S, Madden PA, Männistö S, Manunta P, Marette A, Matise TC, McKnight B, Meitinger T, Moll FL, Montgomery GW, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Ouwehand WH, Pasterkamp G, Peters A, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ritchie M, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Sebert S, Sever P, Shuldiner AR, Sinisalo J, Steinthorsdottir V, Stolk RP, Tardif JC, Tönjes A, Tremblay A, Tremoli E, Virtamo J, Vohl MC; Electronic Medical Records and Genomics (eMEMERGEGE) Consortium; MIGen Consortium; PAGEGE Consortium; LifeLines Cohort Study, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hayes MG, Hui J, Hunter DJ, Hveem K, Jukema JW, Kaplan RC, Kivimaki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Powell JE, Power C, Quertermous T, Rauramaa R, Reinmaa E, Ridker PM, Rivadeneira F, Rotter JI, Saaristo TE, Saleheen D, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Strauch K, Stumvoll M, Tuomilehto J, Uusitupa M, van der Harst P, Völzke H, Walker M, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Zanen P, Deloukas P, Heid IM, Lindgren CM, Mohlke KL, Speliotes EK, Thorsteinsdottir U, Barroso I, Fox CS, North KE, Strachan DP, Beckmann JS, Berndt SI, **Boehnke M**, Borecki IB, McCarthy MI, Metspalu A, Stefansson K, Uitterlinden AG, van Duijn CM, Franke L, Willer CJ, Price AL, Lettre G, Loos RJ, Weedon MN, Ingelsson E, O'Connell JR, Abecasis GR, Chasman DI, Goddard ME, Visscher PM, Hirschhorn JN, and Frayling TM (2014) Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics* 46:1173-1186. PMCID: PMC4250049.

271. Majithia AR, Flannick J, Shahinian P, Guo M, Bray MA, Fontanillas P, Gabriel SB; GoT2D Consortium; NHGRI JHS/FHS Allelic Spectrum Project; SIGMA T2D Consortium; T2D-GENES Consortium, Rosen ED, and Altshuler D (2014) Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proceedings of the National Academy of Sciences USA* 111:13127-13132. PMCID: PMC4246964.

272. H3Africa Consortium, Rotimi C, Abayomi A, Abimiku A, Adabayeri VM, Adebamowo C, Adebiyi E, Ademola AD, Adeyemo A, Adu D, Affolabi D, Agongo G, Ajayi S,

Akarolo-Anthony S, Akinyemi R, Akpalu A, Alberts M, Alonso Betancourt O, Alzohairy AM, Ameni G, Amodu O, Anabwani G, Andersen K, Arogundade F, Arulogun O, Asogun D, Bakare R, Balde N, Baniecki ML, Beiswanger C, Benkahla A, Bethke L, **Boehnke M**, Boima V, Brandful J, Brooks AI, Brosius FC, Brown C, Bucheton B, Burke DT, Burnett BG, Carrington-Lawrence S, Carstens N, Chisi J, Christoffels A, Cooper R, Cordell H, Crowther N, Croxton T, de Vries J, Derr L, Donkor P, Doumbia S, Duncanson A, Ekem I, El Sayed A, Engel ME, Enyaru JC, Everett D, Fadlelmola FM, Fakunle E, Fischbeck KH, Fischer A, Folarin O, Gamieldien J, Garry RF, Gaseitsiwe S, Gbadegesin R, Ghansah A, Giovanni M, Goesbeck P, Gomez-Olive FX, Grant DS, Grewal R, Guyer M, Hanchard NA, Happi CT, Hazelhurst S, Hennig BJ, Hertz- C, Fowler, Hide W, Hilderbrandt F, Hugo-Hamman C, Ibrahim ME, James R, Jaufeerally-Fakim Y, Jenkins C, Jentsch U, Jiang PP, Joloba M, Jongeneel V, Joubert F, Kader M, Kahn K, Kaleebu P, Kapiga SH, Kassim SK, Kasvosve I, Kayondo J, Keavney B, Kekitiinwa A, Khan SH, Kimmel P, King MC, Kleta R, Koffi M, Kopp J, Kretzler M, Kumuthini J, Kyobe S, Kyobutungi C, Lackland DT, Lacourciere KA, Landouré G, Lawlor R, Lehner T, Lesosky M, Levitt N, Littler K, Lombard Z, Loring JF, Lyantagaye S, Macleod A, Madden EB, Mahomva CR, Makani J, Mamven M, Marape M, Mardon G, Marshall P, Martin DP, Masiga D, Mason R, Mate-Kole M, Matovu E, Mayige M, Mayosi BM, Mbanya JC, McCurdy SA, McCarthy MI, McIlleron H, Mc'Ligeyo SO, Merle C, Mocumbi AO, Mondo C, Moran JV, Motala A, Moxey-Mims M, Mpoloka WS, Msefula CL, Mthiyane T, Mulder N, Mulugeta Gh, Mumba D, Musuku J, Nagdee M, Nash O, Ndiaye D, Nguyen AQ, Nicol M, Nkomazana O, Norris S, Nsangi B, Nyarko A, Nyirenda M, Obe E, Obiakor R, Oduro A, Ofori- SF, Ogah O, Ogendo S, Ohene-Frempong K, Ojo A, Olanrewaju T, Oli J, Osafo C, Ouwe Missi Oukem-Boyer O, Ovbiagele B, Owen A, Owolabi MO, Owolabi L, Owusu-Dabo E, Pare G, Parekh R, Patterton HG, Penno MB, Peterson J, Pieper R, Plange-Rhule J, Pollak M, Puzak J, Ramesar RS, Ramsay M, Rasooly R, Reddy S, Sabeti PC, Sagoe K, Salako T, Samassékou O, Sandhu MS, Sankoh O, Sarfo FS, Sarr M, Shaboodien G, Sidibe I, Simo G, Simuunza M, Smeeth L, Sobngwi E, Soodyall H, Sorgho H, Sow Bah O, Srinivasan S, Stein DJ, Susser ES, Swanepoel C, Tangwa G, Tareila A, Tastan Bishop O, Tayo B, Tiffin N, Tinto H, Tobin E, Tollman SM, Traoré M, Treadwell MJ, Troyer J, Tsimako-Johnstone M, Tukei V, Ulasi I, Ulenga N, van Rooyen B, Wachinou AP, Waddy SP, Wade A, Wayengera M, Whitworth J, Wideroff L, Winkler CA, Winnicki S, Wonkam A, Yewondwos M, sen T, Yozwiak N, and Zar H (2014) Research capacity. Enabling the genomic revolution in Africa. *Science* 344:1346-1348. PMCID: PMC4138491.

273. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR, Powell C, Vedantam S, Buchkovich ML, Yang J, Croteau-Chonka DC, Esko T, Fall T, Ferreira T, Gustafsson S, Kutalik Z, Luan J, Mägi R, Randall JC, Winkler TW, Wood AR, Workalemahu T, Faul JD, Smith JA, Zhao JH, Zhao W, Chen J, Fehrmann R, Hedman AK, Karjalainen J, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bolton JL, Bragg-Gresham JL, Buyske S, Demirkan A, Deng G, Ehret GB, Feenstra B, Feitosa MA, Fischer K, Goel A, Gong J, Jackson AU, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Mangino M, Leach IM, Medina-Gomez C, Medland SE, Nalls MA, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Shungin D, Stančákova A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Isaacs A, Albrecht E, Löic J, Arscott GM,

Attwood AP, Bandinelli S, Barrett A, Bas IN, Bellis C, Bennett AJ, Berne C, Blagieva R, Blüher M, Böhringer S, Bonnycastle LL, Böttcher Y, Boyd HA, Bruinenberg M, Caspersen IH, Chen YI, Clarke R, Daw W, de Craen AJM, Delgado G, Dimitriou M, Doney ASF, Eklund N, Estrada K, Eury E, Foldersen L, Fraser RM, Garcia ME, Geller F, Giedraitis V, Gigante B, Go AS, Golay A, Goodall AH, Gordon SD, Gorski M, Grabe H-J, Grallert H, Grammer TB, Gräbler J, Grönberg H, Groves CJ, Gusto G, Haessler J, Hall P, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hengstenberg C, Holmen O, Hottenga J-J, James AL, Jeff JM, Johansson A, Jolley J, Juliusdottir T, Kinnunen L, Koenig W, Koskenvuo M, Kratzer W, Laitinen J, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lo KA, Lobbens S, Lorbeer R, Lu Y, Mach F, Magnusson PKE, Mahajan A, McArdle WL, McLachlan S, Menni C, Merger S, Mihailov E, Milani L, Moayyeri A, Monda KL, Morken MA, Mulas A, Müller G, Müller-Nurasyid M, Musk AW, Nagaraja R, Nöthen MM, Nolte IM, Pilz S, Rayner MW, Renstrom R, Rettig R, Ried JS, Ripke S, Robertson NR, Rose LM, Sanna S, Scharnag H, Scholtens S, Schumacher FR, Scott WR, Seufferlein R, Shi J, Smith AV, Smolonska J, Stanton AV, Steinthorsdottir V, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen A-C, Tan S-T, Tayo BO, Thorand B, Thorleifsson G, Tyrer JP, Uh H-W, Vandenput L, Frank C. Verhulst FC, Vermeulen SH, Zerweij N, Vonk JM, Waite LL, Warren HR, Waterworth D, Weedon MN, Wilkins LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q, The LifeLines Cohort Study, Brennan EP, Choi M, Dastani Z, Drong AW, Eriksson P, Franco-Cereceda A, Gådin JR, Gharavi AG, Goddard ME, Handsaker RE, Huang J, Karpe F, Kathiresan S, Keildson S, Kiryluk K, Kubo M, Lee J-Y, Liang L, Lifton RP, Ma B, McCarroll SA, McKnight AJ, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Okada Y, Perry JRB, Dorajoo R, Reinmaa E, Salem RM, Sandholm N, Scott RA, Stolk L, Takahashi A, Tanaka T, van't Hooft FM, Vinkhuyzen AAE, Westra H-J, Zheng W, Zondervan KT, The ADIPOGen Consortium, The AGEN-BMI Working Group, The CARDIOGRAMplusC4D Consortium, The CKDGen Consortium, The GLGC, The ICBP, The MAGIC Investigators, The MuTHER Consortium, The MIGen Consortium, The PAGE Consortium, The ReproGen Consortium, The GENIE Consortium, The International Endogene Consortium, Heath AC, Arveiler D, Bakker SJL, Beilby J, Bergman RN, Blangero J, Bovet P, Campbell H, Caulfield MJ, Cesana G, Chakravarti A, Chasman DI, Chines PS, Collins FS, Crawford DC, Cupples LA, Cusi D, Danesh J, de Faire U, den Ruijter HM, Dominiczak AF, Erbel R, Erdmann J, Eriksson JG, Farrall M, Felix SB, Ferrannini E, Jean Ferrières J, Ford I, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gejman RV, Gieger C, Gottesman O, Gudnason V, Zyllensten U, Hall AS, Harris TB, Hattersley AT, Hicks AA, Hindorff LA, Hingorani AD, Hofman5 A, Homuth G, Hovingh K, Humphries SE, Hunt SC, Elina Hyppönen E, Illig T, Jacobs KB, Jarvelin J-R, Karl-Heinz Jökel K-H, Johansen B, Jousilahti P, Jukema W, Jula AM, Kaprio J, Kastelein JP, Keinanen-Kiukaanniemi SM, Kiemeney LA, Knekt P, Kooner JA, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Moll FL, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Madden PAF, Pasterkamp G, Peden JF, Peters A, Postma DS, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen R, Rao DC, Rice TK, Ridker PM, Rioux JD, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies

J, Sarzynski MA, Schunkert H, Schwarz PEH, Sever P, Shuldiner AR, Sinisalo J, Stolk RP, Strauch K, Tönjes A, Trégouët D-A, Tremblay A, Tremoli E, Virtamo J, Voh M-C, Völker U, Waeber G, Willemsen G, Witteman JC, Zillikens MC, Adair LS, Amouyel , Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bornstein SR, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PIW, Dedoussis D, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hui J, Hunter DJ, Hveem K, Kaplan RC, Kivimaki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Metspalu A, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CNA, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira R. Saaristo TE, Saleheen D, Sattar N, Schadt EE, Schlessinger D, Slagboom E, Snieder H, Spector TD, Thorsteinsdottir U, Stumvol M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Walker M, Wallaschofski H, Wareham9 NJ, Watkins H, Weir DR, Wichmann HE, Wilson JF, Zanen P, Borecki IB, Deloukas P, Fox CS, Heid IM, O'Connell JR, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, Franke L, Frayling TM, McCarthy MI, Visscher PM, Scherag A, Willer CJ, **Boehnke M**, Mohlke KL, Lindgren CM, Beckmann JS, Barroso I, North KE, Ingelsson E, Hirschhorn JN, Loos RJF, and Speliotes ED (2015) Genetic studies of body mass index yield new insights for obesity biology. *Nature* 518:197-206. PMCID: PMC4382211.

274. F D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, Strawbridge RJ, Pers TH, Fischer K, Justice AE, Workalemahu T, Wu, JMW, Buchkovich ML, Heard-Costa NL, Roman TS, Drong AW, Song C, Gustafsson S, Day FR, Esko T, Fall T, Kutalik Z, Luan J, Randall JC, Scherag A, Vedantam S, Wood AR, Chen J, Fehrmann R, Karjalainen J, Kahali B, Liu C-T, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bragg-Gresham JL, Buyske S, Demirkan A, Ehret GB, Feitosa MF, Goel A, Jackson AU, Johnson T, Kleber ME, Kristiansson K, Mangino M, Leach IM, Medina-Gomez C, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Stančákova A, Sung YJ, Tanaka T, Teumer A, Van Vliet-Ostaptchouk JV, Yeng L, Zhang W, Albrecht E, Ärnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Böhringer S, Bonnet F, Böttcher Y, Bruinenberg M, Carba DB, Caspersen IH, Clarke R, WarwickDaw E, Deelen J, Deelman E, Delgado G, Doney ASF, Eklund N, Erdos MR, Estrada K, Eury E, Friedrich N, Garcia ME, Giedraitis V, Gigante B, Go AS, Golay A, Graller H, Grammer TB, Gräsler J, Grewal J, Grover CJ, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heikkilä K, Herzig K-H, Helmer Q, Hillege HL, Holmen O, Hunt SC, Isaacs A, Ittermann T, James AL, Johansson I, Juliusdottir T, Kalafati I-P, Kinnunen L, Koenig W, Kooner IK, Kratzer W, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Mach F, Magnusson PKE, Mahajan A, McArdle WL, Menni C, Merger S, Mihailov E, Milani L, Mills R, Moayyeri A, Monda KL, Mooijaart SP, Mühleisen TW, Mulas A, Müller G, Müller-Nurasyid M, Nagaraja R, Nalls MA, Narisu N, Glorioso N, Nolte IM, Olden M, Rayner NW, Renstrom F, Reid JS, Robertson NR, Rose LM, Sanna1 S, Scharnag H, Scholtens S, Sennblad B, Seufferlein T, Sitlani CM, Smith AV, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen A-C, Tayo BA, Thorand B, Thorleifsson G, Tomaschitz A, Troffa C, van Oort FVA, Verweij N, Vonk JM, Waite LL, Wennauer R, Wilsgaard T, Wojczynski MK, Wong A, Zhang Q, Zhao JH, Brennan EP, Choi M, Eriksson P, Folkersen L, Franco-Cereceda A, Gharavi AG, Hedman AK, Hivert M-F, Huang J, Kanoni S, Karpe F,

Keildson S, Kiryluk K, Liang, L, Lifton RP, Ma B, McKnight AJ, McPherson R, Metspalu A, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Olsson C, Perry JRB, Reinmaa E, Salem RM, Sandholm N, Schadt EE, Scott RA, Stolk L, Vallejo EE, Westra H-J, Zondervan KT, The ADIPOGen Consortium, The ARDIOGRAMplusC4D Consortium, The CKDGen Consortium, The GEFOS Consortium, The GENIE Consortium, The GLGC, The ICBP, The International Endogene Consortium, The LifeLines Cohort Study, The MAGIC Investigators, The MuTHER Consortium, The PAGE Consortium, The ReproGen Consortium, Amouyel P, Arveiler D, Bakker SJL, Beilby J, Bergman RN, Blangero J, Brown MJ, Burnier M, Campbell H, Chakravarti A, Chines PS, Claudi-Boehm S, Collins FS, Crawford DC, Danesh J, de Faire U, de Geus EJC, Dörr M, Erbell R, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gieger C, Gudnason V, Haiman CA, Harris RB, Hattersley AT, Heliövaara M, Hicks AA, Hingorani AD, Hoffmann W, Hofman A, Homuth G, Humphries SE, Hyppönen E, Illig T, Jarvelin MR, Johansen B, Jousilahti P, Jula AM, Kaprio J, Kee F, Keinanen-Kiukaanniemi SM, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Lakka TA, Langenberg C, Marchand LL, 224, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Musk AW, Möhlenkamp S, Morris AD, Neli M, Ohlsson C, Oldehinkel AJ, Ong KK, Palmer LJ, Penninx BW, Peters A, Pramstaller PP, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PEH, Shuldiner AR, Staessen JA, Steinthorsdottir V, Stolk RP, Strauch K, Tönjes A, Tremblay A, Tremoli E, Vohl M-C, Völker U, Vollenweider P, Wilson JF, Witteman JC, Adair LS, Bochud M, Boehm BO, Bornstein SR, Bouchard C, Cauchi S, Caulfield MJ, Chambers JC, Chasman DI, Cooper RS, Dedoussis G, Ferrucci L, Froguel P, Grabe H-J, Hamsten A, Hui J, Hveem1 K, Jöckel K-H, Kivimaki M, Kuh D, Laakso M, Liu Y, März W, Munroe PB, Njolstad I, Oostra BA, Palmer CAN, Pedersen NL, Perola M, Louis Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sinisalo J, Slagboom E, Sneider H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Veronesi G, Walker M, Wareham NJ, Watkins H, Wichmann H-E, Abecasis GR, Assimes TL, Berndt SI, **Boehnke M**, Borecki IB, Deloukas P, Franke L, Frayling TM, Groop LC, Hunter DJ, Kaplan RC, O'Connell JR, Qi L, Schlessinger D, Strachan DP, Stefansson K, van Duijn CM, Willer CJ, Visscher PM, Yang J, Hirschhorn JN, Zillikens MC, McCarthy MI, Speliotes EK, North KE, Fox CS, Barroso I, Franks PW, Ingelsson E, Heid IM, Loos RJF, Cupples LA, Morris AP, Lindgren CM, and Mohlke KL (2015) New genetic loci link adipose and insulin biology to body fat distribution. *Nature* 518:187-196. PMCID: PMC4338562.

275. Wang Y, Liu A, Mills JL, **Boehnke M**, Wilson AF, Bailey-Wilson JE, Xiong M, Wu CO, and Fan R (2015) Pleiotropy analysis of quantitative traits at gene level by multivarite functional linear models. *Genetic Epidemiology* 39:259-275. PMCID: PMC4443751.

276. Wessel J, Chu AY, Willems SM, Wang S, Yaghootkar H, Brody JA, Dauriz M, Hivert MF, Raghavan S, Lipovich L, Hidalgo B, Fox K, Huffman JE, An P, Lu Y, Rasmussen-Torvik LJ, Grarup N, Ehm MG, Li L, Baldridge AS, Stančáková A, Abrol R, Besse C, Boland A, Bork-Jensen J, Fornage M, Freitag DF, Garcia ME, Guo X, Hara K, Isaacs A,

Jakobsdottir J, Lange LA, Layton JC, Li M, Hua Zhao J, Meidtner K, Morrison AC, Nalls MA, Peters MJ, Sabater-Lleal M, Schurmann C, Silveira A, Smith AV, Southam L, Stoiber MH, Strawbridge RJ, Taylor KD, Varga TV, Allin KH, Amin N, Aponte JL, Aung T, Barbieri C, Bihlmeyer NA, **Boehnke M**, Bombieri C, Bowden DW, Burns SM, Chen Y, Chen YD, Cheng CY, Correa A, Czajkowski J, Dehghan A, Ehret GB, Eiriksdottir G, Escher SA, Farmaki AE, Frånberg M, Gambaro G, Giulianini F, Goddard WA 3rd, Goel A, Gottesman O, Grove ML, Gustafsson S, Hai Y, Hallmans G, Heo J, Hoffmann P, Ikram MK, Jensen RA, Jørgensen ME, Jørgensen T, Karaleftheri M, Khor CC, Kirkpatrick A, Kraja AT, Kuusisto J, Lange EM, Lee IT, Lee WJ, Leong A, Liao J, Liu C, Liu Y, Lindgren CM, Linneberg A, Malerba G, Mamakou V, Marouli E, Maruthur NM, Matchan A, McKean-Cowdin R, McLeod O, Metcalf GA, Mohlke KL, Muzny DM, Ntalla I, Palmer ND, Pasko D, Peter A, Rayner NW, Renström F, Rice K, Sala CF, Sennblad B, Serafetinidis I, Smith JA, Soranzo N, Speliotes EK, Stahl EA, Stirrups K, Tentolouris N, Thanopoulou A, Torres M, Traglia M, Tsafantakis E, Javad S, Yanek LR, Zengini E, Becker DM, Bis JC, Brown JB, Cupples LA, Hansen T, Ingelsson E, Karter AJ, Lorenzo C, Mathias RA, Norris JM, Peloso GM, Sheu WH, Toniolo D, Vaidya D, Varma R, Wagenknecht LE, Boeing H, Bottinger EP, Dedoussis G, Deloukas P, Ferrannini E, Franco OH, Franks PW, Gibbs RA, Gudnason V, Hamsten A, Harris TB, Hattersley AT, Hayward C, Hofman A, Jansson JH, Langenberg C, Launer LJ, Levy D, Oostra BA, O'Donnell CJ, O'Rahilly S, Padmanabhan S, Pankow JS, Polasek O, Province MA, Rich SS, Ridker PM, Rudan I, Schulze MB, Smith BH, Uitterlinden AG, Walker M, Watkins H, Wong TY, Zeggini E; EPIC-InterAct Consortium, Laakso M, Borecki IB, Chasman DI, Pedersen O, Psaty BM, Tai ES, van Duijn CM, Wareham NJ, Waterworth DM, Boerwinkle E, Kao WH, Florez JC, Loos RJ, Wilson JG, Frayling TM, Siscovick DS, Dupuis J, Rotter JI, Meigs JB, Scott RA, and Goodarzi MO (2015) Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications* 6:5897. PMCID: PMC4311266.

277. Mahajan A, Sim X, Ng HJ, Manning A, Rivas MA, Highland HM, Locke AE, Grarup N, Im HK, Cingolani P, Flannick J, Fontanillas P, Fuchsberger C, Gaulton KJ, Teslovich TM, Rayner NW, Robertson NR, Beer NL, Rundle JK, Bork-Jensen J, Ladenvall C, Blancher C, Buck D, Buck G, Burtt NP, Gabriel S, Gjesing AP, Groves CJ, Hollensted M, Huyghe JR, Jackson AU, Jun G, Justesen JM, Mangino M, Murphy J, Neville M, Onofrio R, Small KS, Stringham HM, Syvänen AC, Trakalo J, Abecasis G, Bell GI, Blangero J, Cox NJ, Duggirala R, Hanis CL, Seielstad M, Wilson JG, Christensen C, Brandslund I, Rauramaa R, Surdulescu GL, Doney AS, Lannfelt L, Linneberg A, Isomaa B, Tuomi T, Jørgensen ME, Jørgensen T, Kuusisto J, Uusitupa M, Salomaa V, Spector TD, Morris AD, Palmer CN, Collins FS, Mohlke KL, Bergman RN, Ingelsson E, Lind L, Tuomilehto J, Hansen T, Watanabe RM, Prokopenko I, Dupuis J, Karpe F, Groop L, Laakso M, Pedersen O, Florez JC, Morris AP, Altshuler D, Meigs JB, **Boehnke M**, McCarthy MI, Lindgren CM, Gloyn AL; T2D-GENES consortium and GoT2D consortium (2015) Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. *PloS Genetics* 11:e1004876. PMCID: PMC4307976.

278. Pers TH, Karjalainen JM, Chan Y, Westra HJ, Wood AR, Yang J, Lui JC, Vedantam S, Gustafsson S, Esko T, Frayling T, Speliotes EK; Genetic Investigation of

ANthropometric Traits (GIANT) Consortium, **Boehnke M**, Raychaudhuri S, Fehrmann RS, Hirschhorn JN, and Franke L (2015) Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications* 6:5890. PMCID: PMC4420238.

279. Moutsianas L, Agarwala V, Fuchsberger C, Flannick J, Rivas MA, Gaulton KJ, Albers PK, Go T2D Consortium, McVean G, **Boehnke M**, Altshuler D, and McCarthy MI (2015) The power of gene-based rare varient methods to detect disease-associated variation and test hypotheses About Complex Disease. *PloS Genetics* 11:e1005165. PMCID: PMC4407972.

280. Fan R, Wang Y, **Boehnke M**, Chen W, Li Y, Ren H, Lobach I, and Xiong M (2015) Gene level meta-analysis of quantitative traits by functional linear models. *Genetics* doi:10.1534/genetics. PMID: 26058849.

281. Usher CL, Handsaker RE, Esko T, Tuke MA, Weedon MN, Hastie AR, Cao H, Moon JE, Kashin S, Fuchsberger C, Metspalu A, Pato CN, Pato MT, McCarthy MI, **Boehnke M**, Altshuler DM, Frayling TM, Hirschhorn JN, and McCarroll SA (2015) Structural forms of the human amylase locus and their relationships to SNPs, haplotypes, and obesity. *Nature Genetics* doi:10.1038/ng.3340. PMID: 26098870.

282. Joshi PK, Esko T, Mattsson H, Eklund N, Gandin I, Nutile T, Jackson AU, Schurmann C, Smith AV, Zhang W, Okada Y, Stančáková A, Faul JD, Zhao W, Bartz TM, Concas MP, Franceschini N, Enroth S, Vitart V, Trompet S, Guo X, Chasman DI, O'Connel JR, Corre T, Nongmaithem SS, Chen Y, Mangino M, Ruggiero D, Traglia M, Farmaki AE, Kacprowski T, Bjonnes A, van der Spek A, Wu Y, Giri AK, Yanek LR, Wang L, Hofer E, Rietveld CA, McLeod O, Cornelis MC, Pattaro C, Verweij N, Baumbach C, Abdellaoui A, Warren HR, Vuckovic D, Mei H, Bouchard C, Perry JR, Cappellani S, Mirza SS, Benton MC, Broeckel U, Medland SE, Lind PA, Malerba G, Drong A, Yengo L, Bielak LF, Zhi D, van der Most PJ, Shriner D, Mägi R, Hemani G, Karaderi T, Wang Z, Liu T, Demuth I, Zhao JH, Meng W, Lataniotis L, van der Laan SW, Bradfield JP, Wood AR, Bonnefond A, Ahluwalia TS, Hall LM, Salvi E, Yazar S, Carstensen L, de Haan HG, Abney M, Afzal U, Allison MA, Amin N, Asselbergs FW, Bakker SJ, Barr RG, Baumeister SE, Benjamin DJ, Bergmann S, Boerwinkle E, Bottinger EP, Campbell A, Chakravarti A, Chan Y, Chanock SJ, Chen C, Chen YI, Collins FS, Connell J, Correa A, Cupples LA, Smith GD, Davies G, Dörr M, Ehret G, Ellis SB, Feenstra B, Feitosa MF, Ford I, Fox CS, Frayling TM, Friedrich N, Geller F, Scotland G, Gillham-Nasenya I, Gottesman O, Graff M, Grodstein F, Gu C, Haley C, Hammond CJ, Harris SE, Harris TB, Hastie ND, Heard-Costa NL, Heikkilä K, Hocking LJ, Homuth G, Hottenga JJ, Huang J, Huffman JE, Hysi PG, Ikram MA, Ingelsson E, Joensuu A, Johansson Å, Jousilahti P, Jukema JW, Kähönen M, Kamatani Y, Kanoni S, Kerr SM, Khan NM, Koellinger P, Koistinen HA, Kooner MK, Kubo M, Kuusisto J, Lahti J, Launer LJ, Lea RA, Lehne B, Lehtimäki T, Liewald DC, Lind L, Loh M, Lokki ML, London SJ, Loomis SJ, Loukola A, Lu Y, Lumley T, Lundqvist A, Männistö S, Marques-Vidal P, Masciullo C, Matchan A, Mathias RA, Matsuda K, Meigs JB, Meisinger C, Meitinger T, Menni C, Mentch FD, Mihailov E, Milani L, Montasser ME, Montgomery GW, Morrison A, Myers RH, Nadukuru R, Navarro P, Nelis M, Nieminen MS, Nolte IM, O'Connor GT, Ogunniyi

A, Padmanabhan S, Palmas WR, Pankow JS, Patarcic I, Pavani F, Peyser PA, Pietilainen K, Poulter N, Prokopenko I, Ralhan S, Redmond P, Rich SS, Rissanen H, Robino A, Rose LM, Rose R, Sala C, Salako B, Salomaa V, Sarin AP, Saxena R, Schmidt H, Scott LJ, Scott WR, Sennblad B, Seshadri S, Sever P, Shrestha S, Smith BH, Smith JA, Soranzo N, Sotoodehnia N, Southam L, Stanton AV, Stathopoulou MG, Strauch K, Strawbridge RJ, Suderman MJ, Tandon N, Tang ST, Taylor KD, Tayo BO, Töglhofer AM, Tomaszewski M, Tšernikova N, Tuomilehto J, Uitterlinden AG, Vaidya D, van Hylckama Vlieg A, van Setten J, Vasankari T, Vedantam S, Vlachopoulou E, Vozzi D, Vuoksimaa E, Waldenberger M, Ware EB, Wentworth-Shields W, Whitfield JB, Wild S, Willemsen G, Yajnik CS, Yao J, Zaza G, Zhu X; BioBank Japan Project, Salem RM, Melbye M, Bisgaard H, Samani NJ, Cusi D, Mackey DA, Cooper RS, Froguel P, Pasterkamp G, Grant SF, Hakonarson H, Ferrucci L, Scott RA, Morris AD, Palmer CN, Dedoussis G, Deloukas P, Bertram L, Lindenberger U, Berndt SI, Lindgren CM, Timpson NJ, Tönjes A, Munroe PB, Sørensen TI, Rotimi CN, Arnett DK, Oldehinkel AJ, Kardia SL, Balkau B, Gambaro G, Morris AP, Eriksson JG, Wright MJ, Martin NG, Hunt SC, Starr JM, Deary IJ, Griffiths LR, Tiemeier H, Pirastu N, Kaprio J, Wareham NJ, Pérusse L, Wilson JG, Girotto G, Caulfield MJ, Raitakari O, Boomsma DI, Gieger C, van der Harst P, Hicks AA, Kraft P, Sinisalo J, Knekt P, Johannesson M, Magnusson PK, Hamsten A, Schmidt R, Borecki IB, Vartiainen E, Becker DM, Bharadwaj D, Mohlke KL, **Boehnke M**, van Duijn CM, Sanghera DK, Teumer A, Zeggini E, Metspalu A, Gasparini P, Ulivi S, Ober C, Toniolo D, Rudan I, Porteous DJ, Ciullo M, Spector TD, Hayward C, Dupuis J, Loos RJ, Wright AF, Chandak GR, Vollenweider P, Shuldiner AR, Ridker PM, Rotter JI, Sattar N, Gyllensten U, North KE, Pirastu M, Psaty BM, Weir DR, Laakso M, Gudnason V, Takahashi A, Chambers JC, Kooner JS, Strachan DP, Campbell H, Hirschhorn JN, Perola M, Polašek O, and Wilson JF (2015) Directional dominance on stature and cognition in diverse human populations. *Nature* doi:10.1038/nature14618. PMCID: PMC4516141.

283. Mohlke KL and **Boehnke M** (2015) Recent advances in understanding the genetic architecture of type 2 diabetes. *Human Molecular Genetics* doi:10.1093/hmg/ddv264. PMCID: 4572004.

284. Flickinger M, Jun G, Abecasis GR, **Boehnke M**, and Kang HM (2015) Correcting for sample contamination in genotype calling of DNA sequence data. *American Journal of Human Genetics* 97:284-290. PMID: 26235984.

Publications which have not received peer review

1. Chu EHY, **Boehnke M**, and Hanash SM (1987) Application of two-dimensional electrophoresis to the detection of human somatic mutations at the protein level. In *Banbury Report 28: Mammalian Cell Mutagenesis*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, pp. 203-209.

2. Epstein MP and **Boehnke M** (2002) "Relationship Testing", in RC Elston, JM Olson and L Palmer, editors, *Biostatistical Genetics and Genetic Epidemiology*. John Wiley & Sons, Ltd, Chichester, pp. 673-678.

3. **Boehnke M** (2015) Introduction to the 2014 Curt Stern Award: Gonçalo Abecasis. *American Journal of Human Genetics* 96:361-362. PMCID: PMC4375418.

Book reviews/Letters to the editor

1. **Boehnke M** (1990) (Book Review) Multipoint mapping and linkage analysis based upon affected pedigree members: Genetic Analysis Workshop 6 in *Progress in Clinical and Biological Research*, edited by Elston RC, Spence MA, Hodge SE, and MacCluer JW *American Journal of Human Genetics* 47:1031-1032.

2. **Boehnke M** (1991) Letter to the editor: reply to Chakraborty. *American Journal of Human Genetics* 49:243-244.

3. **Boehnke M** (1992) (Book Review) *Analysis of Human Genetic Linkage, Revised Edition*, by Jürg Ott. *American Journal of Human Genetics* 51:917-918.

4. Schork NJ, **Boehnke M**, Terwilliger JD, Ott J (1994) Letter to the Editor: reply to Sham. *American Journal of Human Genetics* 55:856-858.

5. **Boehnke M** (2000) (Book Review) *Analysis of Human Genetic Linkage, Third Edition*, by Jürg Ott. *American Journal of Human Genetics* 66:1725.

PRESENTATIONS

Talks delivered at professional meetings (2001-present)

New developments in statistical methods for human gene mapping. Invited presentation: US-Japan Symposium in the Cardiovascular Area, Honolulu, Hawaii, January 9, 2001.

Strategies to identify genetic variants responsible for a linkage signal for a complex genetic trait. Invited presentation: AACR Oncogenomics, Phoenix, Arizona, January 31, 2003.

Mapping type 2 diabetes genes on chromosome 20: FUSION and beyond. Invited presentation: American Society of Human Genetics, Toronto, Ontario, Canada, October 28, 2004.

Design considerations in large-scale genetic association studies. Invited presentation: American Society of Human Genetics, Salt Lake City, Utah, October 27, 2005.

Efficient designs for genome-wide association studies. Invited presentation: Genome-Wide Association Studies: Design and Analysis. Yale University, New Haven, Connecticut, October 27, 2006.

Efficient study designs for two-stage genome-wide association studies and application to bipolar disorder. Invited plenary presentation: World Congress of Psychiatric Genetics, Cagliari, Sardinia, Italy, October 30, 2006.

Efficient design of genome-wide association studies with application to type 2 diabetes. Invited plenary presentation: International Genetic Epidemiology Society, Tampa, Florida, November 24, 2006.

Design and analysis of genome-wide association studies: application to type 2 diabetes. Invited presentation: Kenneth Lange Symposium, University of California at Los Angeles, Los Angeles, California, February 9, 2007.

Efficient design and analysis of genome-wide association studies. Invited presentation: Joint Statistical Meetings, Salt Lake City, Utah, July 30, 2007.

A genome-wide association study of type 2 diabetes. GAIN Analysis Workshop II, Bethesda, Maryland, October 18, 2007.

Efficient statistical analysis of genome-wide case-control association data. Joint Statistical Meetings, Denver, Colorado, August 5, 2008.

Genome wide association studies of type 2 diabetes and associated traits. American College of Epidemiology, Tucson, Arizona, September 14, 2008.

Advantages and challenges of large samples and meta-analyses in GWAS of type 2 diabetes. American Society of Human Genetics, Philadelphia, Pennsylvania, November 15, 2008.

Differences in approaches to examining low-frequency (0.5-5%) and really-rare (<0.5%) variants. The dark matter of human genome wide association studies, Bethesda, Maryland, February 3, 2009.

Which GWAS signals should be followed up: choosing regions. The Challenge of Mapping GWAS Signals. Bethesda, Maryland, March 24, 2009.

Genome wide association studies of type 2 diabetes and related traits. Indiana Regional Bioinformatics Conference. Indianapolis, Indiana, July 7, 2009.

Genome wide association studies of type 2 diabetes and related traits. PQG Conference, Boston, November 12, 2009.

The genetics of type 2 diabetes. American Society of Human Genetics, Washington, D.C., November 4, 2010.

Design of GWAS and resequencing-based genetic association studies. International Biometric Society Meeting, Florianpolis, Brazil, December 10, 2010.

Identifying genes for type 2 diabetes and related traits. Diabetes Research Symposium. Chuncheon, Korea, September 9, 2010.

Identifying type 2 diabetes associated variants by exome and genome resequencing: progress report. Genomics of Common Diseases. Sanger Institute, Hinxton, UK, August 30, 2011.

Identifying genes for type 2 diabetes and related traits by genome-wide association and sequencing studies. Institute of Psychiatry, King's College, London, United Kingdom, June 21, 2012.

Genetics of type 2 diabetes in divese populations. 1000 Genomes Project Community Meeting. Ann Arbor, Michigan, July 13, 2012.

Identifying genes for type 2 diabetes and related traits by genome-wide association and sequencing studies. University of Copenhagen, Copenhagen, Denmark, August 21, 2012.

Statistical genetics: opportunities and challenges in human gene mapping. University of Southern Denmark, Odense, Denmark, December 6, 2012.

Identifying genes for type 2 diabetes by genome-wide association and sequencing studies. University of Michigan Health System, Metabolism, Endocrinology, & Diabetes (MEND), Ann Arbor, Michigan, November 15, 2013.

Identifying and correcting for sample contamination in DNA sequencing studies. Department of Biostatistics, Harvard University, Boston, Massachusetts, December 12, 2013.

Identifying and correcting for sample contamination in DNA sequencing studies. Mt. Sinai School of Medicine, New York, New York, April 16, 2014.

Identifying genes for type 2 diabetes and related traits by GWA and sequencing studies. SISu symposium, Helsinki, Finland, August 26, 2014.

Type 2 diabetes knowledge portal: A call to action, community participation, and future directions. American Diabetes Association, Boston, Massachusetts, June 7, 2015.

Seminars (2001-present)

Science Research Club, University of Michigan, Ann Arbor, Michigan, April 3, 2001.

Center for Human Genetics, Duke University, Durham, North Carolina, May 24, 2001.

Department of Biostatistics and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, March 25, 2002.

Rubicon Genomics, Ann Arbor, Michigan, April 12, 2002.

Department of Biostatistics, University of North Carolina, Chapel Hill, North Carolina, Greenberg Lecturer, May 22-24, 2002. Four seminars.

Biogen, Boston, Massachusetts, July 9, 2002.

Department of Human Genetics, University of California at Los Angeles, Los Angeles, California, May 12, 2003.

Wayne State University, Detroit, Michigan, September 8, 2003.

Department of Statistics, Michigan State University, East Lansing, Michigan, November 18, 2003.

McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University, Baltimore, Maryland, February 2, 2004.

Department of Human Genetics, Emory University, Atlanta, Georgia, December 2, 2004.

Universidad Metropolitana, San Juan, Puerto Rico, September 17, 2005.

Department of Mathematics, Howard University, Washington, DC, November 4, 2005.

Department of Genetics, Universidade Federal do Paraná, Curitiba, Brazil, January 24, 2006.

National Institute of Mental Health, Bethesda, Maryland, March 14, 2006.

University of Alabama at Birmingham, Birmingham, Alabama, March 24, 2006.

McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University, Baltimore, Maryland, March 30, 2006.

Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, April 21, 2006.

Queensland Institute of Medical Research, Brisbane, Queensland, Australia, August 25, 2006.

Mount Sinai School of Medicine, December 8, 2006.

Department of Mathematics, Hope College, Holland, Michigan, January 18, 2007.

University of Trondheim, Trondheim, Norway, January 22, 2007.

Department of Genetics, Rutgers University, January 29, 2007.

GlaxoSmithKline, Research Triangle Park, May 30, 2007.

University of California at San Francisco, San Francisco, California, May 2-4, 2007, 2 seminars.

University of Colorado at Denver and Health Sciences Center, Denver, Colorado, Benjamin Stapleton Lecturer, October 11, 2007.

University of Southern California, Los Angeles, California, November 8, 2007.

University of California at Los Angeles, Los Angeles, California, January 10, 2008; January 11, 2008; January 28, 2008.

Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, April 11, 2008.

Department of Genetics, Michigan State University, January 22, 2009

CIDR Board of Governor's Meeting, Rockville, Maryland, February 13, 2009

Fred Hutchinson Cancer Research Center, Seattle, Washington, May 13, 2009

University of Michigan Diabetes Research and Training Center Winter Symposium, March 7, 2009

National University of Singapore, July 16, 2009

Department of Mathematics, Central Michigan University, Mount Pleasant, Michigan, September 10, 2009

Center for Statistical Genetics, University of Michigan, Ann Arbor, Michigan, September 29, 2009

Distinguished University Professor Lecture, University of Michigan, Ann Arbor, Michigan, February 15, 2010

University Program in Genetics and Genomics, Duke University, March 22, 2010

Center for Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, Michigan, March 24, 2010

Department of Medicine, Wayne State University, September 1, 2010

Department of Bioinformatics, Seoul National University, September 6, 2010

Department of Statistics, Seoul National University, September 7, 2010

Korea National Insitute of Health, September 8, 2010

Department of Mathematics, Howard University, Washington DC, October 29, 2010

Department of Mathematics, Spelman College, Atlanta, Georgia, Novmeber 8, 2010

Department of Mathematics, Morehouse College, Atlanta, Georgia, November 9, 2011

CIHR Strategic Training for Advanced Genetic Epidemiology, University of Toronto, Toronto, Ontario, Canada, January 14, 2011

Department of Biostatistics, University of Texas Health Sciences Center, Houston, Texas, January 31, 2011

Department of Human Genetics, University of Pittsburgh, Pittsburgh, Pennsylvania, February 4, 2011

HudsonAlpha Institute, Huntsville, Alabama, February 16, 2011

Center for Human Genetics, Vanderbilt University, Nashville, Tennessee, March 30, 2011

Sanger Insitute, Hinxton, UK, June 3, 2011

Washington University, Saint Louis, Missouri, February 17, 2012

Institute of Psychiatry, Kings College, London, United Kingdom, June 21, 2012

University of Copenhagen, Copenhagen, Denmark, August 21, 2012

University of Southern Denmark, Odensee, Denmark, December 6, 2012

University of Michigan Health System, Metabolism, Endocrinology & Diabetes (MEND), November 15, 2013

Department of Biostatistics, Harvard University School of Public Health, December 12, 2013

Department of Genetics and Genomic Sciences, Mount Sinai School of Medicine, New York City, New York, April 16, 2014

National Institute of Aging, Baltimore, Maryland, May 6, 2014

Department of Genome Sciences, University of Washington, Seattle, Washington, May 22, 2014

Meru University of Science and Technology, Meru, Kenya, June 18, 2014

Department of Genetics and Genome Sciences, Case Western Reserve University, Cleveland, Ohio, September 10, 2014

Interdisciplinary Group Seminar, University of Michigan, Ann Arbor, Michigan, September 16, 2014

Society of Biology Students, University of Michigan, Ann Arbor, Michigan, October 9, 2014

Institute of Genetics, University of Florida, Gainesville, Florida, January 20, 2015

Department of Mathematics, Howard University, Washington, DC, January 23, 2015

Department of Biomathematics, University of California at Los Angeles, Los Angeles, California, March 9, 2015

Department of Biostatistics, Columbia University, New York City, New York, April 2, 2015

Department of Public Health Sciences, University of Chicago, Chicago, Illinois, April 15, 2015

Center for Biomedicine, European Academy, Bolzano, Italy, June 23 and 25, 2015

CURRENT SPONSORED RESEARCH (as Principal Investigator)

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/10-6/30/15, 5% effort, P.I. Michael Boehnke, $3,616,237.

Whole Genome and Exome Sequencing for Bipolar Disorder, NIH NIMH R01 MH 094145, 8/30/11-6/30/15, 7% effort, P.I. Michael Boehnke, $1,843,345.

Identifying T2D Variants by DNA Sequencing in Multiethnic Samples, NIH NIDDK U01 DK085584, 9/20/09-7/31/15, 4% effort, P.I. Michael Boehnke, $3,605,640.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 1/11/11-12/31/15, 33% effort, P.I. Michael Boehnke, $2,118,261.

The Impact of Human Gene Knockouts in Type 2 Diabetes and Related Traits, NIH R01 DK098032, 9/15/12-7/31/16, 9% effort, contact P.I. Michael Boehnke (joint with David Altshuler and Mark McCarthy), $580,453.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 6/1/14-5/31/18, 13.2% effort, P.I. Michael Boehnke, $2,844,816.

Whole Genome Sequencing for Schizophrenia and Bipolar Disorder in the GPC, NIH U01 MH105653, 9/19/14-6/30/18, 12.7% effort, P.I. Michael Boehnke, $2,280,989.

SPONSORED RESEARCH: GRANTS TO BE FUNDED SOON (as Principal Investigator)

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/15-6/30/20, 10% effort, P.I. Michael Boehnke, $4,486,970. Impact Score: 10.

Accelerating Medicines Partnership: Enhancement of the Type 2 Diabetes Knowledge Portal, 6/1/15-5/31/17, FNIH, P.I. Michael Boehnke (joint with Gonçalo Abecasis), 1.1% effort, $2,567,844.

Accelerating Medicines Partnership: Deposit of METSIM and FUSION data into the Knowledge Portal, 6/1/15-5/31/17, FNIH, P.I. Michael Boehnke (joint with Markku Laakso), 1.1% effort, $294,284.

CURRENT SPONSORED RESEARCH (Not as Principal Investigator)

Targeted Genetic Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 7/1/15-6/30/20, 4% effort, P.I. Karen Mohlke.

Genetic Epidemiology of Rare and Regulatory Variants for Metabolic Traits, NIH/NIDDK R01 DK093757, 9/5/11-7/31/16, 3% effort, P.I. Karen Mohlke.

HUNTing for Myocardial Infarction Genes by Combined Genome and Exome Sequencing, NIH R01 HL109946, 9/1/11-6/30/16, 3% effort, P.I. Cristen Willer.

Computational and Statistical Models for Human Genetics, NIH R01 HG007002, 7/18/12-4/30/17, 4% effort, P.I. Gonçalo Abecasis.

H3Africa Kidney Disease Research Network, NIH/University Ghana Medical School, 8/5/12-7/31/15, 4% effort, P.I. Akinlolu Ojo.

PREVIOUS SPONSORED RESEARCH

Linkage Studies in Neurofibromatosis, NIH NINDS R01 NS23410, 4/1/86-3/31/89, 15% effort, P.I. Robert Erickson.

Comparison of Fixed and Sequential Sampling for Family Studies, Rackham Faculty Research Grant, 1/5/87-12/31/87, 0% effort, P.I. Michael Boehnke, $9,927.

Alzheimer Disease Research Center, subcontract from the University of Washington, Seattle, Michigan, 5/1/87-12/31/87, 20% effort, P.I. Michigan subcontract Michael Boehnke.

Michigan Diabetes Research and Training Center, 9/1/87-8/31/89, 10% effort, P.I. Douglas Greene.

Program Project: The Study of Human Mutation, NIH NCI P01 CA26803, 12/1/87-11/30/90, 10% effort, P.I. Samir Hanash.

Design Issues in Genetic Linkage and Segregation Studies, NIH NCHGR R29 HG00376, 9/28/88-8/31/93, 50% effort, P.I. Michael Boehnke, $349,752.

Macular Genetic Studies of Human X-Chromosomal Retinal Dystrophies, Retinitis Pigmentosa Foundation, 10/1/88-6/30/91, 5% effort, P.I. Paul Sieving.

The Effects of Bilineal Pedigrees in Linkage Analysis, MacArthur Foundation, 3/1/90-2/28/91, 0% effort, P.I. Michael Boehnke, $11,369.

Two-Trait Locus Models for Linkage Analysis of Complex Traits, MacArthur Foundation, 5/1/91-12/31/91, 0% effort, P.I. Michael Boehnke, $7,024.

Efficient Use of Two-Trait Linkage Analysis, MacArthur Foundation, 6/1/92-5/31/93, 0% effort, P.I. Michael Boehnke, $12,800.

Linkage Studies in Neurofibromatosis, NIH NINDS R01 NS23410, 4/1/89-3/31/94, 5% effort, P.I. Francis Collins.

Genomic Technology and Genetic Disease, Statistical Genetics Core, NIH NCHGR P30 HG00209, 9/30/90-7/31/95, 15% effort, P.I. (Core) Michael Boehnke, P.I. (Center) Francis Collins and Miriam Meisler.

Retinitis Pigmentosa Research Center, National Retinitis Pigmentosa Foundation, 7/1/91-6/30/94, 5% effort, P.I. Paul Sieving.

Molecular Genetics of Juvenile Onset Glaucoma, NIH NEI R01 EY09580, 9/30/92-9/29/95, 10% effort, P.I. Julia Richards.

Mapping Genes for Type 2 Diabetes, supplement to Genomic Technology and Genetic Disease, NIH NCHGR P30 HG00209, 6/1/94-7/31/95, 15% effort, P.I. (Supplement) Michael Boehnke, P.I. (Center) Miriam Meisler.

Design and Analysis of Human Gene Mapping Studies, NIH NCHGR R01 HG00376, supplement, 9/1/95-8/31/98, 15% effort, P.I. Michael Boehnke, $310,535.

FUSION: Statistical Analysis and Database Support, NIH, 5/1/97-12/31/00, 15% effort, P.I. Michael Boehnke, $282,321.

Public Health Genetics: An Education Model, NIH NCHGR R01 HG01511, 12/09/96-11/30/99, 5% effort (no salary), P.I. Susan Caumartin.

Isolation of the Gene(s) for Ataxia-Telangiectasia, NIH NCI R01 CA57569, 4/1/97-3/31/00, 2% effort, P.I. Patrick Concannon, Virginia Mason Research Center.

Institutional Training Grant in Genomic Science, NIH NCHGR T32 HG00040, 7/1/95-6/30/00, 5% effort (no salary), P.I. Michael Boehnke, $1,163,746.

Molecular Genetics of Juvenile Onset Glaucoma, NIH NEI R01 EY09580, 12/8/95-11/30/00, 10% effort, P.I. Julia Richards.

Design and Analysis of Human Gene Mapping Studies, NIH NCHGR R01 HG00376, 9/1/98-8/31/01, 50% effort, P.I. Michael Boehnke, $418,108.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH NEI EY11671, 12/1/97-11/30/02, 10% effort, P.I. Julia Richards.

Mental Illness Research, Education, and Clinical Center (MIRECC), United States Department of Veterans Affairs, 10/1/99-9/30/05, 10% effort, P.I. Murray Raskind, University of Washington.

Software for Integrated Linkage and Association Analysis, NIH NIMH R01 MH59528, 4/1/00-3/31/03, 5% effort, P.I. Elizabeth Hauser, Duke University.

Consortium Linkage Studies of Type 2 Diabetes, NIH NIDDK U01 DK58026, 6/1/99-5/31/05, 5% effort, P.I. Nancy Cox, University of Chicago.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG00376, 9/1/01-8/31/05, 50% effort, P.I. Michael Boehnke, $800,000.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/00-6/30/05, 5% effort, P.I. Michael Boehnke, $1,932,942.

Genomic Analysis of Schizophrenia, Veterans Administration Seattle Institute of Biomedical and Clinical Research, 4/1/04-3/31/07, 5% effort, P.I. Gerard Schellenberg.

National Center for Integrative Biomedical Informatics, NIH NIDA U54 DA021519, 9/25/05-8/31/10, 5% effort, P.I. Brian Athey.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 5/1/03-11/30/08, 25% effort, P.I. Michael Boehnke, $3,512,852.

Molecular Epidemiology of Colorectal Cancer, NIH NCI R01 CA81488, 6/1/04-5/31/09. 2% effort, P.I. Stephen Gruber.

Integrated Parametric and Non-Parametric Mapping for Genome-Wide Association Data, NIH NHLBI U01 HL084729, 4/1/06-3/31/09, 4% effort, P.I. Gonçalo Abecasis.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH NEI R01 EY11671, 4/1/04-3/31/09, 8% effort, P.I. Julia Richards.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R56 DK062370, 6/1/08-5/31/09, 0% effort, P.I Michael Boehnke, $382,932

Pritzker Neuropsychiatric Disorders Research Consortium, Pritzker Foundation, 12/1/00-11/30/09, 10% effort, P.I. Stan Watson, Huda Akil.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/05-6/30/10, 5% effort, P.I. Michael Boehnke, $2,135,473.

EpiGen Var Coordinating Center, NIH NHGRI Subaward 3548, 7/01/08-5/31/10, 10% effort, P.I. Tara Matise.

Postdoctoral Training Award, American Diabetes Association, 7/1/06-6/30/10, 0% effort, P.I. Michael Boehnke, $180,000.

Targeted Genetics Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 9/1/05-6/30/10, 5% effort, P.I. Karen Mohlke.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 9/1/05-8/31/10, 40% effort, P.I. Michael Boehnke, $1,261,028.

Quality Control, Genotype Calling and Study Design for 1000 Genomes Project, NIH NHGRI U01 HG005214, 7/01/09-6/30/11, 5% effort, P.I. Goncalo Abecasis

Low-Pass Sequencing and High-Density SNP Genotyping for Type 2 Diabetes, NIH NIDDK RC2 DK088389, 9/30/09-8/31/12, 16% effort, P.I. Michael Boehnke, $17,182,927.

Quality Control, Genotype Calling and Study Design for 1000 Genomes Project, NIH U01 HG005214, 6/30/10-6/30/12, 5% effort, P.I. Michael Boehnke, $1,038,257.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH/NEI R01 EY1167109 A2, 7/1/09-6/30/12, 5% effort, P.I. Julia Richards, $8,325.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 6/1/09-5/31/14, 11% effort, P.I. Michael Boehnke, $6,139,683.

Targeted Genetic Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 7/1/11-5/31/15, 5% effort, P.I. Karen Mohlke, $249,243.

TEACHING

Introduction to Biostatistics: 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1995, 1997, 2000, 2005, 2009, 2012, 2013.
Textbook: D.S. Moore et al., *Introduction to the Practice of Statistics*, seventh edition.

Foundations of Biostatistical Inference: 1984, 1985, 1986.
Textbook: B. Lindgren, *Statistical Theory*.

Statistical Models and Numerical Methods in Human Genetics: 1985, 1987, 1989, 1991, 1993, 1995, 1997, 1999, 2007, 2009.
Introduction to Applied Stochastic Processes: 1986.

Textbook: H.M. Taylor and S. Karlin, *Introduction to Stochastic Modeling*.
Introduction to Mathematical Modeling in Clinical Research: 1986, 1988.

Statistical Computer Packages: 1987.
Readings in Statistical Human Genetics: 1992, 1996, 1997, 1998, 2000, 2004.

Advanced Topics in Genetic Modeling: 1999, 2003, 2005.
Textbook: K. Lange, *Mathematical and Statistical Models for Genetic Analysis*.

Readings in Quantitative Genetics: 2004.
Textbook: M. Lynch and B. Walsh, *Genetics and Analysis of Quantitative Traits*.

DOCTORAL COMMITTEE SERVICE: CHAIR OR CO-CHAIR

Lynn M. Ploughman, Department of Biostatistics, 1990. Chair. Linkage Analysis: Power Estimation and Comparison of Methods. Current position: Bristol-Myers Squibb, Princeton, New Jersey.

Nicholas Schork, Department of Epidemiology, 1994. Co-Chair. Advances in the Genetic-Epidemiologic Analysis of Complex Phenotypes. Current position: Professor of Molecular and Experimental Medicine, The Scripps Research Institute, San Diego, California. Professor of Psychiatry and Biostatistics, University of California at San Diego, San Diego, California.

Kathryn Lunetta, Department of Biostatistics, 1996. Chair. Models and Experimental Design for Radiation Hybrid Mapping. Current position: Professor of Biostatistics, Boston University, Boston, Massachusetts.

Elizabeth Hauser, Department of Biostatistics, 1998. Chair. Methods for Linkage Analysis of Complex Genetic Disease. Current position: Professor of Medical Genetics, Duke University, Durham, North Carolina.

Carl Langefeld, Department of Biostatistics, 1999. Chair. The Application of Statistical Methods for Highly Stratified Data to Linkage and Association Analysis of Complex Genetic Traits. Current position: Professor of Biostatistical Sciences, Wake Forest University, Winston-Salem, North Carolina.

Heather Stringham, Department of Biostatistics, 2000. Chair. Bayesian Solutions to Problems of Uncertainty in Genetic Data. Current position: Research Area Specialist Lead, Department of Biostatistics, University of Michigan, Ann Arbor, Michigan.

Ethan M. Lange, Department of Biostatistics, 2001. Chair. Methods for Mapping Disease Susceptibility Genes Using Allele-Sharing Statistics. Current position: Associate Professor of Genetics, University of North Carolina, Chapel Hill, North Carolina.

Julie A. Douglas, Department of Biostatistics, 2001. Chair. Methods for Resolving Genotype and Haplotype Ambiguity in Human Genetic Data. Current position: Associate Professor of Human Genetics, University of Michigan, Ann Arbor, Michigan.

Michael P. Epstein, Department of Biostatistics, 2002. Co-Chair. Statistical Methods in Gene Mapping of Familial Traits. Current position: Professor of Human Genetics, Biostatistics and Bioinformatics, Emory University, Atlanta, Georgia.

Chun Li, Department of Biostatistics, 2003. Chair. Association Methods for Mapping Genes for Complex Diseases. Current position: Associate Professor of Epidemiology and Biostatistics, Case Western Reserve University.

Tasha E. Fingerlin, Department of Epidemiology, 2003. Co-Chair. Application of Association and Linkage Methods in Studies of Complex Traits. Current position: Director of the Center for Genes, Environment and Health and Director of the Quantitative Genetics Program at National Jewish Health, Denver, Colorado.

Mingyao Li, Department of Biostatistics, 2005. Co-Chair. Statistical Methods in Gene Mapping of Complex Diseases. Current position: Associate Professor of Biostatistics, University of Pennsylvania, Philadelphia, Pennsylvania.

Andrew Skol, Department of Biostatistics, 2006. Chair. Efficient Methods for Gene Mapping of Complex Diseases. Current position: Assistant Professor of Genetic Medicine, University of Chicago, Chicago, Illinois.

Karen N. Conneely, Department of Biostatistics, 2008. Chair. Methods for Large-Scale Genetic Association Studies. Current position: Assistant Professor of Human Genetics, Emory University, Atlanta, Georgia.

Yun Li, Department of Biostatistics, 2009. Co-Chair. *In Silico* Haplotyping, Genotyping and Analysis of Resequencing Data Using Markov Models. Current position: Assistant Professor of Genetics and Biostatistics, University of North Carolina, Chapel Hill, North Carolina.

Rui Xiao, Department of Biostatistics, 2009. Chair. Statistical Methods in Genetic Association Studies. Current position: Assistant Professor of Biostatistics, University of Pennsylvania, Philadelphia, Pennsylvania.

Weihua Guan, Department of Biostatistics, 2010. Co-Chair. Models and Methods for Genome-Wide Association Studies. Current position: Assistant Professor of Biostatistics, University of Minnesota, Minneapolis, Minnesota.

Ryan Welch, Program in Bioinformatics, 2013. Co-Chair. Bioinformatics Software and Methods for Genome-Wide Association and Chip-Seq Studies. Current position: Research Area Specialist Lead, Department of Biostatistics, University of Michigan, Ann Arbor, Michigan.

Clement Ma, Department of Biostatistics, 2014. Chair. Statistical methods for low-frequency and rare genetic variants. Current position: Lead Biostatistician, Division of Pediatric Oncology and Hematology, Dana-Farber/Boston Children's Cancer Center, Boston, Massachusetts.

Matthew Flickinger, Department of Biostatistics. Chair.

DOCTORAL COMMITTEE SERVICE: MEMBER

Daniel J. Odenheimer, Department of Epidemiology, 1985. An Evaluation of the Validity of Complex Segregation Analysis in Identifying an Individual's Genotype at a Major Locus.

Ann R. G. Schwartz, Department of Epidemiology, 1986. A New Method for Detecting Familial Heterogeneity of Cancer Risk: A Population-Based Study in Metropolitan Detroit.

Mark Graves, Department of Electrical Engineering and Computer Science, 1994. Theories and Tools for Designing Application-Specific Knowledge Base Data Models.

Kim Papenberg, Department of Human Genetics, 1995. Hereditary Hemorrhagic Telangiectasia: From Linkage to Mutation Analysis.

Benjamin Rybicki, Department of Epidemiology, 1997. Genetic Epidemiology of Sarcoidosis.

Ruzong Fan, Department of Biostatistics, 1998. Mathematical and Statistical Models for Mutant Genes in Nonstationary Populations.

George J. Papanicolaou, Department of Human Genetics, 1999. Genotypic and Phenotypic Analysis of Malignant Melanoma: Analysis of Gene Expression Patterns.

Leslie Lange, Department of Epidemiology, 2000. Identification and Analysis of Candidate Genes for Coronary Artery Calcification.

Anne V. Jackson, Department of Human Genetics, 2000. A Mouse Model System for Quantitative Genetics of Age-Sensitive Traits.

Mohammad Khoshnevisan, Department of Epidemiology, 2001. Selected Genetic and Environmental Risk Factors in the Etiology of Human Oral Clefting.

Cathryn H. Bock, Department of Epidemiology, 2003. Early Detection Practices, Decreasing Age at Diagnosis, and a Linkage Analysis in Prostate Cancer Families.

Erik Ferragut, Department of Mathematics, 2003. Detection of Epistatic Effects in Genetic Data.

Bethany L. Niell, Department of Epidemiology, 2003. Colorectal Cancer Epidemiology: Genes, Environment, and History.

Laura Rozek, Department of Epidemiology, 2003. Candidate Genes for Colorectal Cancer in Structured Populations.

Michelle Cote, Department of Epidemiology, 2003. Early Onset Lung Cancer: Racial Differences in Familial Aggregation, Genetic Polymorphisms and Survival.

Charles Krafchak, Department of Epidemiology, 2004. Genetic Characterization of Posterior Polymorphous Corneal Dystrophy.

Richard McEachin, Department of Human Genetics, 2004. An Integrated Experimental and Computational Approach to Understanding Complex Disease: Differential Gene Expression in Type 2 Diabetes Mellitus.

Jennifer Poynter, Department of Epidemiology, 2005. Molecular Epidemiology of Colorectal Cancer: Mechanisms of Risk and Clues Towards Chemoprevention.

Liming Liang, Department of Biostatistics, 2009. Efficient Methods for Analysis of Genome Scale Data.

Kristen Stevens, Department of Epidemiology, 2010. Epidemiologic Approaches to Understanding Complex Diseases: Applications in Congenital Heart Disease and Cancer.

Jun Ding, Department of Biostatistics, 2010. Statistical Methods for Genome-wide Association Studies of Gene Expression, with Applications to the Genetic Study of Psoriasis.

Alex Tsoi, Department of Biochemistry and Molecular Biology, 2010. Using Ontology Fingerprint to Enhance Analysis of High Throughput Experimental Results.

Jin Zheng, Department of Biostatistics, 2010. Models and Methods for Genetic Linkage and Association Analyses.

Lucy Huang, Department of Bioinformatics, 2011. Genotype Imputation in Diverse Populations: Empirical and Theoretical Approaches.

Wei Chen, Department of Biostatistics, 2011. Statistical Methods and Analysis in Genome Wide Association Studies and Next-Generation Sequencing.

Michael DeGiorgio, Program in Bioinformatics, 2011. Genetic Variation and Modern Human Origins.

Matthew Zawistowski, Department of Biostatistics, 2011. Statistical Methods and Models for Modern Genetic Analysis.

Shyam Gopalakrishnan, Department of Biostatistics, 2011. Methods for Statistical and Population Genetics Analyses.

Chaolong Wang, Program in Bioinformatics, 2012. Statistical Methods for Analyzing Human Genetic Variation in Diverse Populations.

Peng Zhang, Program in Bioinformatics, 2013. The Road to Identifying Disease-Causing Genes: Association Tests, Genotype Imputations, and Sampling Strategies for Sequencing Studies.

Zachary Szpiech, Program in Bioinformatics, 2013. Human Migration, Population Divergence, and the Accumulation of Deleterious Alleles: Insights from Private Genetic Variation and Whole-Exome Sequencing.

Mark Reppell, Department of Biostatistics, 2014. Using Rare Genetic Variation to Understand Human Demography and the Etiology of Complex Traits.

Xiaowei Zhan, Department of Biostatistics, 2014. Statistical Methods and Analysis in Next Generation Sequencing.

POST-DOCTORAL MENTOR

Soumitra Ghosh, 1992-1994. Current position: Executive Director of Immuno-Inflammatory Genetics, GlaxoSmithKline.

Richard M. Watanabe, 1995-1998. Current position: Professor of Preventive Medicine (Biostatistics) and Physiology and Biophysics, University of Southern California.

Laura J. Scott, 2000-2002. Current position: Research Associate Professor, University of Michigan.

Cristen J. Willer, 2004-2010. Current position: Assistant Professor of Cardiovascular Medicine and Human Genetics, University of Michigan.

Christian Fuchsberger, 2010-2014. Current position: Senior Researcher, Center for Biomedicine, Bozen, Italy.

Jeroen Huyghe, 2011-2015. Current position: Staff Scientist, Cancer Prevention Program, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, Washington.

Xueling Sim, 2011-2014. Current position: Assistant Professor, Saw Swee Hock School of Public Health, National University of Singapore, Singapore.

Tanya Teslovich, 2008-present.

Adam E. Locke, 2011-present.

Daniel Taliun, 2014-present.

PROFESSIONAL SERVICE

Associate Editor:

American Journal of Human Genetics	1989-1991
Journal of the American Statistical Association	1993-2003
Human Heredity	1992-present

Editorial Advisory Board:

Genome Research	1995-1999, 2010-2014
Genetic Epidemiology	1997-2010

Referee for:

American Journal of Human Genetics
Annals of Statistics
Annals of Thoracic Surgery
Bioinformatics
Biotechniques
Biological Psychiatry
Biometrics
BMC Medical Genetics
Cell
Cephalalgia
Communications in Statistics
Diabetes
Diabetologia
European Journal of Human Genetics
Genetic Epidemiology
Genetics
Genome Research
Genomics
Human Genetics
Human Genomics
Human Heredity
Human Molecular Genetics
Journal of Clinical Endocrinology and Metabolism
Journal of Clinical Investigation
Journal of Heredity
Journal of the American Statistical Association
Molecular Biology and Evolution
Molecular Medicine
Nature
Nature Genetics

Nature Medicine
New England Journal of Medicine
Pharmacogenomics
PLoS Genetics
PLoS Medicine
Proceedings of the National Academy of Sciences USA
Science
Theoretical and Applied Genetics
Trends in Pharmacological Sciences

Major Grant Review Service

Member, Mammalian Genetics Study Section, 1994-1997.
Member, Center for Inherited Disease Research (CIDR) Access Committee, 1997-2002.
Member, NIGMS Human Mutant Cell Repository Advisory Committee, 1998-2001.
Chair, Genome Research Review Committee (GNOM G) Study Section, 2014-present.

Other:

Co-Organizer (with Nancy Cox), International Type 2 Diabetes Linkage Analysis Consortium. Chair, Steering Committee. Member, Analysis and Mapping Committee.

Member, Genetics Steering Committee, NIMH, 2003-present.

Member, External Advisory Board, International Type 1 Diabetes Genetics Consortium, NIDDK, 2003-2010.

Member, External Advisory Board, European Academy Bolzano Institute for Genetic Medicine, Bolzano, Italy, 2004-present.

Member, Awards Committee, American Society of Human Genetics, 2005-2008.

Member, Board of Directors, American Society of Human Genetics, 2006-2008.

Co-Organizer (with Mark McCarthy and David Altshuler), DIAGRAM Consortium.

Steering Committee Member of the MAGIC, GIANT, and Global Lipids Genetics Genome-Wide Association Study Consortia.

Member, Council, National Human Genome Research Institute, 2009-2012.

Nominating Committee, American Society of Human Genetics, 2009-2010. Member, 2009. Chair, 2010.

Chair, Steering Committee, T2D-GENES, 2009-present.