CURRICULUM VITAE
James E. Hixson, Ph.D.

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University of Texas Health Science Center at Houston (UTHealth)
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Education:

	Degree	Date	Major Field
University of Texas, Austin, Texas	B.A.	1978	Anthropology
University of Michigan, Ann Arbor, Michigan	Ph.D.	1983	Human Genetics
Stanford University Medical School, Stanford, CA	Postdoctoral	1985	Molecular Genetics

Present Position:

2000-Present Professor (tenured 2002), Human Genetics Center, EHGES Division, School of Public Health, UTHealth, Houston, TX.

Previous Positions:

1978 – 1983 Predoctoral Fellow and Trainee, Human Genetics, Genetics Training Grant (NIH), University of Michigan, Ann Arbor, MI.

1983 – 1985 Postdoctoral Fellow, Pathology Department, Stanford University Medical School, Stanford, CA.

1985 - 1989 Assistant Scientist, Department of Genetics, Southwest Foundation for Biomedical Research (SFBR), San Antonio, TX.

1986 - 1990 Assistant Professor, Department of Cellular and Structural Biology, University of Texas Health Science Center at San Antonio (UTHSCSA) San Antonio, TX.

1990 – 1993 Associate Scientist, Department of Genetics, SFBR, San Antonio, TX.

1990 - 1993 Associate Professor, Department of Cellular and Structural Biology, UTHSCSA, San Antonio, TX.

1994 – 1999 Chairman and Scientist, Department of Genetics, SFBR, San Antonio, TX.

1994 – 1999 Professor, Department of Cellular and Structural Biology, UTHSCSA, San Antonio, TX

Editorial Boards:

Current Genetic Medicine Reports

Awards:

Phi Beta Kappa, 1978
NIH Predoctoral Traineeship, 1978 - 1982
University of Michigan Cancer Research, 1983
American Cancer Society Postdoctoral Fellowship, 1983 – 1985
Gilbert W. Beebe Fellowship, The National Academies of Sciences, 2003-2004
UTHealth GSBS: Outstanding contribution towards graduate education as the Chair of the Curriculum Committee ($1,000) 2016

Manuscript Reviewer:

American Journal of Human Genetics
Arteriosclerosis, Thrombosis, and Vascular Biology
Atherosclerosis
BMC Medical Genomics
Circulation
European Journal of Clinical Investigation
Genomics
Human Biology
Journal of Lipid Research
Nature Medicine
New England Journal of Medicine
Plos One

Grant Reviewer:

National Institutes of Health

ACADEMIC ACTIVITIES

UTHealth School of Public Health
MPH and DrPH Committees
MS and PhD Committees

UTHealth
Faculty member, UT Medical School at Houston Medical Genetics Training Program

UTHealth Graduate School of Biomedical Sciences (GSBS)
Director, Human and Molecular Genetics Program (2006-2008)
Chair, GSBS Curriculum Committee (2015-2016)
Member, GSBS Curriculum Committee (2014-present)
MS and PhD Committees

Teaching
Co-Instructor, "NIH Proposal Development"
Lecturer, "Genetic Epidemiology of Chronic Disease"

Doctoral Students (Hixson Advisor)
Chung, Charlie C. (UT-GSBS) 2001-2007
Dissertation: Glucocorticoid Receptor gene variation and effects on hypertension

Mak, Solida (UT-GSBS) 1999-2007
Dissertation: Expression study of atherosclerotic mouse aorta revealed significant disturbance of calcium signaling pathway

Leduc, M (UT-GSBS) 2002-2007
Dissertation: Identification of genetic variation influencing apolipoprotein E levels: Follow-up of genome-wide linkage scans in the GENOA study

Montasser, May E. (UT-SPH) 2001-2008
Dissertation: Gene and Smoking Interaction in hypertension

Polfus, Linda M. (UTSPH-H) 2009-2013
Dissertation: GENOA Rochester GWAS analysis,
GXE Traineeship recipient from Buroughs-Wellcome

RESEARCH SUPPORT

Current

R01-HL111362 Herrington (PI) 4/01/18 - 1/31/22
Genomic and Proteomic Architecture of Atherosclerosis
This project will use proteomic and RNA-Seq technologies to characterize the molecular changes that produce arterial atherosclerotic plaques that ultimately cause ischemic cardiovascular events. The UT-Houston laboratory will be responsible for RNA-Seq analysis of autopsied arterial specimens collected at multiple sites, with and without atherosclerotic lesions.
Role: Co-Investigator

R01-HD073434 Au (PI) 5/1/14 - 4/30/19
Creating a Myelomingenocele Exome Variant Map
This project will use exome resequencing to find genetic variation that influences myelomingenocele in European and Hispanic Americans.
Role: Co-Investigator

R01-DK101505 Kelly (PI) 8/21/15 - 5/31/20
Whole Exome Sequencing Study of Diabetic Nephropathy
This project will use whole exome sequencing to identify genetic variants that influence chronic kidney disease in diabetic subjects from the Chronic Renal Insufficiency Cohort (CRIC) study.
Role: Co-Investigator

UTHealth Northrup and Hixson (multi-PI) 1/1/17 – 1/30/19
Presidential Collaborative Award
Unlocking the mysteries of folate deficiency and neural tube defects with omics approaches in human cell models.
This project aims to unlock the mysteries of folate deficiency leading to neural tube defects (NTDs) using state of the art omics tools including RNASeq and methylome array to identify changes in human pluripotent cells treated with different concentration of folic acids in vitro.
Role: SPH Principal Investigator

Selected Completed Research Support

R01-HL111362 Herrington (PI) 07/18/12 - 05/31/17
NIH/NHLBI
Genomic and Proteomic Architecture of Atherosclerosis
The UT-Houston laboratory will be responsible for exome resequencing for 1,100 case/controls selected from the multicenter autopsy study entitled “Pathobiological Determinants of Atherosclerosis in Youth” using next generation sequencing technologies. The overall goal is to identify functional genetic variants (both rare and common) that influence development of atherosclerotic lesions as directly measured in arterial specimens.
Role: Co-Investigator

R01-HL111249 Rao (PI) 07/15/12 - 06/30/17
NIH/NHLBI
Rare Variants for Hypertension in Taiwan Chinese

This project will use exome resequencing to find genetic variation that influences blood pressure in Taiwan Chinese families.
Role: Co-Investigator

R01-HL091988 Hixson (PI) 07/01/08 – 05/31/13
NIH/NHLBI
Genes of Oxidative Stress and Atherosclerotic Complications of Hypertension
This project will examine the influence of genetic variation in oxidative stress genes on coronary artery calcification.
Role: Principal Investigator

1RC2-HG005697-01 Hixson (PI) 09/30/09 – 08/31/12
NIH/NHGRI
Next-Generation Medical Resequencing of Gout Disease Genes in the ARIC Cohort
This project will use new massively parallel technologies for medical resequencing to identify genetic variants that underlie susceptibility to uric acid levels and gout.
Role: Principal Investigator

R01-HL091988 Hixson (PI) 07/01/08 – 05/31/13
NIH/NHLBI
Genes of Oxidative Stress and Atherosclerotic Complications of Hypertension
This project will examine the influence of genetic variation in oxidative stress genes on coronary artery calcification.
Role: Principal Investigator

1RC2-HG005697-01 Hixson (PI) 09/30/09 – 08/31/12
NIH/NHGRI
Next-Generation Medical Resequencing of Gout Disease Genes in the ARIC Cohort
This project will use new massively parallel technologies for medical resequencing to identify genetic variants that underlie susceptibility to uric acid levels and gout.
Role: Principal Investigator

R01-HL090682 He (PI) 09/15/08 – 07/31/12
NIH/NHLBI
Family-Based Genome-Wide Association Study for Salt-Sensitivity of Blood Pressure
This project will perform GWAS to identify genes that influence blood pressure response to dietary sodium and potassium in a feeding study of families from rural China.
Role: Co-Investigator

R01-HL072810 Boerwinkle (PI) 06/1/03 – 2/28/13
NIH/NHLBI
Modeling DNA Diversity in Reverse Cholesterol Transport
This project is using GWAS and gene resequencing to characterize the genetic architecture of CVD and HDL-C levels in subjects from the NIH CARDIA Study.
Role: Co-Investigator

R01-HL072810 Boerwinkle (PI) 06/01/03 – 02/28/13
NIH/NHLBI

Modeling DNA Diversity in Reverse Cholesterol Transport
This project is using GWAS and gene resequencing to characterize the genetic architecture of CVD and HDL-C levels in subjects from the NIH CARDIA Study.
Role: Co-Investigator

BIBLIOGRAPHY
James E. Hixson, Ph.D.

INVESTIGATIVE ARTICLES

1. Hixson, J.E. and Clayton, D.A. Initiation of transcription from each of the two mitochondrial promoters requires unique nucleotides at the transcriptional start site. Proc. Natl. Acad. Sci. (USA) 82:2660-2664, 1985.

2. Chang, D.D., Hixson, J.E., and Clayton, D.A. Minor transcription events indicate that both human mitochondrial promoters function bidirectionally. Molec. Cell. Biol. 6:294-301, 1986.

3. Chang, D.D., Wong, T.W., Hixson, J.E., and Clayton, D.A. Regulatory sequences for mammalian mitochondrial transcription and replication. In: Achievements and Perspectives of Mitochondrial Research, Volume 2: Biogenesis; Proceedings of the International Symposium, Rosa Marina, Italy, 1985. Edited by E. Quagliarello, E.C. Slater, F. Palmieri, C. Saccone, and A.M. Kroon. Amsterdam, Elsevier Science Publishing Company, 1986. pp. 99-110.

4 Hixson, J.E. and Brown, W.M. A comparison of the 12S rRNA genes from the mitochondrial DNA of humans and the great apes: Sequence, structure, and evolution. Molec. Biol. Evol. 3:1-18, 1986.

5. Hixson, J.E., Wong, T.W., and Clayton, D.A. Both the conserved stem-loop and divergent 5'-flanking sequences are required for initiation at the human mitochondrial origin of light-strand DNA replication. J. Biol. Chem. 261:2384-2390, 1986.

6. Fisher, R.P., Hixson, J.E., and Clayton, D.A. Mitochondrial transcription factor binds novel control elements of both major promoters of human mtDNA. In: Cetus-UCLA Symposium, Keystone, Colorado, 1986. Edited by D. Granner, M.G. Rosenfeld, and S. Chang. New York, Alan R. Liss, 1987. pp. 103-112.

7. Hixson, J.E. DNA markers in primate models for human disease. Genetica 73:85-90, 1987.

8. Hixson, J.E. and Britten, M.L. The baboon beta-myosin heavy chain gene: Construction and characterization of cDNA clones and gene expression in cardiac tissues. Gene 64:33-42, 1988.

9. Hixson, J.E., Borenstein, S., and Cox, L.A. The baboon apo E gene: Structure, expression, and linkage with the apo C-I gene. Genomics 2:315-323, 1988.

10. Foran, D.R., Hixson, J.E., and Brown, W.M.: Comparisons of ape and human sequences that regulate mitochondrial DNA transcription and D-loop DNA synthesis. Nucleic Acids Res. 16:5841-5861, 1988.

11. Hixson, J.E., Borenstein, S., Cox, L.A., Rainwater, D.L., and VandeBerg, J.L. The baboon gene for apolipoprotein A-I: Characterization of a cDNA clone and identification of DNA polymorphisms for genetic studies of cholesterol metabolism. Gene 74:483-490, 1988.

12. Hixson, J.E., Britten, M.L., Manis, G.S., and Rainwater, D.L. Apo(a) glycoprotein isoforms result from size differences in apo(a) mRNA in baboons. J. Biol. Chem. 264:6013-6016, 1989.

13. Hixson, J.E., Kammerer, C.M., Cox, L.A., and Mott, G.E. Identification of an LDL receptor gene marker associated with altered levels of LDL-cholesterol and apolipoprotein B in baboons. Arteriosclerosis 9:829-835, 1989.

14. Hixson, J.E., Henkel, R.D., Britten, M.L., Vernier, D.T., deLemos, R.A., VandeBerg, J.L., and Walsh, R.A. alpha-myosin heavy chain cDNA structure and gene expression in adult, fetal, and premature baboon myocardium. J. Mol. Cell. Cardiol. 21:1073-1086, 1989.

15. Hixson, J.E., Borenstein, S., and Cox, L.A. PvuII RFLP for the lecithin-cholesterol acyltransferase gene (LCAT) in baboons. Nucleic Acids Res. 18:384, 1990.

16. Hixson, J.E. and Vernier, D.T. Restriction isotyping of human apolipoprotein E by gene amplification and cleavage with HhaI. J. Lipid Res. 31:545-548, 1990.

17. Thieszen, S.L., Hixson, J.E., Nagengast, D.J., Wilson, J.E., and McManus, B.M. Lipid phenotypes, apolipoprotein genotypes and cardiovascular risk factors in nonagenarians. Atherosclerosis 83:137-146, 1990.

18. Pathobiological Determinants of Atherosclerosis in Youth (PDAY) Research Group. Relationship of atherosclerosis in young men to serum lipoprotein cholesterol concentrations and smoking. A preliminary report from the PDAY Research group. JAMA 264: 3018-3024, 1990.

19. Hixson, J.E., Vernier, D.T., and Powers, P. Detection of SstI restriction site polymorphism in human APOC3 by the polymerase chain reaction. Nucleic Acids Res. 19:196, 1991.

20. Hixson, J.E. and Powers, P.K. Restriction isotyping of human apolipoprotein A-IV: Rapid typing of apoA-IV isoforms and detection of a new isoform that deletes a conserved repeat. J. Lipid Res. 32:1529-1535, 1991.

21. Hixson, J.E. and the Pathobiological Determinants of Atherosclerosis in Youth (PDAY) Research Group. Apolipoprotein E polymorphisms affect atherosclerosis in young males. Arteriosclerosis and Thrombosis 11:1237-1244, 1991.

22. Blangero, J., Williams-Blangero, S., and Hixson, J.E. Assessing the effects of candidate genes on quantitative traits in primate populations. Am. J. Primatology 27:119-132,

1992.

23. Rainwater, D.L, Blangero, J., Hixson, J.E., Birnbaum, S., Mott, G.E., and VandeBerg, J.L. A DNA polymorphism for lecithin:cholesterol acyltransferase (LCAT) is associated with altered LCAT activity and HDL size distributions in baboons. Arteriosclerosis and Thrombosis 12:682-690, 1992.

24. Pastorcic, M., Birnbaum, S., and Hixson, J.E. Baboon apolipoprotein C-I: cDNA and gene structure and evolution. Genomics 13:368-374, 1992.

25. Hixson, J.E., McMahan, C.A., McGill, H.C., Jr., Strong, J.P., and the Pathobiological Determinants of Atherosclerosis in Youth (PDAY) Research Group. Apolipoprotein B insertion/deletion polymorphisms affect atherosclerosis in young black but not young white males. Arteriosclerosis and Thrombosis 12:1023-1029, 1992

26. Kammerer, C.M., Hixson, J.E., Aivaliotis, M.J., Porter, P.A., and VandeBerg, J.L. Linkage heterogeneity between LDLR and C3 and between APOA1 and APOA4 loci in baboons. Genomics 14:42-48, 1992.

27. Kammerer, C.M., Hixson, J.E., and Mott, G.E. A DNA polymorphism for lecithin: cholesterol acyltransferase (LCAT) is associated with high density lipoprotein levels in baboons. Atherosclerosis 98:153-163, 1993.

28. Hixson, J.E., Driscoll, D.M., Birnbaum, S., and Britten, M.L. Baboon LCAT: cDNA sequences of two alleles, evolution, and gene expression. Gene 128:295-299, 1993.

29. Hixson, J.E., Powers, P.K., and McMahan, C.A. The human apo B 3' hypervariable region: Detection of eight new alleles and comparison of allele frequencies in blacks and whites. Hum. Genet. 91: 475-479, 1993.

30. Hixson, J.E., Kammerer, C.M., Mott, G.E., Britten, M. L., Birnbaum, S, Powers, P.K., and Vandeberg, J.L. Baboon apoA-IV: Identification of Lys76->Glu that distinguishes two common isoforms and detection of length polymorphisms at the carboxyl terminus. J. Biol. Chem. 268:15667-15673, 1993.

31. Powers, P.K., and Hixson, J.E. BanI and PvuII polymorphisms in intron 2 of selectin E (SELE). Hum. Mol. Gen. 2:1082, 1993.

32. Pathobiological Determinants of Atherosclerosis in Youth (PDAY) Research Group. Natural history of aortic and coronary atherosclerotic lesions in youth. Findings from the PDAY study. Arteriosclerosis and Thrombosis 13:1291-1298, 1993.

33. White, A.L., Rainwater, D.L., Hixson, J.E., Estlack, L.E., and Lanford, R.E. Intracellular processing of apo(a) in primary baboon hepatocytes. Chem. Phys. Lipids 67/68:123-133, 1994.

34. White, A.L., Hixson, J.E., Rainwater, D.L., and Lanford, R.E. Molecular basis for "null" lipoprotein (a) phenotypes and the influence of apolipoprotein(a) size on plasma

lipoprotein(a) level in the baboon. J. Biol. Chem. 269:9060-9066, 1994.

35. Mitchell, B.D., Kammerer, C.M., Hixson, J.E., Atwood, L.D., Hackleman, S., Blangero, J., Haffner, S.M., Stern, M.P., and MacCluer, J.W. Evidence for a major gene affecting post-challenge insulin levels in Mexican Americans. Diabetes 44:284-289, 1995.

36. Hixson, J.E. and Powers, P.K. Detection and characterization of new mutations in the human angiotensinogen gene. Hum. Genet. 96:110-112, 1995.

37. Cole, S.A. and Hixson, J.E. Baboon lipoprotein lipase: cDNA sequence and variable tissue-specific expression of two transcripts. Gene 161:265-269, 1995.

38. Rogers, J., Witte, S.M., Kammerer, C.M., Hixson, J.E., and MacCluer, J.W. Linkage mapping in Papio baboons: Conservation of a syntenic group of 6 markers on human chromosome 1. Genomics 28:251-254, 1995.

39. Mahaney, M.C., Blangero, J., Rainwater, D.L., Comuzzie, A.G., VandeBerg, J.L., Stern, M.P., MacCluer, J.W., and Hixson JE. A major locus for high density lipoprotein cholesterol in the San Antonio Family Heart Study: Segregation and linkage analyses. Arteriosclerosis, Thrombosis, and Vascular Biology 15:1730-1739, 1995.

40. Bowman, B.H., Janse, L., Yang, F., Adrian, G.S., Zhao, M., Atherton, S.S., Buchanan, J.M., Greene, R., Walter, C., Herbert, D.C., Weaker, F.J., Chiodo, L.K., Kagan-Hallet, K. and Hixson, J. E. Discovery of a brain promoter from the human transferrin gene and its utilization for development of transgenic mice that express human APOE alleles. Proc. Natl. Acad.Sci. USA 92:12115-12119, 1995.

41. Comuzzie, A.G., Blangero, J., Mahaney, M.C., Mitchell, B.D., Hixson, J.E., Samollow, P.B., Stern, M.P., and MacCluer, J.W. A major gene with sex-specific effects influences fat mass in Mexican Americans. Genetic Epidemiology 12:475-488, 1995.

42. Kammerer, C.M., VandeBerg, J.L., and Hixson, J.E. Apo B signal peptide length polymorphisms are associated with apo B and LDL-C levels in Mexican Americans. Atherosclerosis 120:37-45, 1996.

43. Cole, S.A., Birnbaum, S., and Hixson, J.E. MspI restriction fragment length polymorphism at the cholesteryl ester transfer protein (CETP) locus in baboons. Anim. Genet. 27:63, 1996.

44. Cole, S.A., Birnbaum, S., and Hixson, J.E. TaqI restriction fragment length polymorphism at the hepatic lipase (LIPC) locus in baboons. Anim. Genet. 27:63, 1996.

45. Hixson, J.E., Jett, C., and Birnbaum, S. Identification of promoter sequences in the 5' untranslated region of the baboon apo (a) gene. J. Lipid Res., 37:2324-2331, 1996.

46. Mitchell, B.D., Kammerer, C.M., Blangero, J., Mahaney, M.C., Rainwater, D.L., Dyke, B., Hixson, J.E., Henkel, R.D., Sharp, M.R., Comuzzie, A.G., VandeBerg, J.L., Stern, M.P., and MacCluer, J.W. Genetic and environmental contributions to cardiovascular

risk factors in Mexican Americans: the San Antonio family heart study, Circulation, 94:2159-2170, 1996.

47. Hixson, J.E., McMahan, C.A., Malcom, G.T., Strong, J.P., and the PDAY Research Group. Polymorphism in the apolipoprotein (a) gene promoter region and atherosclerosis in right coronary artery of young white males. Pennington Center Nutrition Series: Nutrition, Genetics, and Heart Disease, 6:224-238, 1996.

48. Blangero, J., Williams-Blangero, S., Mahaney, M.C., Comuzzie, A.G., Hixson, J.E., Samollow, P.B., Sharp, R.M., Stern, M.P., and MacCluer, J.W. A major gene for apolipoprotein AI concentration is thyroid hormone dependent in Mexican Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 16:1177-1183, 1996.

49. Bowman, B.H., Yang, F., Buchanan, J.M., Adrian, G.S., Martinez, A.O., Jansen, L., Zhao, M., Atherton, S.L., Hixson, J.E. Human APOE protein localized in brains of transgenic mice. Neuroscience Letters 219:57-59, 1996.

50. Comuzzie, A.G., Hixson, J.E., Almasy, L., Mitchell, B.D., Mahaney, M.C., Dyer, T.D., Stern, M.P., MacCluer, J.W., and Blangero, J. A major quantitative trait locus determining serum leptin levels and fat mass is located on human chromosome 2. Nature Genet., 15:273-276, 1997.

51. Rainwater, D.L., Kammerer, C.M., VandeBerg, J.L., and Hixson, J.E. Characterization of the genetic elements controlling lipoprotein(a) concentrations in Mexican Americans. Evidence for at least three controlling elements linked to LPA, the locus encoding apolipoprotein(a). Atherosclerosis 128:223-244, 1997.

52. Cole, S.A., Birnbaum, S., and Hixson, J.E. Recent polymorphic insertion of an Alu repeat in the baboon lipoprotein lipase (LPL) gene. Gene, 193:197-201, 1997.

53. Atwood, L.D., Kammerer, C.M., Samollow, P.B., Hixson, J.E., Shade, R.E., and MacCluer, J.W. Linkage of essential hypertension to the angiotensinogen locus in Mexican Americans. Hypertension, 30:326-330, 1997.

54. Cole, S.A., Chen, S., Isaacson, C.J., and Hixson, J.E. Ban II restriction fragment length polymorphism at the apolipoprotein E (ApoE) locus in baboons. Anim. Genet., 28:319, 1997.

55. Mitchell, B.D., Blangero, J., Comuzzie, A.G., Almasy, L.A., Shuldiner, A.R., Silver, K., Stern, M.P., MacCluer, J.W., and Hixson, J.E. A paired sibling analysis of the beta-3 adrenergic receptor and obesity in Mexican Americans. J. Clin. Invest. 101(3): 584-587, 1998.

56. Rainwater, D.L., Kammerer, C.M., Hixson, J.E., Carey, K.D., Rice, K.S., Dyke, B., VandeBerg, J.F., Slifer, S.H., Atwood, L.D., McGill, H.C., Jr., and VandeBerg, J.L. Two major loci control variation in b-lipoprotein cholesterol and response to dietary fat and cholesterol in baboons. Arterioscler., Thromb., and Vasc. Biol. 18:1061-1068, 1998.

57. Cox, L.A., Jett, C., and Hixson, J.E. Molecular basis of the apolipoprotein(a) null phenotype: a splice site mutation is associated with deletion of a single exon in a null

allele, J. Lipid Res., 39:1319-1326, 1998.

58. Rainwater, D.L., Almasy, L., Blangero, J., Cole, S.A., VandeBerg, J.L., MacCluer, J.W., and Hixson, J.E. A genome search identifies major quantitative trait loci on human chromosomes 3 and 4 that influence cholesterol concentrations in small LDL particles. Arterioscler., Thromb., and Vasc. Biol., 19:777-783, 1999.

59. MacCluer, J.W., Stern, M.P., Almasy, L., Atwood, L.A., Blangero, J., Comuzzie, A.G., Dyke, B., Haffner, S.M., Henkel, R.D., Hixson, J.E., Kammerer, C.M., Mahaney, M.C., Mitchell, B.D., Rainwater, D.L., Samollow, P.B., Sharp, R.M., VandeBerg, J.L., and Williams, J. Genetics of atherosclerosis risk factors in Mexican Americans, Nutrition Reviews 57:S59-S65, 1999.

60. Hixson, J.E., Almasy, L., Cole, S., Birnbaum, S., Mitchell, B.D., Mahaney, M.C., Stern, M.P., MacCluer, J.W., Blangero, J., and Comuzzie, A.G. Normal variation in leptin levels is associated with polymorphisms in the pro-opiomelanocortin gene, *POMC*. J. Clin. Endicrol. and Metab. 84:3187-3191, 1999.

61. Mitchell, B.D., Cole, S.A., Comuzzie, A.G., Almasy, L., Blangero, J. MacCluer, J.W., and Hixson, J.E. A quantitative trait locus influencing body mass index maps to the region of the beta-3 adrenergic receptor. Diabetes 48:1863-1867, 1999.

62. Almasy, L., Hixson, J.E., Rainwater, D.L., Cole, S., Williams, J.T., Mahaney, M.C., VandeBerg, J.L., Stern, M.P., MacCluer, J.W., and Blangero, J. Human pedigree-based QTL mapping: localization of two genes influencing HDL cholesterol metabolism. Am. J. Hum. Genet. 64:1686-1693, 1999.

63. Hixson, J.E., and Blangero, J. Genomic searches for genes that influence atherosclerosis and its risk factors. In: Atherosclerosis V, the Fifth Saratoga International Conference. Eds. F. Numano and M.A. Gimbrone, Jr. Ann. N.Y. Acad. Sci. 902:1-7, 2000.

64. Cole, S.A., Mitchell, B.D., Hsueh, W.C., Pinetda P, Beamer, B.A., Shuldiner, A.R., and Hixson, J.E. The Pro12Ala variant of peroxisome proliferator-activated receptor g-2 is associated with measures of obesity in Mexican Americans. Int. J. Obes. Relat. Metab. Disord 24:522-524, 2000.

65. Mitchell, B.D., Cole, S.A., Bauer, R.L., Iturria, S.J., Blangero, J., Rodriguez, E.A., MacCluer, J.W., and Hixson, J.E. Genes influencing variation in serum osteocalcin concentrations are linked to regions on chromosomes 16q and 20q. J. Clin. Endocrinol. Metab. 85:1362-1366, 2000.

66. Mitchell, B.D., Cole, S.A., Hsueh, W.C., Comuzzie, A.G., Blangero, J. MacCluer, J.W., and Hixson, J.E. Linkage of serum insulin concentrations to chromosome 3p in Mexican Americans. Diabetes 49:513-516, 2000.

67. Comuzzie, A.G., Almasy, L., Cole, S.A., Stern, M.P., Macluer, J.W., Blangero, J., and Hixson J.E. Linkage exclusion analysis of the chromosome 11 region containing UCP2 and UCP3 with obesity phenotypes in Mexican Americans. Int J Obes Relat Metab Disord 24:1065-1068, 2000.

68. Hsueh, W.C., Mitchell, B.D., Hixson, J.E. Rainwater, D.L. Effects of the apoE polymorphism on plasma lipoproteins in Mexican Americans. Annals of Epidemiol. 10:524-531, 2000.

69. Atwood, L.D., Samollow, P.B., Hixson, J.E., Stern, M.P., and MacCluer, J.W. Genome-wide linkage analysis of blood pressure in Mexican Americans. Genetic Epidemiology 20:373-382, 2001.

70. Atwood, L.D., Samollow, P.B., Hixson, J.E., Stern, M.P., and MacCluer, J.W. Genome-wide linkage analysis of pulse pressure in Mexican Americans. Hypertension 37:425-428, 2001.

71. Martin, L.J., Blangero, J., Rogers, J., Mahaney, M.C., Hixson, J.E., Carey, K.D., Morin, P.A., Comuzzie, A.G . A quantitative trait locus influencing estrogen levels maps to a region homologous to human chromosome 20. Physiological Genomics. 5:75-80, 2001.

72. Hsueh W.C., Cole, S.A., Shuldiner, A.R., Beamer, B.A., Blangero, J., Hixson, J.E., MacCluer. J.W., Mitchell, B.D. Interactions between variants in the b3-adrenergic receptor and peroxisome proliferator-activated receptor-g2 genes and obesity. Diabetes Care 24:672-677, 2001.

73. Arya, R., Duggirala, R., Almasy, L., Rainwater, D.L., Mahaney, M.C., Cole, S., Dyer, T.D., Williams, K., Leach, R.J., Hixson, J.E., MacCluer, J.W., O'Connell, P., Stern, M.P., Blangero, J. Evidence for Linkage of High Density Lipoprotein-Cholesterol (HDL-C) Concentrations to a Genetic Location on Chromosome 9p in Mexican Americans, Nature Genetics 30:102-5, 2001.

74. Martin L.J., Blangero J., Rogers J., Mahaney M.C., Hixson J.E., Carey K.D., Comuzzie A.G. A quantitative trait locus influencing activin-to-estrogen ratio in pedigreed baboons maps to a region homologous to human chromosome 19. Hum Biol. 73:787-800, 2001.

75. Martin L.J., Mahaney M.C., Almasy L., Hixson J.E., Cole S.A., MacCluer J.W., Jaquish C.E., Blangero J., Comuzzie A.G. A quantitative trait locus on chromosome 22 for serum leptin levels adjusted for serum testosterone. Obes Res. 10:602-607, 2002.

76. Martin, L.J., Cole, S.A., Hixson, J.E., Mahaney, M., Czerwinski, S.A., Almasy, L., Blangero, J., Comuzzie, A.G. Genotype by smoking interaction for leptin levels in the San Antonio Family Heart Study, Genetic Epidemiology 22:105-115, 2002.

77. Mahaney, M.C., Almasy, L., Rainwater, D.L., VandeBerg, J.L., Cole, S.A., Hixson, J.E., Blangero, J., and MacCluer, J.W. A Quantitative Trait Locus on Chromosome 16q Influences Normal Variation in Plasma HDL-C Levels in Mexican Americans. Arteriosclerosis, Thrombosis, and Vascular Biology 23:339-345, 2003.

78. Austin, M.A., Edwards, K.L., Monks, S.A., Koprowicz, K., Brunzell, J.D., Motulsky, A.G., Mahaney, M.C., Hixson, J.E. Genomewide scan for LDL particle size in Familial Combined Hyperlipidemia and Familial Hypertriglyceridemia. Journal of Lipid Research, 44:2161-2168, 2003.

79. Kammerer, C.M., Schneider, J.L., Cole, S.A., Hixson, J.E., Samollow, P.B., O'Connell,

J.R., Perez, R., Dyer, T.D., Almasy, L., Blangero, J., Bauer, R.L., and Mitchell, B.D. Quantitative trait loci on chromosomes 2p, 4p, and 12q influence bone mineral density of the forearm and hip in Mexican Americans. Journal of Bone and Mineral Research 18:2245-2252, 2003.

80. Comuzzie, A.G., Mitchell, B.D., Cole, S., Martin, L.J., Hsueh, W-C, Rainwater, D.L,., Almasy, L., Stern, M., Hixson, J.E., MacCluer, J.W., Blangero, J. The genetics of obesity in Mexican Americans: the evidence from genome scanning efforts in the San Antonio Family Heart Study, Human Biology 75:635-646, 2003.

81. Kammerer CM, Gouin N, Samollow PB, VandeBerg JF, Hixson JE, Cole SA, MacCluer JW, Atwood LD. Two quantitative trait loci affect ACE activities in Mexican-Americans. Hypertension. 43:466-470, 2004.

82. Martin L.J., Cianflone K., Zakarian R., Nagrani G., Almasy L., Rainwater D.L., Cole S., Hixson J.E., MacCluer J.W., Blangero J., Comuzzie A.G. Bivariate linkage between acylation-stimulating protein and BM and high-density lipoproteins, Obesity Research 12:669-678, 2004.

83. Rainwater, D.L., Mahaney, M.C., VandeBerg, J.L., Brush, G., Almasy, L., Blangero, J., Cole, S.A., Dyke, B., Hixson, J.E., Cole, S.A., Stern, M.P., and MacCluer, J.W. A quantitative trait locus influences coordinated variation in measures of apoB-containing lipoproteins. Atherosclerosis 176:379-386, 2004.

84. Scheer, W.D., Boudreau, D.A., Hixson, J.E., McGill, H.C., Newmann, W.P., Tracy, R.E., Zieske, A.W., and Strong, J. P. ACE insert/delete polymorphism and atherosclerosis. Atherosclerosis 178:241-247, 2005.

85. Klos K.L.E., Kardia S.L.R, Hixson J.E., Turner S.T., Hanis C., Boerwinkle E., Sing CF. Linkage evidence from three ethnic groups for multiple genes with context-dependent effects on inter-individual variation in plasma apolipoprotein E. Annals of Human Genetics 69:157-167, 2005.

86. Almasy, L., Rainwater, D.L., Cole, S., Mahaney, M.C., VandeBerg, J.L., Hixson, J.E., Stern, M.P., MacCluer, J.W., and Blangero, J. Joint linkage and association analysis of the hepatic lipase promoter polymorphism and lipoprotein size phenotypes. Human Biology 77:17-25, 2005.

87. Clark, A.G., Boerwinkle, E., Hixson, J.E., and Sing, C.F. Determinants of the success of whole-genome association testing. Genome Research 15:1463-1467, 2005.

88. Brown, C.M., Rea,T.J., Hamon, S.C., Hixson, J.E., Boerwinkle, E., Clark, A.G., and Sing, C.F. The contribution of individual and pairwise combinations of SNPs in the APOA1 and APOC3 genes to interindividual HDL-C variability. Journal of Molecular Medicine 84:561-72, 2006.

89. North, K.E., Carr, J.J., Borecki, I.B., Kraja, A., Province, M., Pankow, J.S., Wilk, J.B., Hixson, J.E., Heiss, G. for the FHS Investigators. QTL-specific genotype-by-smoking interaction and burden of calcified coronary atherosclerosis: The NHLBI Family Heart Study. Atherosclerosis 193:11-19, 2006.

90. Klos, K.L.E., Sing, C.F., Boerwinkle, E., Hamon, S., Rea, T., Clark, A., Fornage, M., Liu, K., and Hixson, J.E. Consistent effects of reverse cholesterol transport candidate gene variation on plasma lipid and apolipoprotein levels in Cardia participants. Arteriosclerosis, Thrombosis, and Vascular Biology 26:1828-1836, 2006.

91. Payseur, B.A., Clark, A.G., Hixson, J.E., Boerwinkle, E., and Sing, C.F. Contrasting multi-site genotypic distributions among discordant quantitative phenotypes: the APOA1/C3/A4/A5 gene cluster and cardiovascular disease risk factors. Genetic Epidemiology 30:508-518, 2006.

92. Corella, D., Arnett, D.K., Tsai, M.Y., Kabagambe, E.K., Peacock, J.M., Hixson, J.E., Straka, R.J., Province, M., Lai, C.Q., Parnell, L.D., Borecki, I., and Ordovas, J.M. The -256T>C Polymorphism in the Apolipoprotein A-II Gene Promoter Is Associated with Body Mass Index and Food Intake in the Genetics of Lipid Lowering Drugs and Diet Network Study. Clinical Chemistry 53:1144-1152, 2007.

93. Lai, C.Q., Arnett, D.K., Corella, D., Straka, R.J., Tsai, M.Y., Peacock, J.M., Adiconis, X., Parnell, L.D., Hixson, J.E., Province, M.A., and Ordovas, J.M. Fenofibrate Effect on Triglyceride and Postprandial Response of Apolipoprotein A5 Variants. The GOLDN Study. Arteriosclerosis, Thrombosis, and Vascular Biology 27:1417-1425, 2007.

94. Shimmin, L., Natarajan, S., Ibarguen, H., Montasser, M., Kim, D-K., Hanis, C.L., Boerwinkle, E., Wadhwa, P.D. and Hixson J.E. Coricotropin Releasing Hormone (CRH) gene variation: comprehensive variant and molecular haplotype discovery for disease association and evolutionary studies. DNA Sequence 18:432-442, 2007.

95. Shen, J., Arnett, D.K., Peacock, J.M., Parnell, L.D., Kraja, A., Hixson, J.E., Tsai, M.Y., Lai, C.Q., Kabagambe, E.K., Straka, R.J., and Ordovas, J.M. Interleukin1-beta genetic polymorphisms interact with polyunsaturated fatty acids to modulate risk of the metabolic syndrome. Journal of Nutrition 137:1846-1851, 2007.

96. Gu, D., Rice, T., Wang, S., Yang, W., Gu, C., Chen, C.S., Hixson, J.E., Jaquish, C.E., Yao, Z.J., Liu, D.P., Rao, D.C., and He, J. Heritability of blood pressure responses to dietary sodium and potassium intake in a Chinese population. Hypertension 50:116-22, 2007. PMCID 2258208

97. Andrés, A.M., Clark, A.G., Shimmin, L., Boerwinkle, E., Sing, C.F., and Hixson, J.E. Assessing the accuracy of statistical haplotype inference with sequence data of known phase. Genetic Epidemiology 31:659-671, 2007. PMCID 2291540

98. The GenSalt Collaborative Research Group. GenSalt: rationale, design, methods and baseline characteristics of study participants. Journal of Human Hypertension 2:639-646. 2007.

99. Bielinski, S.J, Pankow, J.S., Hopkins, P.N., Eckfeldt, J.H., Hixson, J.E., Liu, Y., Register, T., Myers, R.H., and Arnett, D.K. Circulating MCP-1 levels show linkage to chemokine receptor gene cluster on chromosome 3: the NHLBI Family Heart Study follow-up examination. Genes and Immunity 8:684-90, 2007.

100. Jiao, L., Doll, M.A., Hein, D.W., Bondy, M.L., Hassan, M.M., Hixson, J.E., Abbruzzese, J.L., and Li, D. Haplotype of N-acetyltransferase 1 and 2 and risk of pancreatic cancer. Cancer Epidemiology, Biomarkers, and Prevention 16:2379-2386, 2007. PMCID 2215308

101. Shen, J., Arnett. D.K., Pérez-Martínez, P., Parnell, L.D., Lai, C.Q., Peacock, J.M., Hixson, J.E., Tsai, M.Y., Straka, R.J., Hopkins, P.N., and Ordovás, J.M. The effect of IL6-174C/G polymorphism on postprandial triglycerides metabolism in the GOLDN study. Journal of Lipid Research 49:1839-1845, 2008. PMCID 2444004

102. Shen, J., Arnett, D.K., Parnell, L.D., Peacock, J.M., Lai, C.Q., Hixson, J.E., Tsai, M.Y., Province, M.A., Straka, R.J., and Ordovas, J.M. Association of common C-reactive protein (CRP) gene polymorphisms with baseline plasma CRP levels and fenofibrate response: the GOLDN study. Diabetes Care 31:910-915, 2008.

103. Smith, J.A., Arnett, D.K., Kelly, R.J., Ordovas, J.M., Sun, Y.V., Hopkins, P.N., Hixson, J.E., Straka, R.J., Peacock, J.M., and Kardia, S.L. The genetic architecture of fasting plasma triglyceride response to fenofibrate treatment. European Journal of Human Genetics 16:603-613, 2008. PMCID 2546577

104. Zhang, Q., Lewis, C.E., Wagenknecht, L.E., Myers, R.H., Pankow, J.S., Hunt, S.C., North, K.E., Hixson, J.E., Carr, J., Shimmin, L.C., Borecki, I., and Province, M.A. Genome-wide admixture mapping for coronary artery calcification in African Americans: the NHLBI Family Heart Study. Genetic Epidemiology 32:264-272, 2008.

105. Bielinski, S.J, Miller, M., Pankow, J.S., Hopkins, P.N., Eckfeldt, J.H., Hixson, J.E., Liu, Y., Register, T., Myers, R.H., and Arnett, D.K. Circulating soluble ICAM-1 levels show linkage to ICAM gene cluster region on chromosome 19: the NHLBI Family Heart Study follow-up examination. Atherosclerosis 199:172-178, 2008

106. Klos, K.L.E., Shimmin, L.C., Ballentyne, C., Boerwinkle, E., Clark, A., Coresh, J., Hanis, C., Liu, K., and Hixson J.E. APOE/C1/C4/C2 hepatic control region polymorphism influences plasma apoE and LDL cholesterol levels. Human Molecular Genetics 17:2039-2046, 2008.

107. Chen, J., Gu, D., Jaquish, C.E., Chen, C.S., Rao, D.C., Liu, D., Hixson, J.E., Hamm, L.L., Gu, C.C., Whelton, P.K., and He, J., and the GenSalt Collaborative Research Group. Association between blood pressure responses to the cold pressor test and dietary sodium intervention in a Chinese population. Arch Intern Med. 168:1740-1746, 2008. PMCID 2535851

108. Liu, Y., Ordovas. J.M., Gao, G., Province, M., Straka, R.J., Tsai, M.Y., Lai, C.Q., Zhang, K., Borecki, I., Hixson, J.E., Allison, D.B., Arnett, D.K. The SCARB1 gene is associated with lipid response to dietary and pharmacological interventions. J Hum Genet. 53:709-717, 2008.

109. Leduc, M.S., Shimmin, L.C., Klos, K.L.E., Hanis, C., Boerwinkle, E., and Hixson, J.E. Comprehensive evaluation of apolipoprotein H gene (*APOH*) variation identifies novel associations with measures of lipid metabolism in GENOA. J Lipid Res 49:2648-2656, 2008. PMCID 2582370

110. Yang, W., Gu, D., Chen, J., Jaquish, C.E., Rao, D.C., Wu, X., Hixson, J.E., Duan, X., Kelly, T.N., Hamm, L.L., Whelton, P.K., He, J.; GenSalt Collaborative Research Group. Agreement of blood pressure measurements between random-zero and standard mercury sphygmomanometers. Am J Med Sci 336:373-378, 2008. PMCID 2587170

111. Chung, C.C., Shimmin, L., Natarajan, S., Hanis, C.L., Boerwinkle, E., and Hixson, J.E. A glucocorticoid receptor gene variant in the 3' untranslated region is associated with multiple measures of blood pressure in GENOA J Clin Endocrinol Metab 94:268-276, 2009. PMCID 2630865

112. He, J., Gu, D., Chen, J., Jaquish, C.E., Rao, D.C., Hixson, J.E., Chen, J.C., Duan, X., Huang, J.F., Chen, C.S., Kelly, T.N., Bazzano, L.A., Whelton, P.K.; GenSalt Collaborative Research Group. Gender difference in blood pressure responses to dietary sodium intervention in the GenSalt study. J Hypertens 27:48-54, 2009. PMCID 2882679

113. Liu, Y., Ordovas. J.M., Gao, G., Province, M., Straka, R.J., Tsai, M.Y., Lai, C.Q., Zhang, K., Borecki, I., Hixson, J.E., Allison, D.B., and Arnett, D.K. Pharmacogenetic association of the APOA1/C3/A4 gene cluster and lipid responses to fenofibrate-the genetics of lipid lowering drugs and diet network (GOLDN) study. Pharmacogenetics & Genomics 19:161-169, 2009. PMCID 2733171

114. Warodomwichit, D., Arnett, D.K., Kabagambe, E.K., Tsai, M.Y., Hixson, J.E., Straka, R.J., Province, M., An, P., Lai, C.Q., Borecki, I., Ordovas, J.M. Polyunsaturated fatty acids modulate the effect of TCF7L2 gene variants on postprandial lipemia. J Nutr 139:439-446, 2009. PMCID 2714378

115. Warodomwichit, D., Shen, J., Arnett, D.K., Tsai, M.Y., Kabagambe, E.K., Peacock, J.M., Hixson, J.E., Straka, R.J., Province, M.A., An, P., Lai, C.Q., Parnell, L.D., Borecki, I.B., Ordovas, J.M. ADIPOQ Polymorphisms, monounsaturated fatty acids, and obesity risk: The GOLDN Study. Obesity (Silver Spring) 17:510-517, 2009. PMCID 2753535

116. Chen, J., Gu, D., Huang, J., Rao, D.C., Jaquish, C.E., Hixson, J.E., Chen, C.S., Chen, J., Lu, F., Hu, D., Rice, T., Kelly, T.N., Hamm, L.L., Whelton, P.K., He, J.; GenSalt Collaborative Research Group. Metabolic syndrome and salt sensitivity of blood pressure in non-diabetic people in China: a dietary intervention study. Lancet 373:829-835, 2009. PMCID 2822441

117. Montasser, M.E., Shimmin, L.C., Hanis, C.L., Boerwinkle, E., and Hixson, J.E. Gene by smoking interaction in hypertension: Identification of a major QTL on chromosome 15q for systolic blood pressure in Mexican Americans. J Hypertension 37:491-501, 2009. PMCID 2664514

118. Rasmussen-Torvik, L.J., Pankow, J.S., Peacock, J.M., Borecki, I.B., Hixson, J.E., Tsai, M.Y., Kabagambe, E.K., Arnett, D.K. Suggestion for linkage of chromosome 1p35.2 and 3q28 to plasma adiponectin concentrations in the GOLDN Study. BMC Med Genet. 10:39, 2009. PMCID 2691741

119. Kelly, T.N., Rice, T.K., Gu, D., Hixson, J.E., Chen, J., Liu, D., Jaquish, C.E., Bazzano, L.A., Hu, D., Ma, J., Gu, C.C., Huang, J., Hamm, L.L., and He, J. Novel Genetic

Variants in the alpha-Adducin and Guanine Nucleotide Binding Protein beta-Polypeptide 3 Genes and Salt Sensitivity of Blood Pressure. Am J Hypertens. 22:985-92 Am J Hypertens. 2009. PMCID 2882159

120. Zhao, Q., Gu, D., Chen, J., Bazzano, L.A., Rao, D.C., Hixson, J.E., Jaquish, C.E., Cao, J., Chen, J., Li, J., Rice, T., and He, J. Correlation Between Blood Pressure Responses to Dietary Sodium and Potassium Intervention in a Chinese Population. Am J Hypertens. 22:985-92, 2009. PMCID 2885718

121. Mei, H., Gu, D., Rice, T.K., Hixson, J.E., Chen, J., Jaquish, C.E., Zhao, Q., Chen, C.S., Chen, J.C., Gu, C.C., Kelly, T.N., and He, J. Heritability of blood pressure responses to cold pressor test in a Chinese population. Am J Hypertens 22:1096-1100, 2009. PMCID 2896683

122. Montasser, M.E., Shimmin, L.C., Gu, Donfeng; Chen, Jing; Gu, Charles; Kelly, Tanika N; Jaquish, Cashell E; Rice, Treva; Rao, DC; Cao, Jie; Chen, Jichun; Liu, De-Pei; Whelton, Paul; He, Jiang; and Hixson, James E. Blood pressure response to potassium supplementation is associated with genetic variation in endothelin 1 and interactions with E selectin in rural Chinese. Journal of Hypertension 28: 748–755, 2010. PMCID 2919321

123. Mak, S., Sun, H., Acevedo, F., Shimmin, L.C., Zhao, L., Teng, B.B., Hixson, J.E. Differential expression of genes in the calcium-signaling pathway underlies lesion development in the LDb mouse model of atherosclerosis. Atherosclerosis 213:40-51, 2010. PMCID 2963700

124. Chen, S., Wang, H., Lu, X., Liu, D.P., Chen, J., Jaquish, C.E., Rao, D.C., Hixson, J.E., Kelly, T.N., Hou, L., Wang, L., Huang, J., Chen, C.S., Rice, T.K., Whelton, P.K., He, J., Gu, D. GenSalt Collaborative Research Group. Polymorphisms in the GNB3 and ADD1 genes and blood pressure in a Chinese population. Hum Genet 128:137-143, 2010.

125. Gu, D., Kelly, T.N., Hixson, J.E., Chen, J., Liu, D., Chen, J.C., Rao, D.C., Mu, J., Ma, J., Jaquish, C.E., Rice, T.K., Gu, C., Hamm, L.L., Whelton, P.K., He, J. Genetic variants in the renin-angiotensin-aldosterone system and salt sensitivity of blood pressure. J Hypertens 28:1210-1220, 2010. PMCID 2884148

126. Zhao Q, Gu D, Kelly TN, Hixson JE, Rao DC, Jaquish CE, Chen J, Huang J, Chen CS, Gu CC, Whelton PK, He J. Association of genetic variants in the apelin-APJ system and ACE2 with blood pressure responses to potassium supplementation: the GenSalt study. Am J Hypertens 23:606-613, 2010. PMCID 2890255

127. Zhao Q, Hixson JE, Rao DC, Gu D, Jaquish CE, Rice T, Shimmin LC, Chen J, Cao J, Kelly TN, Hamm LL, He J. Genetic variants in the apelin system and blood pressure responses to dietary sodium interventions: a family-based association study. J Hypertens 28:756-763, 2010. PMCID 2905479

128. Kelly TN, Hixson JE, Rao DC, Mei H, Rice TK, Jaquish CE, Shimmin LC, Schwander K, Chen CS, Liu D, Chen J, Bormans C, Shukla P, Farhana N, Stuart C, Whelton PK, He J, Gu D. Genome-wide Linkage and Positional Candidate Gene Study of Blood Pressure Response to Dietary Potassium Intervention: The GenSalt Study. Circ Cardiovasc Genet 3:539-547, 2010.

129. Shen H, Bielak LF, Ferguson JF, Streeten EA, Yerges-Armstrong LM, Liu J, Post W, O'Connell JR, Hixson JE, Kardia SL, Sun YV, Jhun MA, Wang X, Mehta NN, Li M, Koller DL, Hakonarson H, Keating BJ, Rader DJ, Shuldiner AR, Peyser PA, Reilly MP, Mitchell BD. Association of the Vitamin D Metabolism Gene CYP24A1 With Coronary Artery Calcification. Arterioscler Thromb Vasc Biol 30:2648-54, 2010. PMCID 2988112

130. Wang L, Hou L, Li H, Chen J, Kelly TN, Jaquish CE, Rao DC, Hixson JE, Hu D, Chen CS, Gu C, Chen S, Lu X, Whelton PK, He J, Lu F, Huang J, Liu DP, Gu D; for the GenSalt Collaborative Research Group. Genetic variants in the renin-angiotensin system and blood pressure reactions to the cold pressor test. J Hypertens 28:2422-2428, 2010.

131. Coventry A, Bull-Otterson LM, Liu X, Clark AG, Maxwell TJ, Crosby J, Hixson JE, Rea TJ, Muzny DM, Lewis LR, Wheeler DA, Sabo A, Lusk C, Weiss KG, Akbar H, Cree A, Hawes AC, Newsham I, Varghese RT, Villasana D, Gross S, Joshi V, Santibanez J, Morgan M, Chang K, Iv WH, Templeton AR, Boerwinkle E, Gibbs R, Sing CF. Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nat Commun 1:131, 2010.

132. Kato N, Takeuchi F, Tabara Y, Kelly TN, Go MJ, Sim X, Tay WT, Chen CH, Zhang Y, Yamamoto K, Katsuya T, Yokota M, Kim YJ, Ong RT, Nabika T, Gu D, Chang LC, Kokubo Y, Huang W, Ohnaka K, Yamori Y, Nakashima E, Jaquish CE, Lee JY, Seielstad M, Isono M, Hixson JE, Chen YT, Miki T, Zhou X, Sugiyama T, Jeon JP, Liu JJ, Takayanagi R, Kim SS, Aung T, Sung YJ, Zhang X, Wong TY, Han BG, Kobayashi S, Ogihara T, Zhu D, Iwai N, Wu JY, Teo YY, Tai ES, Cho YS, He J. Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nat Genet. 43:531-538, 2011.

133. Hixson JE, Shimmin LC, Montasser ME, Kim DK, Zhong Y, Ibarguen H, Follis J, Malcom G, Strong J, Howard T, Langefeld C, Liu Y, Rotter JI, Johnson C, Herrington D. Common Variants in the Periostin Gene Influence Development of Atherosclerosis in Young Persons. Arterioscler Thromb Vasc Biol. 31:1661-1667, 2011.

134. Zhao Q, Gu D, Hixson JE, Liu DP, Rao DC, Jaquish CE, Kelly TN, Lu F, Ma J, Mu J, Shimmin LC, Chen J, Mei H, Hamm LL, He J. (2011) Common Variants in Epithelial Sodium Channel Genes Contribute to Salt-Sensitivity of Blood Pressure: The GenSalt Study. Circ Cardiovasc Genet. 4:375-380, 2011.

135. Barbalic M, Reiner AP, Wu C, Hixson JE, Franceschini N, Eaton CB, Heiss G, Couper D, Mosley T, Boerwinkle E. Genome-Wide Association Analysis of Incident Coronary Heart Disease (CHD) in African Americans: A Short Report. PLoS Genet. 7:e1002199, 2011.

136. He J, Gu D, Kelly TN, Hixson JE, Rao DC, Jaquish CE, Chen J, Zhao Q, Gu C, Huang J, Shimmin LC, Chen JC, Mu J, Ji X, Liu DP, Whelton PK; GenSalt Collaborative Research Group. Genetic variants in the renin-angiotensin-aldosterone system and blood pressure responses to potassium intake. J Hypertens. 29:1719-30, 2011.

137. Montasser ME, Gu D, Chen J, Shimmin LC, Gu C, Kelly TN, Jaquish CE, Rice T, Rao DC, Cao J, Chen J, Liu DP, Whelton PK, He J, Hixson JE. Interactions of genetic variants with physical activity are associated with blood pressure in Chinese: the GenSalt study. Am J Hypertens. 24:1035-40, 2011.

138. Bressler J, Shimmin LC, Boerwinkle E, Hixson JE. Global DNA methylation and risk of subclinical atherosclerosis in young adults: The Pathobiological Determinants of Atherosclerosis in Youth (PDAY) study. Atherosclerosis 219:958-962, 2011.

139. Irvin MR, Zhang Q, Kabagambe EK, Perry RT, Straka RJ, Tiwari HK, Borecki IB, Shimmin LC, Stuart C, Zhong Y, Hixson JE, Arnett DK. Rare PPARA variants and extreme response to fenofibrate in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Pharmacogenet Genomics 22:367-372, 2012.

140. Frazier-Wood AC, Ordovas JM, Straka RJ, Hixson JE, Borecki IB, Tiwari HK, Arnett DK. The PPAR alpha gene is associated with triglyceride, low-density cholesterol and inflammation marker response to fenofibrate intervention: the GOLDN study. Pharmacogenomics J. 13:312-317, 2012.

141. Wang L, Chen S, Zhao Q, Hixson JE, Rao DC, Jaquish CE, Huang J, Lu X, Chen J, Cao J, Li J, Li H, He J, Liu DP, Gu D; GenSalt Collaborative Research Group. Association between genetic variants of the ADD1 and GNB3 genes and blood pressure response to the cold pressor test in a Chinese Han population: the GenSalt Study. Hypertens Res. 35:805-810, 2012.

142. Gu D, Zhao Q, Kelly TN, Hixson JE, Rao DC, Cao J, Chen J, Li J, Chen J, Ji X, Hu D, Wang X, Liu DP, He J. The Role of the Kallikrein-Kinin System Genes in the Salt Sensitivity of Blood Pressure: The GenSalt Study. Am J Epidemiol. 176 Suppl 7:S72-80, 2012.

143. Wadhwa PD, Simhan HN, Entringer S, Buss C, Smith R, Hobel CJ, Farhana N, Shimmin L, Hixson JE, Sing CF. Variation in the Maternal Corticotrophin Releasing Hormone-Binding Protein (CRH-BP) Gene and Birth Weight in Blacks, Hispanics and Whites. PLoS One. 7:e43931, 2012.

144. Mei H, Gu D, Hixson JE, Rice TK, Chen J, Shimmin LC, Schwander K, Kelly TN, Liu DP, Chen S, Huang JF, Jaquish CE, Rao DC, He J. Genome-wide Linkage and Positional Association Study of Blood Pressure Response to Dietary Sodium Intervention: The GenSalt Study. Am J Epidemiol. 176 Suppl 7:S81-90, 2012.

145. Okada Y, Sim X, Go MJ, Wu JY, Gu D, Takeuchi F, Takahashi A, Maeda S, Tsunoda T, Chen P, Lim SC, Wong TY, Liu J, Young TL, Aung T, Seielstad M, Teo YY, Kim YJ, Lee JY, Han BG, Kang D, Chen CH, Tsai FJ, Chang LC, Fann SJ, Mei H, Rao DC, Hixson JE, Chen S, Katsuya T, Isono M, Ogihara T, Chambers JC, Zhang W, Kooner JS; KidneyGen Consortium; CKDGen Consortium, Albrecht E; GUGC consortium, Yamamoto K, Kubo M, Nakamura Y, Kamatani N, Kato N, He J, Chen YT, Cho YS, Tai ES, Tanaka T. Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. Nat Genet. 44:904-909, 2012.

146. Köttgen A, Yang Q, Shimmin LC, Tin A, Schaeffer C, Coresh J, Liu X, Rampoldi L,

Hwang SJ, Boerwinkle E, Hixson JE, Kao WH, Fox CS. Association of estimated glomerular filtration rate and urinary uromodulin concentrations with rare variants identified by UMOD gene region sequencing. PLoS One 7:e38311, 2012.

147. Huang J, Chen S, Lu X, Zhao Q, Rao DC, Jaquish CE, Hixson JE, Chen J, Wang L, Cao J, Li J, Li H, He J, Liu DP, Gu D. Polymorphisms of ACE2 are associated with blood pressure response to cold pressor test: the GenSalt study. Am J Hypertens. 25:937-942, 2012.

148. Kelly TN, Rebholz CM, Gu D, Hixson JE, Rice TK, Cao J, Chen J, Li J, Lu F, Ma J, Mu J, Whelton PK, He J. Analysis of Sex Hormone Genes Reveals Gender Differences in the Genetic Etiology of Blood Pressure Salt Sensitivity: The GenSalt Study. Am J Hypertens. 26:191-200, 2013.

149. Defagó MD, Gu D, Hixson JE, Shimmin LC, Rice TK, Gu CC, Jaquish CE, Liu DP, He J, Kelly TN. Common genetic variants in the endothelial system predict blood pressure response to sodium intake: the GenSalt study. Am J Hypertens. 26:643-56, 2013.

150. Kelly TN, Takeuchi F, Tabara Y, Edwards TL, Kim YJ, Chen P, Li H, Wu Y, Yang CF, Zhang Y, Gu D, Katsuya T, Ohkubo T, Gao YT, Go MJ, Teo YY, Lu L, Lee NR, Chang LC, Peng H, Zhao Q, Nakashima E, Kita Y, Shu XO, Kim NH, Tai ES, Wang Y, Adair LS, Chen CH, Zhang S, Li C, Nabika T, Umemura S, Cai Q, Cho YS, Wong TY, Zhu J, Wu JY, Gao X, Hixson JE, Cai H, Lee J, Cheng CY, Rao DC, Xiang YB, Cho MC, Han BG, Wang A, Tsai FJ, Mohlke K, Lin X, Ikram MK, Lee JY, Zheng W, Tetsuro M, Kato N, He J. Genome-Wide Association Study Meta-Analysis Reveals Transethnic Replication of Mean Arterial and Pulse Pressure Loci. Hypertension. 62:853-859, 2013.

151. Agopian AJ, Bhalla AD, Boerwinkle E, Finnell RH, Grove ML, Hixson JE, Shimmin LC, Sewda A, Stuart C, Zhong Y, Zhu H, Mitchell LE. Exon sequencing of PAX3 and T (brachyury) in cases with spina bifida. Birth Defects Res A Clin Mol Teratol. 97:597-601, 2013.

152. Polfus LM, Smith JA, Shimmin LC, Bielak LF, Morrison AC, Kardia SL, Peyser PA, Hixson JE. Genome-wide association study of gene by smoking interactions in coronary artery calcification. PLoS One. 8:e74642, 2013.

153. He J, Kelly TN, Zhao Q, Li H, Huang J, Wang L, Jaquish CE, Sung YJ, Shimmin LC, Lu F, Mu J, Hu D, Ji X, Shen C, Guo D, Ma J, Wang R, Shen J, Li S, Chen J, Mei H, Chen CS, Chen S, Chen J, Li J, Cao J, Lu X, Wu X, Rice TK, Gu CC, Schwander K, Hamm LL, Liu D, Rao DC, Hixson JE, Gu D. Genome-Wide Association Study Identifies Eight Novel Loci Associated with Blood Pressure Responses to Interventions in Han Chinese. Circ Cardiovasc Genet. 6:598-607, 2013.

154. Liu AY, Gu D, Hixson JE, Rao DC, Shimmin LC, Jaquish CE, Liu DP, He J, Kelly TN. Genome-wide linkage and regional association study of obesity-related phenotypes: The Gensalt study. Obesity 22:545-562, 2014.

155. Yang X, He J, Gu D, Hixson JE, Huang J, Rao DC, Shimmin LC, Chen J, Rice TK, Li J, Schwander K, Kelly TN. Associations of Epithelial Sodium Channel Genes With Blood Pressure Changes and Hypertension Incidence: The GenSalt Study. Am J Hypertens.

27:1370-1376. 2014.

156. Montasser ME, Shimmin LC, Gu D, Chen J, Gu C, Kelly TN, Jaquish CE, Rice TK, Rao DC, Cao J, Chen J, Liu DP, Whelton PK, Hamm LL, He J, Hixson JE. Variation in genes that regulate blood pressure are associated with glomerular filtration rate in Chinese. PLoS One. 9:e92468, 2014.

157. Yang X, Gu D, He J, Hixson JE, Rao DC, Lu F, Mu J, Jaquish CE, Chen J, Huang J, Shimmin LC, Rice TK, Chen J, Wu X, Liu D, Kelly TN. Genome-wide linkage and regional association study of blood pressure response to the cold pressor test in Han Chinese: the genetic epidemiology network of salt sensitivity study. Circ Cardiovasc Genet. 2014 7:521-528, 2014.

158, Li C, Yang X, He J, Hixson JE, Gu D, Rao DC, Shimmin LC, Huang J, Gu CC, Chen J, Li J, Kelly TN. A gene-based analysis of variants in the serum/glucocorticoid regulated kinase (SGK) genes with blood pressure responses to sodium intake: the GenSalt Study. PLoS One 9(5):e98432, 2014.

159. Howard TD, Mathias RA, Seeds MC, Herrington DM, Hixson JE, Shimmin LC, Hawkins GA, Sellers M, Ainsworth HC, Sergeant S, Miller LR, Chilton FH. DNA methylation in an enhancer region of the FADS cluster is associated with FADS activity in human liver. PLoS One. 9(5):e97510, 2014.

160. Lu X, Wang L, Lin X, Huang J, Charles Gu C, He M, Shen H, He J, Zhu J, Li H, Hixson JE, Wu T, Dai J, Lu L, Shen C, Chen S, He L, Mo Z, Hao Y, Mo X, Yang X, Li J, Cao J, Chen J, Fan Z, Li Y, Zhao L, Li H, Lu F, Yao C, Yu L, Xu L, Mu J, Wu X, Deng Y, Hu D, Zhang W, Ji X, Guo D, Guo Z, Zhou Z, Yang Z, Wang R, Yang J, Zhou X, Yan W, Sun N, Gao P, Gu D. Genome-wide association study in Chinese identifies novel loci for blood pressure and hypertension. Human Molecular Genetics. 24(3), 865-874, 2015.

161. Hwang JY, Sim X, Wu Y, Liang J, Tabara Y, Hu C, Hara K, Tam CH, Cai Q, Zhao Q, Jee S, Takeuchi F, Go MJ, Hee Ong RT, Ohkubo T, Kim YJ, Zhang R, Yamauchi T, So WY, Long J, Gu D, Lee NR, Kim S, Tomohiro K, Oh J, Liu J, Umemura S, Kim YJ, Jiang F, Maeda S, Chan JC, Lu W, Hixson JE, Adair LS, Jung K, Nabika T, Bae JB, Lee M, Seielstad M, Young TL, Teo YY, Kita Y, Takashima N, Osawa H, Lee SH, Shin MH, Shin DH, Choi BY, Shi J, Gao YT, Xiang YB, Zheng W, Kato N, Yoon M, He J, Shu XO, Ma RC, Kadowaki T, Jia W, Miki T, Qi L, Tai ES, Mohlke KL, Han BG, Cho YS, Kim BJ. Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. Diabetes 64:291-298, 2015.

162. Liu F, He J, Gu D, Rao DC, Huang J, Hixson JE, Jaquish CE, Chen J, Li C, Yang X, Li J, Rice TK, Shimmin LC, Kelly TN. Associations of Endothelial System Genes With Blood Pressure Changes and Hypertension Incidence: The GenSalt Study. Am J Hypertens. 28(6):780-788, 2015.

163. Reynolds L., Wan M., Ding J., Taylor J., Lohman K., Su D., Bennett B., Porter D., Gimple R., Pittman G., Wang X., Howard T., Siscovick D., Psaty B., Shea S., Burke G., Jacobs D., Rich S., Hixson J., Stein J., Stunnenberg H., Barr R., Kaufman J., Post W., Hoeschele I., Herrington D., Bell D., Liu Y. DNA Methylation of the Aryl Hydrocarbon Receptor Repressor Associations with Cigarette Smoking and Subclinical Atherosclerosis.

Circulation: Cardiovascular Genetics. 8(5), 707-716, 2015.

164. He J., Li C., Rao D., Hixson J., Huang J., Cao J., Rice T., Shimmin L., Gu D., Kelly T. Associations of renin-angiotensin-aldosterone system genes with blood pressure changes and hypertension incidence. American Journal of Hypertension. 28(11), 1310-1315, 2015.

165. Li C., Bazzano L., Rao D., Hixson J., He J., Gu D., Gu C., Shimmin L., Jaquish C., Schwander K., Liu D., Huang J., Lu F., Cao J., Chong S., Lu X., Kelly T. Genome-Wide Linkage and Positional Association Analyses Identify Associations of Novel AFF3 and NTM Genes with Triglycerides: The GenSalt Study. Journal of Genetics and Genomics. 42(3), 107-117, 2015.

166. Liu F., Yang X., Mo X., Huang J., Chen J., Kelly T., Hixson J., Rao D., Gu C., Shimmin L., Chen J., Rice T., Li J., Schwander K., He J., Liu D., Gu D. Associations of epithelial sodium channel genes with blood pressure: The GenSalt study. Journal of Human Hypertension. 29(4), 224-228, 2015.

167. Chen G., de las Fuentes L., Gu C., He J., Gu D., Kelly T., Hixson J., Jacquish C., Rao D., Rice T. Aggregate blood pressure responses to serial dietary sodium and potassium intervention: Defining responses using independent component analysis. BMC Genetics. 16(1), 2015.

168. Kato N, Loh M, Takeuchi F, Verweij N, Wang X, Zhang W, Kelly TN, Saleheen D, Lehne B, Mateo Leach I, Drong AW, Abbott J, Wahl S, Tan ST, Scott WR, Campanella G, Chadeau-Hyam M, Afzal U, Ahluwalia TS, Bonder MJ, Chen P, Dehghan A, Edwards TL, Esko T, Go MJ, Harris SE, Hartiala J, Kasela S, Kasturiratne A, Khor CC, Kleber ME, Li H, Mok ZY, Nakatochi M, Sapari NS, Saxena R, Stewart AF, Stolk L, Tabara Y, Teh AL, Wu Y, Wu JY, Zhang Y, Aits I, Da Silva Couto Alves A, Das S, Dorajoo R, Hopewell JC, Kim YK, Koivula RW, Luan J, Lyytikäinen LP, Nguyen QN, Pereira MA, Postmus I, Raitakari OT, Bryan MS, Scott RA, Sorice R, Tragante V, Traglia M, White J, Yamamoto K, Zhang Y, Adair LS, Ahmed A, Akiyama K, Asif R, Aung T, Barroso I, Bjonnes A, Braun TR, Cai H, Chang LC, Chen CH, Cheng CY, Chong YS, Collins R, Courtney R, Davies G, Delgado G, Do LD, Doevendans PA, Gansevoort RT, Gao YT, Grammer TB, Grarup N, Grewal J, Gu D, Wander GS, Hartikainen AL, Hazen SL, He J, Heng CK, Hixson JE, Hofman A, Hsu C, Huang W, Husemoen LL, Hwang JY, Ichihara S, Igase M, Isono M, Justesen JM, Katsuya T, Kibriya MG, Kim YJ, Kishimoto M, Koh WP, Kohara K, Kumari M, Kwek K, Lee NR, Lee J, Liao J, Lieb W, Liewald DC, Matsubara T, Matsushita Y, Meitinger T, Mihailov E, Milani L, Mills R, Mononen N, Müller-Nurasyid M, Nabika T, Nakashima E, Ng HK, Nikus K, Nutile T, Ohkubo T, Ohnaka K, Parish S, Paternoster L, Peng H, Peters A, Pham ST, Pinidiyapathirage MJ, Rahman M, Rakugi H, Rolandsson O, Rozario MA, Ruggiero D, Sala CF, Sarju R, Shimokawa K, Snieder H, Sparsø T, Spiering W, Starr JM, Stott DJ, Stram DO, Sugiyama T, Szymczak S, Tang WH, Tong L, Trompet S, Turjanmaa V, Ueshima H, Uitterlinden AG, Umemura S, Vaarasmaki M, van Dam RM, van Gilst WH, van Veldhuisen DJ, Viikari JS, Waldenberger M, Wang Y, Wang A, Wilson R, Wong TY, Xiang YB, Yamaguchi S, Ye X, Young RD, Young TL, Yuan JM, Zhou X, Asselbergs FW, Ciullo M, Clarke R, Deloukas P, Franke A, Franks PW, Franks S, Friedlander Y, Gross MD, Guo Z, Hansen T, Jarvelin MR, Jørgensen T, Jukema JW, Kähönen M, Kajio H, Kivimaki M, Lee JY, Lehtimäki T, Linneberg A, Miki T, Pedersen O, Samani NJ,

Sørensen TI, Takayanagi R, Toniolo D; BIOS-consortium; CARDIo GRAMplusCD; LifeLines Cohort Study; InterAct Consortium, Ahsan H, Allayee H, Chen YT, Danesh J, Deary IJ, Franco OH, Franke L, Heijman BT, Holbrook JD, Isaacs A, Kim BJ, Lin X, Liu J, März W, Metspalu A, Mohlke KL, Sanghera DK, Shu XO, van Meurs JB, Vithana E, Wickremasinghe AR, Wijmenga C, Wolffenbuttel BH, Yokota M, Zheng W, Zhu D, Vineis P, Kyrtopoulos SA, Kleinjans JC, McCarthy MI, Soong R, Gieger C, Scott J, Teo YY, He J, Elliott P, Tai ES, van der Harst P, Kooner JS, Chambers JC. Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nat Genet. 47(11):1282-93, 2015.

169. Guo L., Liu F., Chen S., Yang X., Huang J., He J., Jaquish C., Zhao Q., Gu C., Hixson J., Gu D. Common variants in the Na+-coupled bicarbonate transporter genes and salt sensitivity of blood pressure: the GenSalt study. Journal of Human Hypertension. J Hum Hypertens. 30:543-548, 2016.

170. Wen W., Kato N., Hwang J., Guo X., Tabara Y., Li H., Dorajoo R., Yang X., Tsai F., Li S., Wu Y., Wu T., Kim S., Guo X., Liang J., Shungin D., Adair L., Akiyama K., Allison M., Cai Q., Chang L., Chen C., Chen Y., Cho Y., Choi B., Gao Y., Go M., Gu D., Han B., He M., Hixson J., Hu Y., Huang T., Isono M., Jung K., Kang D., Kim Y., Kita Y., Lee J., Lee N., Lee J., Wang Y., Liu J., Long J., Moon S., Nakamura Y., Nakatochi M., Ohnaka K., Rao D., Shi J., Sull J., Tan A., Ueshima H., Wu C., Xiang Y., Yamamoto K., Yao J., Ye X., Yokota M., Zhang X., Zheng Y., Qi L., Rotter J., Jee S., Lin D., Mohlke K., He J., Mo Z., Wu J., Tai E., Lin X., Miki T., Kim B., Takeuchi F., Zheng W., Shu X.Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. Scientific Reports. Jan 20;6:17958. doi: 10.1038/srep17958, 2016.

171. Pattaro C., Teumer A., Gorski M., Chu A., Li M., Mijatovic V., Garnaas M., Tin A., Sorice R., Li Y., Taliun D., Olden M., Foster M., Yang Q., Chen M., Pers T., Johnson A., Ko Y., Fuchsberger C., Tayo B., Nalls M., Feitosa M., Isaacs A., Dehghan A., D'Adamo P., Adeyemo A., Dieffenbach A., Zonderman A., Nolte I., Van Der Most P., Wright A., Shuldiner A., Morrison A., Hofman A., Smith A., Dreisbach A., Franke A., Uitterlinden A., Metspalu A., Tonjes A., Lupo A., Robino A., Johansson Å., Demirkan A., Kollerits B., Freedman B., Ponte B., Oostra B., Paulweber B., Krämer B., Mitchell B., Buckley B., Peralta C., Hayward C., Helmer C., Rotimi C., Shaffer C., Müller C., Sala C., Van Duijn C., Saint-Pierre A., Ackermann D., Shriner D., Ruggiero D., Toniolo D., Lu Y., Cusi D., Czamara D., Ellinghaus D., Siscovick D., Ruderfer D., Gieger C., Grallert H., Rochtchina E., Atkinson E., Holliday E., Boerwinkle E., Salvi E., Bottinger E., Murgia F., Rivadeneira F., Ernst F.Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nat Commun. 2016 Jan 21;7:10023. doi: 10.1038/ncomms1002, 2016.

172. Lu X., Huang J., Mo Z., He J., Wang L., Yang X., Tan A., Chen S., Chen J., Gu C., Chen J., Li Y., Zhao L., Li H., Hao Y., Li J., Hixson J., Li Y., Cheng M., Liu X., Cao J., Liu F., Huang C., Shen C., Shen J., Yu L., Xu L., Mu J., Wu X., Ji X., Guo D., Zhou Z., Yang Z., Wang R., Yang J., Yan W., Peng X., Gu D. Genetic Susceptibility to Lipid Levels and Lipid Change over Time and Risk of Incident Hyperlipidemia in Chinese Populations. Circulation: Cardiovascular Genetics. 9(1), 37-44, 2016.

173. Li C, He J, Chen J, Zhao J, Gu D, Hixson JE, Rao, DC, Jaquish, CE, G, C, Chen J, Huang J, Chen S, Kelly TN. Genome-Wide Gene-Sodium Interaction Analyses on Blood Pressure. Hypertension. 68:348-355, 2016.

174. Perez-Martinez, P., Alcala-Diaz, J.F., Kabagambe, E.K., Garcia-Rios, A., Tsai, M.Y., Delgado-Lista, J., Kolovou, G., Straka, R. J., Gomez-Delgado, F., Hopkins, P.N., Marin, C., Borecki, I., Yubero-Serrano, E.M., Hixson, J.E., Camargo, A.A., Province, M.A., Lopez-Moreno, J., Rodriguez-Cantalejo, F., Tinahones, F. J., Mikhailidis, D. P., Perez-Jimenez, F., Arnett, D.K., Ordovas, J.M., Lopez-Miranda, J. Assessment of postprandial triglycerides in clinical practice. Journal of Clinical Lipidology.10:1163-1171, 2016.

175. Chappell CL, Darkoh C, Shimmin L, Farhana N, Kim DK, Okhuysen PC, Hixson J. Fecal Indole as a Biomarker of Susceptibility to Cryptosporidium Infection. Infect Immun. 84:2299-2306, 2016.

176. Shah RH, Northrup H, Hixson JE, Morrison AC, Au KS. Genetic association of the glycine cleavage system genes and myelomeningocele. Birth Defects Res A Clin Mol Teratol. 10:847-853, 2016 PMID: 27620832 PubMed Central PMCID: PMC5074854

177. Chen, S., Huang, J., Zhao, Q., Chen, J., Jaquish, C. E., He, J., Lu, X., Yang, X., Gu, C., Hixson, J.E., Liu, F., Rice, T.K., Cao, J., Chen, J., Gu, D. Associations between Genetic Variants of the Natriuretic Peptide System and Blood Pressure Response to Dietary Sodium Intervention. American Journal of Hypertension. 29(3), 397-404, 2016.

178. Ray EC, Chen J, Kelly TN, He J, Hamm LL, Gu D, Shimmin LC, Hixson JE, Rao DC, Sheng S, Kleyman TR. Human Epithelial Na+ Channel Missense Variants Identified in the GenSalt Study Alter Channel Activity. Am J Physiol Renal Physiol. 5:F908-F914, 2016. PubMed PMID: 27582106; PubMed Central PMCID: PMC5130461.

179. Hu Z, Liu F, Li M, He J, Huang J, Rao DC, Hixson JE, Gu C, Kelly TN, Chen S, Gu D, Yang X. Associations of Variants in the CACNA1A and CACNA1C Genes With Longitudinal Blood Pressure Changes and Hypertension Incidence: The GenSalt Study. Am J Hypertens. 2016 Jul 14. pii: hpw070. [Epub ahead of print] PubMed PMID: 27418245; PubMed Central PMCID: PMC5055736.

180. Zhang D, Gu D, He J, Hixson JE, Rao DC, Li C, He H, Chen J, Huang J, Chen J, Rice TK, Chen S, Kelly TN. Associations of the Serum/Glucocorticoid Regulated Kinase Genes With BP Changes and Hypertension Incidence: The Gensalt Study. Am J Hypertens. 30:95-101, 2017.

181. Li C, Kim YK, Dorajoo R, Li H, Lee IT, Cheng CY, He M, Sheu WH, Guo X, Ganesh SK, He J, Lee J, Liu J, Hu Y, Rao DC, Tsai FJ, Koh JY, Hu H, Liang KW, Palmas W, Hixson JE, Han S, Teo YY, Wang Y, Chen J, Lu CH, Zheng Y, Gui L, Lee WJ, Yao J, Gu D, Han BG, Sim X, Sun L, Zhao J, Chen CH, Kumari N, He Y, Taylor KD, Raffel LJ, Moon S, Rotter JI, Ida Chen YD, Wu T, Wong TY, Wu JY, Lin X, Tai ES, Kim BJ, Kelly TN. Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. Circ Cardiovasc Genet. 2017

182. Han X, Hu Z, Chen J, Huang J, Huang C, Liu F, Gu C, Yang X, Hixson JE, Lu X, Wang

L, Liu DP, He J, Chen S, Gu D. Associations Between Genetic Variants of NADPH Oxidase-Related Genes and Blood Pressure Responses to Dietary Sodium Intervention: The GenSalt Study. Am J Hypertens. 30:427-434, 2017.

183. Kelly TN, Li C, Hixson JE, Gu D, Rao DC, Huang J, Rice TK, Chen J, Cao J, Li J, Anderson CE, He J. Resequencing Study Identifies Rare Renin-Angiotensin-Aldosterone System Variants Associated With Blood Pressure Salt-Sensitivity: The GenSalt Study. Am J Hypertens. 30:495-501, 2017.

184. Hixson JE, Jun G, Shimmin LC, Wang Y, Yu G, Mao C, Warren AS, Howard TD, Heide RSV, Van Eyk J, Wang Y, Herrington DM. Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. Sci Rep. 7:4091, 2017.

185. Findley TO, Tenpenny JC, O'Byrne MR, Morrison AC, Hixson JE, Northrup H, Au KS. Mutations in folate transporter genes and risk for human myelomeningocele. Am J Med Genet A. 2017 Nov;173(11):2973-2984. doi: 10.1002/ajmg.a.38472. Epub 2017 Sep 26. PubMed PMID: 28948692; PubMed Central PMCID: PMC5650522.

186. Rahbar E, Ainsworth HC, Howard TD, Hawkins GA, Ruczinski I, Mathias R, Seeds MC, Sergeant S, Hixson JE, Herrington DM, Langefeld CD, Chilton FH. Uncovering the DNA methylation landscape in key regulatory regions within the FADS cluster. PLoS One. 2017 Sep 28;12(9):e0180903. doi: 10.1371/journal.pone.0180903. eCollection 2017. PubMed PMID: 28957329; PubMed Central PMCID: PMC5619705.

187. Li C, He J, Chen J, Zhao J, Gu D, Hixson JE, Rao DC, Jaquish CE, Rice TK, Sung YJ, Kelly TN. Genome-Wide Gene-Potassium Interaction Analyses on Blood Pressure: The GenSalt Study (Genetic Epidemiology Network of Salt Sensitivity). Circ Cardiovasc Genet. 2017 Dec;10(6). pii: e001811. doi: 10.1161/CIRCGENETICS.117.001811. PubMed PMID: 29212900; PubMed Central PMCID: PMC5728702.

188. Nierenberg JL, Li C, He J, Gu D, Chen J, Lu X, Li J, Wu X, Gu CC, Hixson JE, Rao DC, Kelly TN. Blood Pressure Genetic Risk Score Predicts Blood Pressure Responses to Dietary Sodium and Potassium: The GenSalt Study (Genetic Epidemiology Network of Salt Sensitivity). Hypertension. 2017 Dec;70(6):1106-1112. doi: 10.1161/HYPERTENSION AHA.117.10108. Epub 2017 Oct 9. PubMed PMID: 28993450.

189. Gu X, Gu D, He J, Rao DC, Hixson JE, Chen J, Li J, Huang J, Wu X, Rice TK, Shimmin LC, Kelly TN. Resequencing Epithelial Sodium Channel Genes Identifies Rare Variants Associated With Blood Pressure Salt-Sensitivity: The GenSalt Study. Am J Hypertens. 2018 Jan 12;31(2):205-211. doi: 10.1093/ajh/hpx169. PubMed PMID: 29036630; PubMed Central PMCID: PMC5861537.

190. Li H, Han X, Hu Z, Huang J, Chen J, Hixson JE, Rao DC, He J, Gu D, Chen S. Associations of NADPH oxidase-related genes with blood pressure changes and incident hypertension: The GenSalt Study. J Hum Hypertens. 2018 Apr;32(4):287-293. doi: 10.1038/s41371-018-0041-6. Epub 2018 Feb 20. PubMed PMID: 29463833; PubMed Central PMCID: PMC5889722.

191. Herrington DM, Mao C, Parker SJ, Fu Z, Yu G, Chen L, Venkatraman V, Fu Y, Wang Y,

Howard TD, Jun G, Zhao CF, Liu Y, Saylor G, Spivia WR, Athas GB, Troxclair D, Hixson JE, Vander Heide RS, Wang Y, Van Eyk JE. Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation. 2018 Jun 19;137(25):2741-2756. doi: 10.1161/CIRCULATIONAHA.118.034365.

EDITORIALS, REVIEW ARTICLES, BOOK CHAPTERS, AND BOOK REVIEWS

1. Hixson, J.E. Review of Short Protocols in Molecular Biology. In: American Journal of Human Biology 2:172-173, 1990.

2. Boerwinkle, E., and Hixson, J.E. Genes and normal lipid variation. Current Opinion in Lipidology 1:151-159, 1990.

3. Hixson, J.E. Molecular genetics of atherosclerosis in human and nonhuman primates. Chapter in: Molecular Applications in Biological Anthropology, ed: Eric J. Devor , Cambridge University Press, Cambridge, pp. 56-75, 1992.

4. Hixson, J.E. Review of Fundamentals of Molecular Evolution. In: Human Biology 64:661-662, 1993.

5. Rogers, J.A., and Hixson, J.E. Insights from model systems. Baboons as an animal model for genetic studies of common human disease. Am. J. Hum. Genet. 61:489-493, 1997.

6. Cole, S.A., and Hixson, J.E. PCR methodology applied to genetic studies of lipoprotein metabolism and atherosclerosis. In: Lipoprotein Protocols, editor: Jose M. Ordovas, Humana Press, Inc., 110:1-34, 1998.

7. Hixson, J.E. Genomic searches for genes that influence common disease in human and nonhuman primate families. In: Common Disease: Genetic and Pathogenetic Aspects of Multifactorial Diseases, editors: H. Imura, M. Kasuga and K. Nakao, Elsevier Science B.V., 251-259, 1999.

8. Boerwinkle, E., Hixson, J.E., and Hanis, C.L. Peeking under the peaks: following-up genome wide linkage analyses. Circulation 102:1877-1878, 2000.

9. Chang, B.H.-J., Hixson, J.E., Ma, K., and Chan, L. Current genomic investigation of lipid disorders. In: Lipid and Atherosclerosis Annual 2001, editors: A. Gaw and J. Shepherd, Taylor and Francis Publishing Group, pp. 321-332, 2001.

10. Hixson, J.E. Genetics of cardiovascular disease: From candidate genes to genomic screens and back again. In: Proceedings of the US-Japan Symposium on Genetic Research in Cardiovascular Disease. Japanese Heart Journal 45:S3-S8, 2004