Professor Nicole Soranzo, BSc, PhD

Curriculum Vitae

Present addresses:

Department of Human Genetics
Wellcome Trust Sanger Institute
Wellcome Genome Campus
Hinxton, CB10 1HH, UK
Tel. +44 (0)1223 492364
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Department of Haematology
School of Clinical Medicine
University of Cambridge
Cambridge Biomedical Research Campus
Hills Road, Cambridge, CB2 0XY, UK
Tel. +44 (0)1223 762046
ns545@medschl.cam.ac.uk

Qualifications and research experience

1989-1994	Bachelor of Science in Biological Sciences (110/110 cum laude), University of Milan, Italy
1996-1999	PhD in Genetics and Biotechnology, University of Dundee, UK
1999-2002	Post-doctoral research fellow, University of Milan, Italy
2002-2005	Post-doctoral research fellow, University College London, UK
2005-2007	Senior Scientist, Pharmacogenomics Department, Johnson and Johnson Pharmaceutical Research and Development, Raritan, NJ, USA
2007-2009	Senior Staff Scientist, Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK
2008-2009	Honorary Lecturer, Kings College London School of Medicine, London, UK
2009-2011	Honorary Senior Lecturer, Kings College London School of Medicine, London, UK
2009-2012	Head of Human Complex Traits Group (Career Development Fellow), Wellcome Trust Sanger Institute, Hinxton, UK
2013-2015	Principal of Research, University of Cambridge, Cambridge, UK
June 2012-	Head of Human Complex Traits Group (Group Leader), Wellcome Trust Sanger Institute, Hinxton, UK
Oct 2015-	Professor of Human Genetics, University of Cambridge Clinical School, Cambridge, UK

Web profiles

http://www.sanger.ac.uk/people/directory/soranzo-nicole
http://www.cardiovascular.cam.ac.uk/directory/nsoranzo
http://platelets.group.cam.ac.uk/people/nicole-soranzo
http://donorhealth-btru.nihr.ac.uk/contact.html
http://orcid.org/0000-0003-1095-3852
https://scholar.google.co.uk/citations?user=WH1kIMIAAAAJ&hl=en

Awards and honours

Outstanding performance (Johnson & Johnson Pharmaceutical Research and Development), 2006
Outstanding performance (Johnson & Johnson Pharmaceutical Research and Development), 2007
Outstanding platform presentation (EU Bloodomics Project Annual Meeting), 2009
Paula und Richard von Hertwig-Preis for International Cooperation, 2010
MRC Suffrage Science Heirloom (by Dame Sally Davies), 2012
Top Italian Scientist, Virtual Italian Academy, 2014
Movers and Shakers in Biobusiness, BioBeats, 2014
Club of Italian Female Researchers and Scientists of Impact, National Observatory for Women's Health, Italy, 2016

Grant Funding

Dates	Title	Awarding body	Total award amount	Total amount to PI	Role
2009 - 2010	Replication for blood cell indices associations	Wellcome Trust (WT)	£29,568	£29,568	Sole PI
2009 - 2011	WTCCC3 Renal Transplant Dysfunction	Wellcome Trust (WT)	£10M	£3.2M	Co-applicant
2009-2010	In-depth characterization of cardiometabolic risk factors using metabolomics profiling	Pfizer	£1.8M	£300,000	Co-applicant
2009-2010	FP6 - ENGAGE Exchange and Mobility Program to Ann-Kristin Petersen	EU FP6 - ENGAGE	£9,458	£9,458	Sole PI
2009-2014	Premature cardiovascular disease and platelet quantitative traits	British Heart Foundation	£1,042,372	Awarded through University of Cambridge	Co-applicant
2010-2013	"10,000 UK genome sequences: accessing the role of rare genetic variants in health and disease"	Wellcome Trust (WT)	£10.4M	£2.4M	Co-applicant (Theme Leader)
2011-2013	Next Generation Sequencing in Extremes to Identify Functional Genetic Variants affecting Red Blood Cell Volume	LSBR (Netherlands)	€368,969	Awarded through University of Cambridge	Co-applicant
2011-2016	A BLUEPRINT of Hematopoietic Genomes	EU FP7	€35M	-	Co-applicant (Theme Leader)
2012-2017	NIHR Cambridge Biomedical Research Centre	NIHR	£110,073,288	Awarded through University of Cambridge	Co-applicant
2012-2015	EpiGeneSys RISE 1 new investigator award	EU FP7	€ 199,995	€ 199,995	Sole PI
2013-2017	ESPOD fellowship to Valentina Iotchkova	WT/ EMBL	£162,000	£81,000	Co-applicant
2015-2018	Center for Therapeutic Target Validation	GSK/EMBL/WT	£131,336	£131,336	Sole PI
2015-2020	NIHR Biomedical Research Unit in Donor Health and Genomics	NIHR	£4,099,619	£217,022	Co-applicant (Theme Leader)
2015-2018	ESPOD fellowship to Na Cai	WT/ EMBL	£162,000	£81,000	Co-applicant

Committee Memberships

Steering Committee and Chair, HaemGen Consortium, 2009-
Steering Committee, MAGIC (Meta-Analyses of Glucose and Insulin related traits Consortium), 2009-2012
Steering Committee, GBPG (Global Blood Pressure Genetics) Consortium, 2009-2012
Steering Committee, Wellcome Trust Case Control Consortim Phase 3, 2009-2012
Steering Committee and Co-chair of Cohorts project, UK10K Project, 2011-2015
Steering Committee, EU FP7 BLUEPRINT Project, 2011-2016
Chair of the Scientific Advisory Council, Wellcome Trust Sanger Institute, 2012-2014
Award Committee, Wellcome Trust-Royal Society Sir Henry Dale Junior Investigator, 2012-
Steering Committee and Theme Leader, NIHR BTRU, 2015-2021
Scientific Advisory Board, GECCO (Genetics and Epidemiology of Colorectal Cancer Consortium, Fred Hutchinson Cancer Research Center), 2012-2017
Selection Committee, Head of Division of Genetics and Molecular Medicine, King's College London, 2015
Scientific Advisory Board, WT Strategic Award to Peter Donnelly, Doug Higgs (University of Oxford), 2016-2021
Award Committee, Academy of Finland Investigator Awards, 2016-
Steering Committee, BHF Cambridge Centre of Excellence (CRE), 2016-

Scientific Journals

Editorial Board, Cardiogenetics, 2011-
Guest Editor, PLoS Genetics, 2011-2012
Editorial Board, BMC Cardiovascular Disorders, 2011-
Guest Editor, Cardiogenetics, 2012
Editorial Board, European Journal of Genetic Epidemiology, 2014-
Editorial Board, Molecular Biology and Evolution, 2015-
Editorial Board, Trends in Genetics, 2015-

Academic Service

Postgraduate courses regularly taught

PhD Programme, Sanger Institute, University of Cambridge, 2009-
PhD Programme, British Heart Foundation, University of Cambridge, 2011-
Sardinia Genetics Summer School, 2012-
Leena Peltonen School of Human Genomics, 2012-

PhD advisor

Aparna Radhakrishnan (Secondary advisor), 2010-2014
Jie Huang (Primary advisor), 2012-2015
Alice Stanley (Primary advisor), 2014-2017

PhD advisory committee

Dirk Paul (Advisor P. Deloukas), 2009-2012
Zihao Ding (Advisor R. Durbin), 2011-2014
Leyland Taylor (Advisors F. Collins/E. Birney), 2013-2017
Fernando Riveros-Mackay (Advisor I. Barroso), 2014-2018

PhD First-year Viva Examiner (Sanger Institute)

Jimmy Liu (Advisor C. Anderson, 2012)
Kaur Alasoo (Advisor D. Gaffney, 2014)
Vagheesh Narasimhan (Advisor R. Durbin, 2015)
Jan Botthof (Advisor A. Cveic, 2015)

PhD Viva Examiner (External)
Michael Inouye, University of Leiden, 2010
Suthesh Sivapalaratnam, University of Amsterdam, 2012
Gad Abraham, University of Melbourne, 2012
Maria Gutierrez-Arcelus, University of Geneva, 2014
Donal Gorman, University of Cambridge, 2014
Massimo Mezzavilla, University of Trieste, 2015
Dragana Vuckovic, University of Trieste, 2015
Manuel Rivas, University of Oxford, 2015
Claudia Giambartolomei, University College London, 2015
Ilaria Gandin, University of Trieste, 2016
Serena Sanna, University of Groningen, 2016

Current Team
Lu Chen, Post-doctoral fellow, EU BLUEPRINT, 2011-
Klaudia Walter, Staff scientist, Wellcome Trust, 2011-
Louella Vasquez, Post-doctoral fellow, EU EpiGeneSys, 2012-
Valentina Iotchkova, Post-doctoral fellow, WT/EMBL ESPOD, 2013- (with Ewan Birney)
Stephen Watt, Senior Research Assistant, Wellcome Trust, 2013-
Alice Stanley, PhD Student, Wellcome Trust, 2014-
Ying Yan, Senior Bioinformatician, EU BLUEPRINT, 2014-
Heather Elding, Post-doctoral fellow, NIHR, 2014-
Daniel Mead, Project manager, Wellcome Trust, 2014-
Kousik Kundu, Post-doctoral fellow, NIHR, 2015
Lorenzo Bomba, Post-doctoral fellow, WT/EMBL/GSK, 2015
Na Cai, Post-doctoral fellow, WT/EMBL ESPOD, 2016 (with Oliver Stegle)

Alumni
Aparna Radhakrishnan, 2009-2011 (Current: in-between jobs and maternity leave)
So-Youn Shin, 2009-2013 (Current: Oak Foundation Research Fellow, University of Bristol)
Yasin Memari, 2009-2012 (Current: Post-doctoral fellow, R. Durbin group, Sanger Institute)
Chris Franklin, 2011-2014 (Current: Statistical Geneticist, Genomics Plc.)
Jie Huang, 2012-2014 (Current: Junior Faculty at VA Healthcare Boston, USA)
Massimiliano Cocca, 2013 (Current: PhD student, University of Trieste, Italy)
Matthias Geihs, 2014 (Current: PhD student, Technische Universität Darmstadt, Germany)
Heleen Bouman 2014-2015 (Current: Medical Doctor, Netherlands)
Dragana Vuckovic, 2015 (Current: post-doctoral fellow, University of Doha, Qatar)

Platform Talks, Keynotes and Invited Seminars (since 2009)

2009
- King's College London, London, UK, April 2009
- Cardiogenics Annual Meeting, Lubeck, Germany, April 2009
- European Society of Human Genetics, Vienna, Austria, May 2009
- Helmoltz Zentrum Munich, Munich, Germany, May 2009
- University of Verona, Verona, Italy, Sept 2009
- Amsterdam Medical Center, Amsterdam, The Netherlands, Oct 2009
- ASHG Meeting, Honolulu, Hawaii, USA, Oct 2009
- Triticaeae Meeting, Lodi, Italy, Oct 2009
- Bloodomics Meeting, Madingley, UK, Nov 2009
- Yang-Ming Institute of Public Health, Taiwan, Nov 2009
- National Yang Ming University, Taiwan, Nov 2009
- Academia Sinica, Taiwan, Nov 2009

2010
- Scandinavian Human Genetics Meeting, Oslo, Norway, Apr 2010

- BHF PhD program, Cambridge, UK, June 2010
- American Diabetes Association, Orlando, USA, June 2010
- First OpenGENE Young Investigator Workshop, Tartu, Estonia, Aug 2010
- Leena Peltonen School of Human Genetics, Hinxton, Aug 2010

2011
- Cardiogenics Annual Meeting, Lubeck, Germany, Feb 2011
- Graziella Persico Lecture, Naples, Italy, Mar 2011
- Burlo Garofolo Children Hospital, Trieste, Italy, Apr 2011
- A Global View of Human Disease Genomics, Helsinki, Finland, May 2011
- San Raffaele Medical institute, Milano, Italy, July 2011
- Leena Peltonen School of Human Genomics, Hinxton, Aug 2011
- Sardinia Genetics Summer School, Pula, Italy, Sept 2011
- School of Hygiene and Tropical Medicine, London, UK, June 2011
- Cambridge Statistics Initiative, Cambridge, UK, Sept 2011
- ISHG, Montreal, Canada, Oct 2011
- Statistics Workshop, Paris, France, Oct 2011
- Rotterdam SNP Course, Rotterdam, Netherlands, Nov 2011

2012
- University of Leicester, Leicester, UK, Feb 2012
- Convegno "Studiando il Sangue verso la Medicina", Verona, Italy, Mar 2012
- V International meeting on complex traits and genetic isolates, Trieste, Italy, Mar 2012
- IPCAT, Cambridge, Apr 2012
- University of Washington, Seattle, USA, Apr 2012
- University of Reading, Reading, UK, May 2012
- EMBL-EBI Industry Programme & MetaboLights Project Workshop, Hinxton, May 2012
- University College London, London, May 2012
- Leena Peltonen School of Human Genomics, Cambridge, Aug 2012
- Genomics of Common Diseases 2012, Potomac, MD, USA, Sept 2012
- Genetic Summer School 2012, Pula, Italy Sept 2012
- WT Advanced course on "Design and Analysis of Genetic-based Association Studies", Hinxton, Sept 2012
- University of Reading, Nov 2012
- Rotterdam SNP Course, Rotterdam, Netherlands, Nov 2012

2013
- Keystone Symposium on New Frontiers in Cardiovascular Genetics beyond GWAS, Tahoe City, USA, Jan 2013. (Keynote)
- Genomic Disorders 2013, Hinxton, April 2013
- University of Cambridge, Cambridge, UK, April 2013
- Stanford University, Stanford, USA, May 2013
- Biology of Genomes, Cold Spring Harbor, USA, May 2013
- CB2 conference, Basel, July 2013
- Q-bit, Tuebingen, July 2013
- Sardinia Summer School, Pula, It, Aug 2013
- WT Advanced course on "Design and Analysis of Genetic-based Association Studies", Hinxton, Sept 2013
- Oxford Autumn genomics Forum, Oxford, Oct 2013 (Keynote)
- IHEC/BLUEPRINT meeting, Berlin, Nov 2013
- MRC Integrative Epidemiology Unit Launch, Bristol, Nov 2013
- EpigGeneSys annual investigator meeting, Babraham, Dec 2013

2014
- GECCO investigator meeting, Seattle, February 2014
- Wellcome Trust Investigator Retreat, Ashford, March 2014

- BLUEPRINT meeting- Amsterdam, April 2014
- European Society of Human Genetics, Milano, June 2013
- Genetic Epidemiology of Malaria, Hinxton, June 2014
- 1000 Genomes Project and Beyond, Cambridge, June 2014
- EMBO trairing course in Genomics, Hinxton, June 2014
- University of Minneapolis, Minneapolis, July 2014
- Leena Peltonen School of Human Genomics, Cambridge, Aug 2014
- American Society of Human Genetics, San Diego, Oct 2014
- BLUEPRINT/IHEC meeting, Rome, Oct 2014-06-05
- IHEC meeting, Vancouver, Canada, Oct 2014
- From Functional Genomics to Systems Biology, Heidelberg, Nov 2014
- University of Cambridge, Cambridge, Nov 2014
- McGill University, Toronto, Canada, Nov 2014

2015
- New York Genome Centre, New York, Jan 2015
- International Symposium on Genome Science 2015, Tokyo, Japan, Jan 2015
- Biology of Genomes, Cold Spring Harbor, USA, May 2015
- WT researchers meeting, Farnham, Feb 2015
- Sardinia Summer School, Pula, It, June 2015
- ISAFG2015, Piacenza, Italy, July 2015
- Genomics of Common Diseases, Hinxton, Sept 2015
- Sanger Institute Graduate PhD Programme, Oct 2015
- Target Validation using Genomics and Informatics, Hinxton, Dec 2015

2016
- Jesus college, Cambridge, March 2016 (Career talk)
- Sanger/EBI Seminar Series, Hinxton, March 2016
- International Congress of Human Genetics (ICHG 2016), Kyoto, April 2016
- Sanger post-doctoral fellows retreat, Cambridge, Apr 2016 (Career talk)
- Keystone Symposia on Understanding the Function of Human Genome Variation, Uppsala, Sweden, June 2016
- BLUEPRINT jamboree, Madrid, June 2016
- WT Advanced course on "Human Genome Analysis: Genetic Analysis of Multi-factorial Diseases" - Hinxton, July 2016 (Guest Speaker)
- Leena Peltonen School of Human Genomics, Hinxton, Aug 2016 (PhD talk and tutor)
- BLUEPRINT meeting, Brussels, Sept 2016 (Keynote)
- 28th International IGB Workshop: "Cross-talk between population genomics of human and non-human organisms, Capri, Italy, Oct 2016 (Keynote)
- International Genetic Epidemiology Society Meeting, Toronto, Canada, Oct 2016 (Keynote)
- Merck seminar Series, Boston, Oct 2016

Publications

For manuscripts with greater than 10 authors, the first and last author are indicated, with the number of other authors and the relative position of Soranzo, N indicated in square brackets. In blue are manuscripts with first-or last (including joint) author contribution, which also contain the following notation:

* Joint first author
** Joint last author
§ Corresponding author

Peer reviewed

1. Provan, J., **Soranzo, N.**, Wilson, N.J., McNicol, J.W., Forrest, G.I., Cottrell, J., and Powell, W. (1998). Gene-pool variation in Caledonian and European Scots pine (*Pinus sylvestris* L.) revealed by chloroplast simple-sequence repeats. Proc Biol Sci 265, 1697-1705.

2. **Soranzo, N.**, Provan, J., and Powell, W. (1998). Characterization of microsatellite loci in *Pinus sylvestris* L. Mol Ecol 7, 1260-1261.
3. Muluvi, G.M., Sprent, J.I., **Soranzo, N.**, Provan, J., Odee, D., Folkard, G., McNicol, J.W., and Powell, W. (1999). Amplified fragment length polymorphism (AFLP) analysis of genetic variation in Moringa oleifera Lam. Mol Ecol 8, 463-470.
4. **Soranzo, N.,** Provan, J., and Powell, W. (1999). An example of microsatellite length variation in the mitochondrial genome of conifers. Genome 42, 158-161.
5. Provan, J., **Soranzo, N.**, Wilson, N.J., Goldstein, D.B., and Powell, W. (1999). A low mutation rate for chloroplast microsatellites. **Genetics** 153, 943-947.
6. Soranzo, N., Alia, R., Provan, J., and Powell, W. (2000). Patterns of variation at a mitochondrial sequence-tagged-site locus provides new insights into the postglacial history of European Pinus sylvestris populations. Mol Ecol 9, 1205-1211.
7. Rockman, M.V., Hahn, M.W., **Soranzo, N.**, Goldstein, D.B., and Wray, G.A. (2003). Positive selection on a human-specific transcription factor binding site regulating IL4 expression. Curr Biol 13, 2118-2123.
8. **Soranzo, N.**, Sari Gorla, M., Mizzi, L., De Toma, G., and Frova, C. (2004). Organisation and structural evolution of the rice glutathione S-transferase gene family. Mol Genet Genomics 271, 511-521.
9. Hahn, M.W., Rockman, M.V., **Soranzo, N.**, Goldstein, D.B., and Wray, G.A. (2004). Population genetic and phylogenetic evidence for positive selection on regulatory mutations at the factor VII locus in humans. **Genetics** 167, 867-877.
10. Rockman, M.V., Hahn, M.W., **Soranzo, N.**, Loisel, D.A., Goldstein, D.B., and Wray, G.A. (2004). Positive selection on MMP3 regulation has shaped heart disease risk. Curr Biol 14, 1531-1539.
11. **Soranzo, N.**, Cavalleri, G.L., Weale, M.E., Wood, N.W., Depondt, C., Marguerie, R., Sisodiya, S.M., and Goldstein, D.B. (2004). Identifying candidate causal variants responsible for altered activity of the ABCB1 multidrug resistance gene. Genome Res 14, 1333-1344.
12. Ahmadi, K.R., [14 authors, **Soranzo, N.**: 4], and Goldstein, D.B. (2005). A single-nucleotide polymorphism tagging set for human drug metabolism and transport. **Nat Genet** 37, 84-89.
13. Colombo, S.*, **Soranzo, N.***[10 authors], and Swiss H.I.V. Cohort Study (2005). Influence of ABCB1, ABCC1, ABCC2, and ABCG2 haplotypes on the cellular exposure of nelfinavir in vivo. Pharmacogenet Genomics 15, 599-608.
14. Rockman, M.V., Hahn, M.W., **Soranzo, N.**, Zimprich, F., Goldstein, D.B., and Wray, G.A. (2005). Ancient and recent positive selection transformed opioid cis-regulation in humans. **PLoS Biol** 3, e387.
15. **Soranzo, N.**, Bufe, B., Sabeti, P.C., Wilson, J.F., Weale, M.E., Marguerie, R., Meyerhof, W., and Goldstein, D.B. (2005). Positive selection on a high-sensitivity allele of the human bitter-taste receptor TAS2R16. Curr Biol 15, 1257-1265.
16. Tate, S.K., [12 authors, **Soranzo, N.**: 6], and Goldstein, D.B. (2005). Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. **Proc Natl Acad Sci U S A** 102, 5507-5512.
17. **Soranzo, N.**, Goldstein, D.B., and Sisodiya, S.M. (2005). The role of common variation in drug transporter genes in refractory epilepsy. Expert Opin Pharmacother 6, 1305-1312.
18. Ho, G.T., **Soranzo, N.**, Nimmo, E.R., Tenesa, A., Goldstein, D.B., and Satsangi, J. (2006). ABCB1/MDR1 gene determines susceptibility and phenotype in ulcerative colitis: discrimination of critical variants using a gene-wide haplotype tagging approach. **Hum Mol Genet** 15, 797-805.
19. Ho, G.T., **Soranzo, N.**, Tate, S.K., Drummond, H., Nimmo, E.R., Tenesa, A., Arnott, I.D., and Satsangi, J. (2006). Lack of association of the pregnane X receptor (PXR/NR1I2) gene with inflammatory bowel disease: parallel allelic association study and gene wide haplotype analysis. **Gut** 55, 1676-1677.
20. Cavalleri, G.L., [21 authors, **Soranzo, N.**: 3], and Sisodiya, S.M. (2007). A multicenter study of BRD2 as a risk factor for juvenile myoclonic epilepsy. Epilepsia 48, 706-712.
21. Loeuillet, C., [13 authors, **Soranzo, N.**: 5], and Telenti, A. (2007). Promoter polymorphisms and allelic imbalance in ABCB1 expression. Pharmacogenet Genomics 17, 951-959.
22. **Soranzo, N.**, Kelly, L., Martinian, L., Burley, M.W., Thom, M., Sali, A., Kroetz, D.L., Goldstein, D.B., and Sisodiya, S.M. (2007). Lack of support for a role for RLIP76 (RALBP1) in response to treatment or predisposition to epilepsy. **Epilepsia** 48, 674-683.

23. Liu, Y.Z., [22 authors, **Soranzo, N.**: 9], and Deng, H.W. (2008). Identification of PLCL1 gene for hip bone size variation in females in a genome-wide association study. **PLoS One** 3, e3160.
24. Loos, R.J., [141 authors, **Soranzo, N.**: 85], and Mohlke, K.L. (2008). Common variants near MC4R are associated with fat mass, weight and risk of obesity. **Nat Genet** 40, 768-775.
25. Richards, J.B., [28 authors, **Soranzo, N.**: 5], and Spector, T.D. (2008). Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study. **Lancet** 371, 1505-1512.
26. Richards, J.B., [22 authors, **Soranzo, N.**: 13], and Mooser, V. (2008). Male-pattern baldness susceptibility locus at 20p11. **Nat Genet** 40, 1282-1284.
27. Weedon, M.N., [42 authors, **Soranzo, N.**: 35], and Frayling, T.M. (2008). Genome-wide association analysis identifies 20 loci that influence adult height. **Nat Genet** 40, 575-583.
28. Coronary Artery Disease Consortium, [12 authors, **Soranzo, N.**: 9], and Ziegler, A. (2009). Large scale association analysis of novel genetic loci for coronary artery disease. **Arterioscler Thromb Vasc Biol** 29, 774-780.
29. Falchi, M., [16 authors, **Soranzo, N.**: 10], and Spector, T.D. (2009). Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. **Nat Genet** 41, 915-919.
30. * Ganesh, S.K., [62 authors, **Soranzo, N.**: 4], and Lin, J.P. (2009). Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. **Nat Genet** 41, 1191-1198.
31. Lindgren, C.M., [146 authors, **Soranzo, N.**: 14], and Giant, C. (2009). Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. **PLoS Genet** 5, e1000508.
32. Mangino, M., Richards, J.B., **Soranzo, N.**, Zhai, G., Aviv, A., Valdes, A.M., Samani, N.J., Deloukas, P., and Spector, T.D. (2009). A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. J Med Genet 46, 451-454.
33. Meisinger, C., [22 authors, **Soranzo, N.**: 4], and Doring, A. (2009). A genome-wide association study identifies three loci associated with mean platelet volume. **Am J Hum Genet** 84, 66-71.
34. Newton-Cheh, C., [159 authors, **Soranzo, N.**: 124], and Munroe, P.B. (2009). Genome-wide association study identifies eight loci associated with blood pressure. **Nat Genet** 41, 666-676.
35. Nolte, I.M., [40 authors, **Soranzo, N.**: 6], and Jamshidi, Y. (2009). Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. **PLoS One** 4, e6138.
36. Perry, J.R., [39 authors, **Soranzo, N.**: 27], and Murabito, J.M. (2009). Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. **Nat Genet** 41, 648-650.
37. * Prokopenko, I., [108 authors, **Soranzo, N.**: 5], and Abecasis, G.R. (2009). Variants in MTNR1B influence fasting glucose levels. **Nat Genet** 41, 77-81.
38. Richards, J.B., [35 authors, **Soranzo, N.**: 24], and Genetic Factors for Osteoporosis Consortium (2009). Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. Ann Intern Med 151, 528-537.
39. Richards, J.B., [67 authors, **Soranzo, N.**: 10], and Consortium, G. (2009). A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. **PLoS Genet** 5, e1000768.
40. § **Soranzo, N.**, [38 authors], and Deloukas, P. (2009). Meta-analysis of genome-wide scans for human adult stature identifies novel Loci and associations with measures of skeletal frame size. **PLoS Genet** 5, e1000445.
41. Rivadeneira, F., [36 authors, **Soranzo, N.**: 23], and Genetic Factors for Osteoporosis Consortium. (2009). Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. **Nat Genet** 41, 1199-1206.
42. § **Soranzo, N.**, [29 authors], and Ouwehand, W.H. (2009). A novel variant on chromosome 7q22.3 associated with mean platelet volume, counts, and function. **Blood** 113, 3831-3837.
43. Timpson, N.J., [21 authors, **Soranzo, N.**: 4], and Evans, D.M. (2009). Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. **Hum Mol Genet** 18, 1510-1517.
44. § **Soranzo, N.**, [80 authors], and Gieger, C. (2009). A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. **Nat Genet** 41, 1182-1190.
45. Stolk, L., [23 authors, **Soranzo, N.**: 11], and Uitterlinden, A.G. (2009). Loci at chromosomes 13, 19 and 20 influence age at natural menopause. **Nat Genet** 41, 645-647.

46. * Southam, L., **Soranzo, N.**, Montgomery, S.B., Frayling, T.M., McCarthy, M.I., Barroso, I., and Zeggini, E. (2009). Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants? Diabetologia 52, 1846-1851.
47. Takeuchi, F., [15 authors, **Soranzo, N.**: 6], and Deloukas, P. (2009). A genome-wide association study confirms VKORC1, CYP2C9, and CYP4F2 as principal genetic determinants of warfarin dose. **PLoS Genet** 5, e1000433.
48. Willer, C.J., [147 authors, **Soranzo, N.**: 26], and Genetic Investigation of Anthropometric Traits Consortium (2009). Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. **Nat Genet** 41, 25-34.
49. Zhai, G., [17 authors, **Soranzo, N.**: 6], and Spector, T.D. (2009). A genome-wide association study suggests that a locus within the ataxin 2 binding protein 1 gene is associated with hand osteoarthritis: the Treat-OA consortium. J Med Genet 46, 614-616.
50. Chambers, J.C., [94 authors, **Soranzo, N.**: 71], and Kooner, J.S. (2010). Genetic loci influencing kidney function and chronic kidney disease. **Nat Genet** 42, 373-375.
51. Codd, V., [29 authors, **Soranzo, N.**: 10], and Samani, N.J. (2010). Common variants near TERC are associated with mean telomere length. **Nat Genet** 42, 197-199.
52. Duffy, D.L., [21 authors, **Soranzo, N.**: 9], and Montgomery, G.W. (2010). IRF4 variants have age-specific effects on nevus count and predispose to melanoma. **Am J Hum Genet** 87, 6-16.
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