Prepared: April 26, 2022

University of California, San Francisco

CURRICULUM VITAE

Name: Mark Seielstad, PhD

Position: Professor, Step 3
Laboratory Medicine
School of Medicine

Address: Institute for Human Genetics
513 Parnassus Ave, Med Sci, 965H
University of California San Francisco
San Francisco, CA 94143-0794
Voice: 415-476-0625
Email: Mark.Seielstad@ucsf.edu
Web: https://profiles.ucsf.edu/mark.seielstad

EDUCATION

1988 - 1992	Stanford University, Stanford, CA	B.S.	with Honors, Biological Sciences	
1988 - 1992	Stanford University, Stanford, CA	A.B.	Classical Studies	
1992 - 1998	Harvard University, Cambridge, MA	Ph.D.	Biology	R.C. Lewontin & L. L. Cavalli-Sforza
1998 - 2000	Harvard School of Public Health, Boston, MA	postdoc	Population Genetics	

LICENSES, CERTIFICATION

2020 UCSF Diversity Equity and Inclusion Champion Training

PRINCIPAL POSITIONS HELD

2000 - 2001	Harvard School of Public Health	Research Associate	Population Genetics
2002 - 2009	Harvard School of Public Health	Assistant Professor	(tenure track)
2002 - 2004	Genome Institute of Singapore	Group Leader	Population Genetics
2004 - 2009	Genome Institute of Singapore	Associate Director & Senior Group Leader	Human Genetics

2010 - 2015	University of California, San Francisco	Associate Professor	Laboratory Medicine
2011 - 2015	University of California, San Francisco	Associate Professor	Epidemiology and Biostatistics
2015 - present	University of California, San Francisco	Professor	Laboratory Medicine
2015 - present	University of California, San Francisco	Professor	Epidemiology and Biostatistics

OTHER POSITIONS HELD CONCURRENTLY

1994 - 1996	Stanford University	Visiting Scholar	Genetics
1995 - 1995	Addis Ababa University, Ethiopia	Visiting Scholar	Biology
2000 - 2002	University of Khartoum, Sudan	Visiting Assistant Professor	(Third World Academy of Sciences, Trieste, Italy)
2004 - 2010	National University of Singapore	Adjunct Associate Professor	Centre for Molecular Epidemiology
2005 - 2008	Harvard School of Public Health	Adjunct Assistant Professor	Genetics and Complex Diseases
2009 - 2010	Harvard School of Public Health	Adjunct Assistant Professor	Epidemiology
2010 - 2012	Genome Institute of Singapore	Adjunct Investigator	Human Genetics
2012 - 2012	Monash University Malaysia Campus	Visiting Professor	Human Genetics
2010 - 2018	Blood Systems Research Institute	Associate Investigator	Epidemiology
2012 - present	University of California San Francisco	Faculty Affiliate	Institute for Global Health Sciences
2010 - present	University of California San Francisco	Faculty Affiliate	Institute for Human Genetics
2010 - present	University of California San Francisco	Investigator	Quantitative Biosciences Institute (QBI)

HONORS AND AWARDS

1985	French Government -- Société Honoraire de Français Scholarship for study in France	
1990	Classics Undergraduate Prizes (1990, 1991, and 1992)	Stanford University
1990	Lionel Pearson Award for study at the Intercollegiate Center for Classical Studies (Rome) and for archeological study in Tunisia and Turkey.	Stanford University
1991	Travel Award for excavation work in Panakton, Greece and for archeological study in Jordan and Egypt.	Stanford University
1991	Howard Hughes Medical Institute Major Grant for thesis research on the molecular systematics of the butterfly genus, Colias.	Stanford University
1992	National Institutes of Health Genetics Trainee	Harvard University
1993	National Science Foundation Predoctoral Fellow	Harvard University
1994	U.S. National Science Foundation -- Graduate University for Advanced Studies,Yokohoma; Summer Research Fellowship at the Japanese National Institute of Genetics, Mishima	
1994	Arthur Green Fund (Harvard University) Grants for field research in Sudan (1994 and 1998); Ethiopia (1995); and Thailand and Vietnam (1997-1998)	Harvard University
1996	L.S.B. Leakey Society Award for field research in Mali (1996); Thailand and Vietnam (1997-8)	Harvard University
2000	National Research Service Award, National Institute of General Medical Sciences (F32 GM20425-01) (declined)	Harvard University
2000	Principal Investigator, Research Career Award, U.S. National Human Genome Research Institute (K22 HG00053-01; US$1,047,678) (2000-2002).	Harvard University
2002	The Keville-DePalma Founders Lecture.	Salem State University

2002	The Horning Lecture in the Humanities	Oregon State University
2016	The Sir John Monash Lecture	Monash University
2019	Fulbright Senior Scholar	Academia Sinica, Taiwan
2021	Elected Member, at-Large	Sigma Xi
2020	Honorary Fellow (Biological Sciences)	American Association for the Advancement of Science (AAAS)

KEYWORDS/AREAS OF INTEREST

human genetics, population genetics, genomics, genetic epidemiology, immunogenetics, autoimmunity, infectious diseases, immunology, type 2 diabetes, metabolism, evolution, anthropology.

PROFESSIONAL ACTIVITIES

MEMBERSHIPS

1998 - present	American Society of Human Genetics
1998 - 2013	Genetics Society of America
2002 - present	American Association for the Advancement of Science
2003 - present	Human Genome Organization (HUGO)
2007 - present	International Genetic Epidemiology Society
2011 - 2012	International Society of Computational Biology
2021 - present	European Society of Human Genetics

SERVICE TO PROFESSIONAL ORGANIZATIONS

2009 - 2010	Illumina Genotyping Advisory Panel (unpaid)	
2014 - present	American Society of Human Genetics	DNA Day Judge (annually)
2015 - 2018	International Genetic Epidemiology Society	Education Committee
2015 - present	American Association for the Advancement of Science (AAAS)	Student Poster Judge
2021 - present	European Society of Human Genetics	Essay Judge
2022 - 2026	American Society of Human Genetics (ASHG)	Nominating Committee

SERVICE TO PROFESSIONAL PUBLICATIONS

2007 - 2014	Editorial Board, The HUGO Journal (formerly titled Genomic Medicine)
2008 - present	Senior Editor, Annals of Human Genetics

2009 - present Associate Editor, BMC Medical Genomics

2011 - 2019 Review Editor, Frontiers in Evolutionary and Population Genetics

2010 - present Frequent ad hoc referee for Science; Nature Genetics; The American Journal of Human Genetics; Genome Research; Human Molecular Genetics; Vaccine; DNA and Cell Biology; Tissue Antigens; PLoSONE; Scientific Reports; JAMA; Current Biology; Immunological Investigations; and Journal of Human Genetics. Grant reviewer for the National Science Foundation Physical Anthropology Section. Grant Reviewer for the LSB Leakey Foundation.

INVITED PRESENTATIONS - INTERNATIONAL

1997 Trinational Workshop on Molecular Evolution, University of Munich (June 5-7, 1997).

1997 Department of Biological Anthropology Colloquium, University of Cambridge, UK (June 19, 1997).

1997 Department of Biology Seminar, Chiang Mai University, Thailand (November, 1997).

1999 Department of Epidemiology Seminar, Beijing Medical University (November 8, 1999).

2000 Department of Bio. Anthropology Seminar, University of Oxford (March 17, 2000).

2001 Eijkman Institute for Molecular Biology, Jakarta, Indonesia (July 9, 2001).

2001 Genome Institute of Singapore, Singapore (September 25, 2001).

2002 Institute of Mathematical Sciences, Workshop on Population and Statistical Genetics; National University of Singapore (March 26, 2002).

2002 6th Annual NUS-NUH Annual Scientific Meeting, Singapore (August 16, 2002).

2003 Biomedical Research Council Symposium, Singapore (July 31, 2003).

2004 3rd International Eijkman Symposium, Yogyakarta (Oct. 1, 2004).

2004 5th HUGO Pacific Meeting, Pattaya, Thailand (November 18, 2004).

2005 Royal Dutch Academy of Sciences Open Science Meeting, Yogyakarta (Sept. 28, 2005).

2005 Institute of Mathematical Sciences, Workshop on Genomics, Singapore (Nov. 15, 2005).

2006	Affymetrix User Group Meeting, Singapore (Nov. 12, 2006).
2006	8th International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Bangkok (Nov. 30, 2006).
2006	7th International Symposium on Host Genetic Epidemiology, Seoul National University (Dec. 8, 2006).
2007	Symposium & Workshop on Forensic DNA, Jakarta (5th February 2007).
2007	Illumina User Group Meeting, Siena, Italy (26th April 2007).
2007	Center for Molecular Medicine, Karolinska Institutet, Stockholm (9th May 2007).
2007	International Medical & Health Conference, Kota Bahru, Malaysia (25th May 2007).
2007	Instituto Nacional de Medicina Genomica, Mexico City (4th September 2007).
2007	Clinician Scientist Unit, National University Hospital, Singapore (29th October 2007).
2007	Singapore Eye Research Institute, Singapore (31st October 2007).
2007	Eijkman International Symposium, Bali (16th November 2007).
2008	Indian Society of Human Genetics, Annual Meetings, Vishakhapatnam (12th February 2008).
2008	Centre for Cellular and Molecular Biology, Hyderabad (14th February 2008).
2008	1st Asia Pacific Inflammatory Bowel Disease Scientific Meeting & Postgraduate Course, Singapore (24th February 2008).
2008	Illumina User Group Meeting, Cebu, the Philippines (31st March 2008).
2008	Combined Analysis of Three Genome-Wide Scans Reveals Novel Loci Associated with Rheumatoid Arthritis. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (5th April 2008).
2008	The Population Genetics of SNPs and CNVs in Southeast Asian Populations. Affymetrix Integrated Genomics Solution Seminar. Singapore. (22nd September 2008).

2008	Genome-Wide Studies for Chronic Diseases. The Singapore Epidemiology of Eye Diseases Symposium. (13th October 2008).
2009	Korean National Institutes of Health, Seoul, Korea (April 27, 2009).
2009	Global Diabetes Consortium Meeting, Hong Kong (March 15, 2009).
2010	Genetics of Nasopharyngeal Carcinoma Workshop, National Cancer Centre, Singapore (February 20th, 2010)
2016	University of the Philippines Manila and Diliman.
2019	Institute for Biomedical Sciences, Academia Sinica, Taipei Taiwan
2019	Tzu Chee University School of Medicine, Hualien, Taiwan
2020	Monash University Malaysia

KEYNOTE

2001	The 2nd Annual Conference on Sex and Gene Expression of the Society for Women's Health Research. (March 8-11, 2001).
2006	The Malaysian Society of Molecular Biology and Biochemistry. Bangi, Malaysia (August 17, 2006).
2007	The Genes That Cause Autoimmune Disease. Federation of Clinical Immunology Societies Annual Meeting, San Diego (11th June 2007).
2008	Mapping Human Genetic History in Asia. Opening Plenary. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (2nd April 2008).
2008	Mapping Human Genetic History in Asia. Special Plenary. Human Genome Meetings 2008 (HUGO), Hyderabad, India (28th September 2008).
2009	Japan College of Rheumatology International Symposium, Tokyo, Japan (April 24th, 2009).
2011	University of Sao Paulo, Brazil. (April 4th, 2011)
2011	Hemocentro Sao Paulo, Brazil. (April 5th, 2011)
2011	The inaugural Affymetrix Pan-Asian GWAS Meeting, Shanghai, China (May 16, 2011).
2011	The European Society of Human Genetics Annual Meeting, Amsterdam, the Netherlands (May 30, 2011)

2011	The Wellcome Trust Sanger Centre, Hinxton, the United Kingdom (June 13, 2011)
2012	Monash University Malaysia Campus, Seminar (April 26, 2012)
2012	University Malaya, Seminar (April 26, 2012)
2013	Joint Human Genome Meeting and 21st International Congress of Genetics, Singapore (April 15, 2013)
2016	Sir John Monash Lecture, Monash University
2019	Asia Society of Human Genetics Meetings, Manila, Philippines (November 7, 2019)

INVITED PRESENTATIONS - NATIONAL

2000	Division of Human Genetics Seminar, Washington University (March 22, 2000).
2005	Seminar, Center for Human Genetics, University of California, San Francisco (Sept. 9, 2005).
2006	Illumina User Group Meeting, San Diego (March 14, 2006).
2009	Program for Quantitative Genetics, Harvard School of Public Health, Boston, MA (October 27, 2009).
2009	Session Chair, Program for Quantitative Genetics Annual Conference, Harvard University, Boston, MA (November 12, 2009).
2011	Third biennial Affymetrix Best Practices in Genotyping Meeting, Chicago, IL (July 13, 2011).

INVITED PRESENTATIONS - REGIONAL AND OTHER INVITED PRESENTATIONS

2011	Blood Systems Research Institute Epidemiology Site Visit (February 25, 2011)	Program Presenter
2011	Biomedical Sciences (BMS) Ph.D. Program Retreat (October 8, 2011)	speaker
2012	Blood Systems Research Institute, Scientific Retreat (September 24, 2012).	speaker
2016	SF General Hospital, Endocrinology Department	speaker

GOVERNMENT AND OTHER PROFESSIONAL SERVICE

2009 - 2015	U01 supported Type 2 Diabetes GENES (T2D-GENES) Steering Committee (10 members comprised of representatives from the Broad Institute, Oxford University, University of Chicago, Southwest Foundation Medical Research Institute, and University of Michigan	Member
2010 -	GenomeBC (British Columbia), Genomics and Health: Personalized Medicine Program	Review Panel Member
2011 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2012 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2012 -	Grant Review Committee for the Wellcome Trust, UK.	Member
2012 -	Malaria Genomics Grant Review Committee for Gates Foundation	Member
2013 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2013 -	NIH Genotype and Tissue Expression (GTEx) Special Emphasis Study Section	Member
2013 -	NIDDK Special Emphasis study section to evaluate Inflammatory Bowel Disease Program Project application	Member
2014 -	NIH Special Emphasis study section to evaluate Genetics of Zoster, Zoster Pain and Immune Responses to Zoster Vaccine Program Project Application	Member
2015 - 2018	International Genetic Epidemiology Society (IGES) Education Committee	Member
2015 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (J3)	Member
2015 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (M3)	Member
2016 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (M3)	Member
2017 -	NIH (NIDDK) Study Section Digestive Diseases and Nutrition C Subcommittee (DDK-C)	Member
2017 -	Health Research Board (Ireland)	Proposal Reviewer
2018 -	National Eye Institute (NEI) Special Emphasis Panel (ZEY VSN (01))	Member

2018 -	NIH Special Emphasis Panel: Chronic Disease and Epidemiology	Member
2019 -	NEI Special Emphasis Panel R13/R21/R01 Review	Member
2020 -	NIDDK DDK-C Study Section Subcommittee	Member
2022 -	NIDDK ZDK1 GRB-Q (M2) Study Section	Member

UNIVERSITY AND PUBLIC SERVICE

SERVICE ACTIVITIES SUMMARY

I serve actively on multiple mostly Senate Committees and have advanced to the Leadership of the Rules and Jurisdiction Committee. In addition, I have actively and continuously served on the Basic Research in HIV Study Section for RAP/CFAR and have reviewed multiple grants in twice annual meetings since 2010. I assist actively in the admissions and recruitment for 2 Ph.D. programs, Biomedical Sciences (BMS) and Biological and Medical Informatics (BMI).

UNIVERSITY SERVICE

UC SYSTEM AND MULTI-CAMPUS SERVICE

2016 - 2017	UC Systemwide Committee Representative	Member
2017 - 2020	UC Systemwide Library and Scholarly Information Advisory Committee (SLASIAC)	Member
2018 - 2020	SLASIAC□s Standing Subcommittee on Copyright Policy (SSCP)	Member
2021 -	President's Postdoctoral Fellowship Program (PPFP)	Review Panel

UCSF CAMPUSWIDE

2010 - present	Basic Research in HIV Study Section for RAP/CFAR	member
2010 - present	application screener for BMI PhD student applications	
2011 - 2021	application screener for BMS PhD student applications	
2011 - 2014	Graduate Council	member
2011 - 2011	San Diego State University outreach visit and talk to minority/disadvantaged students interested in UCSF's undergraduate summer programs and graduate study at UCSF (September 23, 2011).	speaker/discussion leader
2014 - 2017	OSR Service Partnership Agreement Committee	member
2015 - 2018	APB Campus Finance Subcommittee	member
2015 - 2018	Committee on Library and Scholarly Communication (COLASC)	member
2015 - 2019	Rules and Jurisdiction Committee	member

2016 - 2019	Standing Panel for Faculty Code of Conduct Investigations	member
2016 - 2017	Rules and Jurisdiction Committee	Vice-Chair
2017 - 2019	Rules and Jurisdiction Committee	Chair
2017 - 2019	UCSF Senate Executive Council	member
2017 - 2021	Biomedical Sciences (BMS) Ph.D. Program Admissions Committee	member
2020 - present	Biological and Medical Informatics (BMI) Ph.D. Program Admissions Committee	member
2020 - present	Biological and Medical Information (BMI) Ph.D. Program Diversity, Equity and Inclusion Committee	member
2021 - 2024	UCSF Senate Sustainability Committee	member
2021 -	UCSF Health Awards (Health Hub)	Judge

DEPARTMENTAL SERVICE

2012 - 2012	Organized BSRI Scientific Retreat	
2013 - 2016	Laboratory Medicine Committee on Advancements and Promotions	Member

COMMUNITY AND PUBLIC SERVICE

2021 - 2022	San Francisco Civil Grand Jury	Parliamentarian

CONTRIBUTIONS TO DIVERSITY

CONTRIBUTIONS TO DIVERSITY Contributions to Diversity, Equity & Inclusion Guidance

I have actively mentored several Filipino (considered by UCSF to be under-represented) students in the context of a collaboration with the University of the Philippines in Diliman and Manila. Two of these students (Maria Elizabeth Mercado and Alvin Lirio) were enrolled in the Clinical and Translational Science Program in the Department of Epidemiology and Biostatistics. Currently, one (Maria Elizabeth Mercado) is a faculty member at the University of the Philippines, and another (Alvin Lirio) is employed by the Philippine Genome Center in addition to practicing medicine at the University of the Philippines in Manila.

Another (Dominic Albao) is entering (Fall 2020) a Ph.D. program at Scripps in Florida. The other, Margarette Mariano, who I employed and mentored for several years as a research assistant is soon to enter her 3rd year in the Albert Einstein College of Medicine Ph.D. Program.

As a Hispanic myself, I have been sought out by several Latinx students at UCSF, and have mentored three here at UCSF: including Roxana Ordonez in the BMI Ph.D. Program; Carlos Rojo (currently a faculty member at San Jose City College) in the BMS Ph.D. Program; and

have co-mentored and served on the thesis committee of Raul Torres in the BMS Ph.D. Program.

My research has largely been conducted in non-European populations, especially East Asian populations. This has brought much needed diversity to the study and understanding of complex disease genetics. Whether East Asian populations are under-represented in the ranks of an Institution like ours, unquestionably these populations have not been well represented until recently (partly on account of my own work) in genetic studies.

TEACHING AND MENTORING

TEACHING SUMMARY

I participate actively in three Ph.D. programs: Biomedical Sciences (BMS), Biological and Medical Informatics (BMI), and Epidemiology & Translational Science. I have lectured in courses for BMI and BMS; participated actively in annual retreats; journal clubs; pizza talks; and student coaching. I have also led weekly student discussion sessions for core BMS courses.

I have also supervised one student□s rotation project in the Epidemiology and Translational Science Program; and have supervised what became a one-year terminal Master□s project by an NSF-funded Ph.D. student in the BMI program, Roxana Ordonez. Currently, I am the advisor for Carlos Rojo, a student in the BMS program.

I have been and expect to continue to be fully engaged in these programs by participating in annual retreats, admissions activities for applicants, as well as informal and formal seminars, classroom teaching etc.

I have also was sole supervisor, over two and a half years, of a Clinical and Translational Research (CTR) Fellow (formerly known as the PACTRR program). This highly talented UCSF M.D. student (Dustin Long) was a remarkable addition to my lab, and has performed from day-one at the level of an advanced Ph.D. student. I also supervised and examined his thesis for the M.D. with Distinction degree, through the Pathways to Discovery in Molecular Medicine. After finishing a one year internship with Kaiser after graduating from UCSF in 2013, he recently began a residency in Anesthesiology at the Massachusetts General Hospital.

Finally, I am active in teaching at the Blood Systems Research Institute and participate in their summer student program.

FORMAL TEACHING

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	1992 - 1992	Teaching Assistant, Biological Sciences 2, Harvard University, Cambridge, MA	Graduate TA		300
	1996 - 1996	Teaching Assistant, Molecular Biology Core (Science B-46), Harvard College, Cambridge, MA	Graduate TA		30

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	2000 - 2000	Lecturer, Course on Human Genome Diversity, ICGEB, Islamabad, Pakistan	Lecturer		50
	2004 - 2004	Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet - National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology	Course Director and Lecturer		25
	2006 - 2006	Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet - National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology	Course Director and Lecturer		25
	2006 - 2006	Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).	Lecturer		100
	2008 - 2008	Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).	Lecturer		30

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	2010 - 2010	BMI 206; Bioinformatics & Computational Biology	1 lecture + 1 student-led paper discussion	Grad	7
	2011 - 2011	Controversies in IBD: 2011; Office of Continuing Medical Education	Delivered a half hour lecture summarizing genetic advances and potential in IBD research.	Medicine	200
	2012 - 2012	BMS 255B; Tissue and Organ Biology (Genetics)	2 lectures	Grad	28
	2013 - 2013	BMS 255B; Tissue and Organ Biology (Genetics)	2 lectures	Grad	22
	2013 - 2013	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	9
	2014 - 2014	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	12
	2015 - 2015	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2016 - 2016	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2017 - 2017	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2016 - 2017	IDS121A-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	9
	2016 - 2017	IDS121B-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2016 - 2017	IDS121C-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2016 - 2017	IDS121E-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	2020 -	IDS121E-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2017 - 2017	BMS 260	Student Proposal & Presentation Evaluator	Grad	30
	2019 -	Wu Ta You Foundation Summer School on Biomedical Sciences	Lecturer and small group facilitator	Grad	110
	2020 - 2021	IDS121A-CIC Core Inquiry Curriculum	Small Group Facilitator	Medicine	11

INFORMAL TEACHING

2010 - present Frequent participation and speaking at BMI and BMS student retreats

2010 - present Annually coach 2-5 BMI and BMS students in their journal club presentations

2010 - present Present 1-3 times each year at student journal clubs

2010 - present Give informal research "pizza talks" to first and second year students, 1-2 times per year

MENTORING SUMMARY

Since Summer 2017, I am the primary advisor for Elizabeth "Aprille" Mercado, M.D., who is pursuing an M.Sc. in the Master's Degree Program in Clinical Research in the Department of Epidemiology and Biostatistics at UCSF.

Since mid-2016 I have mentored an Assistant Clinical Research Coordinator, hired on my diabetes grant, Ms. Margarette Mariano. This has involved intensive co-mentoring with Drs. Sarah Kim and Lisa Murphy of the Department of Endocrinology; and is centered on the enrollment of research subjects in the CRS and at outside sites. In addition, I am mentoring to Student volunteers who assist on this project, Ms. Irah Rubio and Matthew Roces.

From 2010-2013, I have mentored Assistant Adjunct Professor Adam Lauring, M.D., Ph.D., an infectious disease physician and expert in viral evolution and diversity, as he sought exposure to and training in human genetics. The two of us collaborated closely and published on 2 or 3 projects centered on identifying human genetic variation that determines varying susceptibilities and outcomes to infections. He has since begun his first tenure track Assistant Professor position at the University of Michigan.

Beginning in October 2011, BSRI hired a new senior scientist in Bioinformatics, Dr. Xutao Deng, whom I have co-mentored on projects in human genetics and genomics -- subjects with which he had had some, but not the deepest exposure previously. The collaborative work has been both enjoyable and incredibly productive.

PREDOCTORAL STUDENTS SUPERVISED OR MENTORED

Dates	Name	Program or School	Mentor Type	Role	Current Position
2002 - 2006	Methawee Srikummool	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Lecturer, Narasuen University, Phitsanulok, Thailand
2003 - 2007	Jatupol Kampuansai	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Assistant Professor, Chiang Mai University, Chiang Mai, Thailand
2008 - 2012	Wibhu Kutanan	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Assistant Professor, Khon Kaen University, Thailand.
2006 - 2012	Eileen Png	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	postdoc at Genome Institute of Singapore
2007 - 2012	Chee Seng Ku	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc at National University of Singapore, Cancer Centre
2008 - 2011	Rajkumar Dorajoo	ASTAR-Imperial University, London, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc in Singapore
2009 - 2012	Rick T.H. Ong	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc at National University of Singapore

Dates	Name	Program or School	Mentor Type	Role	Current Position
2010 - 2011	Roxanna Ordonez	BMI, UCSF	Research/Scholarly Mentor,Project Mentor	advisor	pursued a Master's thesis in my lab
2011 - 2011	Shenhaochen Zhu	BSRI summer student (from SFSU)	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	industry
2011 - 2013	Dustin Long	M.D. w/ Distinction, UCSF; Clinical and Translational Fellow	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	Anesthesia Resident, Massachusetts General Hospital
2012 - 2012	Evan McCartney-Melstad	BSRI summer student	Project Mentor	advisor	Ph.D. student, UCLA
2012 - 2012	Katherine Nishimura	Epidemiology and Translational Science Ph.D., UCSF	Project Mentor,Career Mentor	rotation advisor	Ph.D. candidate
2014 - 2014	Carlos Rojo	BMS, UCSF	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	faculty, City College of San José
2014 - present	Raul Torres	BMS, UCSF	Project Mentor,Career Mentor	thesis committee chair	employed in industry
2016 - 2018	Matthew Roces	UC Berkeley	Research/Scholarly Mentor,Project Mentor	advisor	M.D. student at UCSF
2016 - 2018	Irah Rubio	UC Berkeley	Research/Scholarly Mentor,Project Mentor	advisor	pursuing Physician's Assistant

Dates	Name	Program or School	Mentor Type	Role	Current Position
2017 - 2019	Elizabeth "Aprille" Mercado	Master's Degree Program in Clinical Research	Research/Scholarly Mentor,Project Mentor,Career Mentor	primary mentor/advisor	Faculty, University of the Philippines
2018 - present	Wesley Marin	BMI, UCSF	Co-Mentor/Clinical Mentor	thesis committee member	Ph.D. candidate

POSTDOCTORAL FELLOWS AND RESIDENTS MENTORED

Dates	Name	Fellow	Mentor Role	Faculty Role	Current Position
2004 - 2008	Terry KL Toh	postdoc		Research Supervision	Clinical Scientist, National University Hospital, Singapore
2005 - 2007	Jenny Hui Hui Tan	postdoc		Research Supervision	Instructor, Ministry of Education, Singapore
2006 - 2010	Vikrant Kumar	postdoc		Research Supervision	Research Associate, Genome Institute of Singapore
2009 - 2010	Devindri Perera	postdoc		Research Supervision	Lecturer, Murdoch University (Australia)
2013 - 2013	Jonathan Esensten	resident		Research Supervision	Assistant Professor, UCSF

FACULTY MENTORING

Dates	Name	Position while Mentored	Mentor Type	Mentoring Role	Current Position

Dates	Name	Position while Mentored	Mentor Type	Mentoring Role	Current Position
2010 - 2012	Adam Lauring, M.D., Ph.D.	Assistant Adjunct Professor		supervised his K project as he moved from viral evolution into human genetics.	Assistant Professor University of Michigan

VISITING FACULTY MENTORED

2013 - 2013	Prof. Maude Phipps	Monash University Malaysia
2015 - 2015	Prof. Maude Phipps	Monash University Malaysia

RESEARCH AND CREATIVE ACTIVITIES

RESEARCH AND CREATIVE ACTIVITIES SUMMARY
RESEARCH INTERESTS

My research centers on the identification of inherited variation that influences disease risk in humans. The hope is that this will lead to tangible improvements in public and individual health, via the identification of novel genes and pathways involved in the physiology of a particular disease process or non-disease phenotype. Neither of these rather lofty aims - the identification of disease related variation, nor the translation into clinical utility - has been realistic for complex diseases until recently. But with the completion of the human genome project and rapid developments in SNP genotyping and DNA sequencing technology, progress has been accelerated greatly. Results from genome-wide association studies (GWAS) have demonstrated both their feasibility, and their potential for identifying unexpected pathways of disease physiology - pathways that seem likely, in many cases, to be the targets of successful new therapies and predictive risk assessments.

I have been fortunate to have designed, executed, and led numerous such studies, each of which has led directly to years of productive follow-up research. I have chosen to concentrate particularly on disorders of immunity and metabolism for several reasons. First is my belief that deaths from epidemics or famine are likely to have been among the two greatest selective forces in our evolutionary past. This leads to the expectation that the magnitude of genetic effects contributing to susceptibility to infection, autoimmunity, and metabolic disease is significant, and probably larger than for many other complex diseases that have so far proved refractory to genetic analysis. This should increase the likelihood of identifying relevant genes via population-based association studies, and should serve as a better testing ground for methodology that might then be more successfully applied to diseases with more subtle genetic etiologies. It also leads to the attractive hypothesis (which my research program aims to test) that our adaptations to survive infections and periods of food scarcity have left us maladapted to modern life in which infectious mortality has been sharply reduced by improvements in hygiene, antibiotics/antivirals, and vaccines; and in which an overabundance of food poses a greater threat to the health of a growing fraction of the global population, than does its scarcity. In addition to susceptibility to infections and overt autoimmune conditions; immune genes are now known to play key roles in many cancers, allergic and hyper-responsive disorders of rapidly increasing incidence such as asthma, metabolic disease/diabetes, as well cardiac and vascular disease. By using pathogens, vaccines, and autoimmune diseases as probes of functionally relevant immunogenetic variation, I believe we can gain a broader understanding of numerous other diseases that all converge in one way or

another on the nexus of immune genes - and my research program at UCSF seeks to uncover the genetic underpinnings of both immune-related and metabolic diseases of humans.

Among the most productive recent projects, with funding from a U01 grant from the NIDDK, has been my participation and leadership within the T2D-GENES consortium. In this consortium, working with leading researchers from the University of Chicago, University of Michigan, the Broad Institute (of Harvard and MIT) and, the University of Oxford; we are performing whole genome sequencing of 1,000 Latino pedigree members with a high diabetes prevalence, and exome sequencing of 20,000 case and control individuals from diverse global populations, including Asians and African-Americans. As a program for the follow-up of GWAS studies of diabetes, the scale and comprehensiveness are unprecedented and world-leading. For the first time, we are also able to examine the role of low-frequency genetic variation in the etiology of complex human disease on a genome-wide level. I will increasingly be applying genome-scale sequencing to a variety of infectious, autoimmune and metabolic diseases.

RESEARCH AWARDS - CURRENT

1. A127149 PI 20 % effort Seielstad (PI)

   Philippine Commission on Higher Education 01/01/2016 01/31/2022

   Metagenomic Contributions to Type 2 Diabetes Among Filipino Populations $ 384,324 direct/yr 1 $ 980,000 total

   Our goal is to characterize the gene-environment interactions that drive T2D susceptibility in Filipinos, leading to interventions that may begin to reduce the incidence and cost curves of this rapidly increasing disease.

   Designed study, convened co-investigators, wrote proposal. Will oversee all aspects of the research study, beginning from the enrollment of case and control subjects in both the Bay Area and the Philippines; will supervise all aspects of the genomic data collection (in the Philippines); and will design and oversee the data analysis. There will also be a substantial teaching and training component.

RESEARCH AWARDS - SUBMITTED

1. 1 R01 AG052869-01 PI 25 % effort Seielstad (PI)

   NIAID 09/01/2018 07/31/2023

   Genetic Susceptibility to Herpes Zoster: a Model for Immunosenescence $ 292,613.00 direct/yr 1 $ 874,704.00 total

   Herpes zoster (HZ), caused by the reemergence of the chicken pox virus, occurs most often in the elderly and is characterized by a painful and often debilitating skin rash. Using HZ as a model, the goal of the proposed research study is to identify genes and other biological factors that cause the immune system to weaken with age. Results may help focus HZ prevention efforts, including use of the vaccine, and may inform the epidemiology of other infections in the elderly.

   PI, responsible for overseeing all aspects of design, research conduct, analysis and publication.

2. 1 R01 AI153529-01 PI 25 % effort Seielstad (PI)

   NIH 2020 2024

Identifying determinants of hepatitis b viral immunity via genomic and focused HLA-KIR gene studies — $ 250,000 direct/yr 1 — $ 1,000,000 total

We intend to identify host genetic variation impacting both HBV vaccine response, AND the ability to spontaneously clear an HBV infection, by analyzing a large, extant cohort of serologically and genetically characterized Chinese individuals living in Taiwan.

PI. Conceived and wrote the proposal.

RESEARCH AWARDS - PAST

1. 5R01CA104021-02 — co-investigator
   NIH/NCI — 2005-09-01 — 2010-06-30
   Genetic determinants of postmenopausal breast cancer. — $ 1,264,708 direct/yr 1

2. N01 HB-57181 — co-investigator — Busch (PI)
   NHLBI — 01/01/2011 — 06/30/2011
   Retrovirus Epidemiology Donor Study-II (REDS-II) - Central Laboratory. Central laboratory for all REDS specimen testing, including specific project — $ 139,015 direct/yr 1 — $ 139,015 total

3. GIS/05-PB2101 — PI
   Genome Institute of Singapore (GIS) intramural — 2005-04-01 — 2009-03-31
   High-Throughput SNP Genotyping Facility — $ 2,983,900 direct/yr 1

4. GIS/09-BR2102 — PI
   Genome Institute of Singapore Intramural Funding — 2005-04-01 — 2010-03-31
   $ 5,979,847 direct/yr 1

5. N66001-08-C-2014 — PI
   DARPA (USA) — 2008-05-01 — 2009-08-31
   Genetic Biomarkers for Prediction of Vaccine Response — $ 830,829 direct/yr 1

6. W911QY-06-C-0085 — PI

	DARPA	2006	2007
	Genetic Biomarkers for Prediction of Vaccine Response	$ 325,000 direct/yr 1	
7.	Susan G. Komen Breast Cancer Foundation	co-investigator	
	Genetic and environmental determinants of postmenopausal breast cancer	2004	2006
		$ 952,057 direct/yr 1	
8.	05/1/36/19/413	co-investigator	
	Biomedical Research Council, Singapore	2006	2009
	The Genetics of High Density Lipoprotein Cholesterol Metabolism	$ 886,250 direct/yr 1	
9.	National Medical Research Council, Singapore	collaborator	
	Genome-wide case-control studies to identify genetic variants and gene-environment interactions involved in the pathogenesis of type 2 diabetes mellitus in Chinese, Malays and Asian Indians living in Singapore	2008	2011
		$ 500,000 direct/yr 1	
10.	NMRC/1111/2007	co-investigator	
	National Medical Research Council, Singapore	2007	2010
	Environmental and genetic determinants of adiponectin in Chinese, Malays and Asian Indians, National Medical Research Council, Singapore		$ 150,000 total
11.	National Medical Research Council, Singapore	collaborator	
	Translational Research Innovations in Ocular Surgery		
		$ 3,600,000 direct/yr 1	

12. 1U01DK085545-01	principal investigator		Seielstad (PI)
NIH/NIDDK		09/20/2009	07/31/2015
Identifying Variants Causal for Type 2 Diabetes in Major Human Populations		$ 547,230 direct/yr 1	$ 2,500,000 total

13. 1R01DK080720-01A1	co-investigator		Pereira (PI)
NIH/NIDDK		03/01/2009	02/28/2015
Genetic and Environmental Determinants of Type 2 Diabetes in Chinese Singaporeans.		$ 681,811 direct/yr 1	

14. HHSF223201210412A	co-investigator		Klein (PI)
FDA		09/17/2012	03/31/2015
A Genome-Wide Association Study to Examine Genes Associated with an Increased Risk of Febrile Seizure in Children Following Measles Containing Vaccines		$ 306,377 direct/yr 1	$ 306,377 total

15. 5R01AR065174-02	co-investigator	3.54 % effort	Liao (PI)
NIAMS		07/19/2013	05/31/2018
Identification of causal variants in Psoriasis		$ 465,839 direct/yr 1	$ 1,848,109 total

Genome-wide association studies (GWAS) have successfully identified approximately 36 psoriasis susceptibility loci. However, the causal variants at these loci remain largely unknown, and it is very likely that a large number of additional loci remain to be identified. In this proposal, we pursue a comprehensive strategy to identify both common and rare causal variants in psoriasis, and then perform targeted functional studies of these variants.

Genetics expertise.

16. NHLBI-HB-11-01	co-investigator	10 % effort	Busch (PI)
NHLBI		01/14/2013	09/30/2018
Recipient Epidemiology and Donor Evaluation Study-III (REDS-III) □ Central Laboratory. Genome-wide search for genetic variation increasing risk of HLA-alloimmunization following pregnancy or blood transfusion.		$ 1,212,889 direct/yr 1	$ ~$7,000,000 total

Improving blood component safety and availability in the U.S. and internationally through the conduct of epidemiologic, survey, and laboratory studies is the cornerstone of the REDS program.

Genetics and genotyping expertise for multiple genetics related sub-projects.

17. NHLBI-HB-11-04	co-investigator	5 % effort	Busch (PI)
NHLBI		03/01/2014	09/30/2018
Recipient Epidemiology and Donor Evaluation Study-III (REDS-III) □ International Sites. Compilation of extensive blood donor/donation data/specimens; 4 projects on critical TM issues in Latin America.		$ 1,074,774 direct/yr 1	$ ~$6,000,000 total

Improving blood component safety and availability in the U.S. and internationally through the conduct of epidemiologic, survey, and laboratory studies is the cornerstone of the REDS program.

Genetics and genotyping expertise.

PEER REVIEWED PUBLICATIONS

1. **Seielstad** MT, Hebert JM, Lin AA, Underhill PA, Ibrahim M, Vollrath D, Cavalli-Sforza LL (1994) Construction of human Y-chromosomal haplotypes using a new polymorphic A to G transition. Human Molecular Genetics, 3:2159-61.
2. Ruiz-Linares A, Nayar K, Goldstein DB, Hebert JM, **Seielstad** MT, Underhill PA, Lin AA, Feldman MW, and Cavalli-Sforza LL (1996) Geographic clustering of human Y chromosome haplotypes. Annals of Human Genetics , 60:401-408.
3. Wells RS, **Seielstad** M, Bunce M, Tyan DB, Bekele E, and Parham P (1997) Cw*1701 defines a divergent African HLA-C allelic lineage. Immunogenetics, 46:173-180.
4. Perez-Lezaun A, Calafell F, Seielstad M, Mateu E, Comas D, Bosch E, and Bertranpetit J (1997) Population genetics of Y-chromosome short tandem repeats in humans. Journal of Molecular Evolution, 45:265-270.
5. Seielstad M, Minch E, and Cavalli-Sforza LL (1998) Genetic evidence for a higher female migration rate in humans. Nature Genetics, 20:278-280.
6. Seielstad M, Bekele E, Ibrahim M, Touré A, and Traoré M (1999) A view of modern human origins from Y chromosome microsatellite variation. Genome Research, 9:558-567.
7. Pritchard JK, Seielstad MT, Perez-Lezaun A, and Feldman MW (1999) Population growth of human Y chromosomes: a study of Y chromosome microsatellites. Molecular Biology and Evolution, 16:1791-1798.
8. Jorde LB, Watkins WS, Bamshad MJ, Dixon ME, Ricker CE, Seielstad MT and Batzer MA (2000) The distribution of human genetic diversity: a comparison of mitochondrial, autosomal and Y-chromosome data. American Journal of Human Genetics, 66:979-988.
9. Underhill PA, Shen P, Lin AA, Jin L, Passarino G, Yang WH, Kauffman E, Bonné-Tamir B, Bertranpetit J, Francalacci P, Ibrahim M, Jenkins T, Kidd J, Mehdi SQ, Seielstad MT, Wells RS, Piazza A, Davis RW, Feldman M, Cavalli-Sforza LL and Oefner PJ. (2000) The architecture of Y-chromosome biallelic haplotype diversity: an emerging portrait of mankind. Nature Genetics, 26:358-361.
10. Su B, Xiao C, Deka R, Seielstad M, Kangwanpong D, Xiao J, Lu D, Underhill P, Cavalli-Sforza L, Chakraborty R and Jin L (2000) Y chromosome haplotypes reveal prehistorical migrations to the Himalayas. Human Genetics, 107:582-90.

11. Y Ke, B Su, X Song, D Lu, L Chen, H Li, C Qi, S Marzuki, R Deka, P Underhill, C Xiao, M Shriver, J Lell, D Wallace, S Wells, M Seielstad, P Oefner, D Zhu, J Jin, W Huang, R Chakraborty, Z Chen, L Jin (2001) African Origin of Modern Humans in East Asia: A tale of 12,000 Y chromosomes. Science 292:1151-1153.

12. Niu T, Seielstad M, Zeng X, Apffel A, Li G, Hahnenberger K, Xu X. (2001) Detection of novel ALAD gene polymorphisms using denaturing high-performance liquid chromatography. Human Biology, 73:429-42.

13. Ardlie K, Lunetta K and Seielstad M (2002) Testing for population subdivision and association in four case-control studies. American Journal of Human Genetics, 71:304-311.

14. Bereir RE, Mohamed HS, Seielstad M, El Hassani AM, Khalil EA, Peacock CS, Blackwell JM, Ibrahim ME. (2003) Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. Genetica, 119:57-63.

15. Seielstad M, Yuldasheva N, Singh N, Underhill P, Oefner P, Shen P, Wells RS (2003) A novel Y-chromosome variant puts an upper limit on the timing of first entry into the Americas. American Journal of Human Genetics, 73:700-705.

16. Chia KS, Lee JJM, Cheung P, Cheung KH, Seielstad M, Liu E (2004) Twin births in Singapore: a population-based study using the national birth registry. Annals Academy of Medicine Singapore, 33:195-199.

17. Zhang C, Bailey DK, Awad T, Liu G, Xing G, Cao M, Valmeekam V, Retief J, Matsuzaki H, Taub M, Seielstad M, Kennedy GC. (2006) A whole genome long-range haplotype (WGLRH) test for detecting imprints of positive selection in human populations. Bioinformatics 22:2122-8.

18. Teo YY, Fry AE, Clark TG, Tai ES, & Seielstad M. (2007) On the Usage of HWE for Identifying Genotyping Errors. Ann Hum Genet. 71:701-3.

19. Besaggio D, Fuselli S, Srikummool M, Kampuansai J, Castrì L, Tyler-Smith C, Seielstad M, Kangwanpong D and Bertorelle G. Genetic variation in Northern Thailand Hill Tribes: origins and relationships with social structure and linguistic differences. (2007). BMC Evolutionary Biology 7(Suppl 2):S12 doi:10.1186/1471-2148-7-S2-S12

20. Plenge RM*, Seielstad M*, Padyukov L, Lee AT, Remmers EF, Ding B, Liew A, Khalili MSH, Chandrasekaran A, Davies LRL, Li W, Tan AKS, Bonnard C, Ong RTH, Thalamuthu A, Pettersson S, Liu C, Tian C, Chen WV, Carulli JP, Altshuler D, Alfredsson L, Criswell LA, Amos CI, Seldin MF, Kastner DL, Klareskog L, Gregersen PK. Genome-wide association study in rheumatoid arthritis identifies TRAF1-C5 as a new susceptibility locus (2007). The New England Journal of Medicine 357:1199-209.
*equal contributions

21. S Nejentsev, T Thye, J S Szeszko1, H Stevens, Y Balabanova, A M Chinbuah, M Hibberd, E van de Vosse, B Alisjahbana, R van Crevel, THM Ottenhoff, E Png, F Drobniewski, J A Todd, M Seielstad and R D Horstmann. (2008) Analysis of association of the MAL/TIRAP variant and tuberculosis in 9,441 subjects from three populations. Nature Genetics 40: 261 - 262.

22. Teo YY, Inouye M, Small KS, Fry AE, Potter SC, Dunstan SJ, Seielstad M, Barroso I, Wareham NJ, Rockett KA, Kwiatkowski DP, Deloukas P. (2008) Whole genome-amplified DNA: insights and imputation. Nature Methods. 5:279-80.

23. Tan JT, Dorajoo R, Seielstad M, Sim XL, Ong RT, Chia KS, Wong TY, Saw SM, Chew SK, Aung T, Tai ES. (2008) FTO Variants Are Associated With Obesity in the Chinese and Malay Populations in Singapore. Diabetes. 57:2851-7.

24. Raychaudhuri S, Remmers EF, Lee AT, Hackett R, Guiducci C, Burtt NP, Gianniny L, Korman BD, Padyukov L, Kurreeman FA, Chang M, Catanese JJ, Ding B, Wong S, van der Helm-van Mil AH, Neale BM, Coblyn J, Cui J, Tak PP, Wolbink GJ, Crusius JB, van der Horst-Bruinsma IE, Criswell LA, Amos CI, Seldin MF, Kastner DL, Ardlie KG, Alfredsson L, Costenbader KH, Altshuler D, Huizinga TW, Shadick NA, Weinblatt ME, de Vries N, Worthington J, Seielstad M, Toes RE, Karlson EW, Begovich AB, Klareskog L, Gregersen PK, Daly MJ, Plenge RM. (2008) Common variants at CD40 and other loci confer risk of rheumatoid arthritis. Nature Genetics 40:1216-23.

25. Chen H, Toh TK, Szeverenyi I, Ong RT, Theng CT, McLean WH, Seielstad M, Lane EB. (2008) Association of Skin Barrier Genes within the PSORS4 Locus Is Enriched in Singaporean Chinese with Early-Onset Psoriasis. Journal of Investigative Dermatology. 129:606-14.

26. Thuong NTT, Dunstan SJ, Chau TTH, Thorsson V, Simmons CP, Quyen NTH, Thwaites GE, Lan NTN, Hibberd M, Teo YY, Seielstad M, Aderem A, Farrar JJ and Hawn TR. (2008) Identification of Tuberculosis Susceptibility Genes with Human Macrophage Gene Expression Profiles. PLoS Pathogens 4:e1000229.

27. Davila S, Hibberd ML, Dass RH, Wong HEE, Sahiratmadja E, Bonnard C, Alisjahbana B, Szeszko JS, Balabanova Y, Drobniewski F , van Crevel R, van de Vosse E, Nejentsev S, Ottenhoff THM, Seielstad M (2008) Genetic Association and Expression Studies Indicate a Role of Toll-Like Receptor 8 in Pulmonary Tuberculosis. PLoS Genetics 4:e1000218.

28. Tai ES, Sim XL, Ong TH, Wong TY, Saw SM, Aung T, Kathiresan S, Orho-Melander M, Ordovas JM, Tan JT, Seielstad M. (2008) Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. J Lipid Res. 50:514-20.

29. Ding B, Padyukov L, Lundström E, Seielstad M, Plenge RM, Oksenberg JR, Gregersen PK, Alfredsson L, Klareskog L. (2009) Different patterns of associations with anti-citrullinated protein antibody-positive and anti-citrullinated protein antibody-negative rheumatoid arthritis in the extended major histocompatibility complex region. Arthritis Rheum. 60:30-8.

30. Lim LS, Tai ES, Aung T, Tay WT, Saw SM, Seielstad M, Wong TY. (2009) Relation of Age-related Cataract With Obesity and Obesity Genes in an Asian Population. Am J Epidemiol. 169:1267-74.

31. Lee YC, Raychaudhuri S, Cui J, De Vivo I, Ding B, Alfredsson L, Padyukov L, Costenbader KH, Seielstad M, Graham RR, Klareskog L, Gregersen PK, Plenge RM, Karlson EW. (2009) The PRL -1149 G/T polymorphism and rheumatoid arthritis susceptibility. Arthritis Rheum. 60:1250-4.

32. Tan JT, Dorajoo R, Seielstad M, Sim XL, Ong RT, Chia KS, Wong TY, Saw SM, Chew SK, Aung T, Tai ES. (2008) FTO variants are associated with obesity in the Chinese and Malay populations in Singapore. Diabetes. 57:2851-7.

33. Chen J, Zheng H, Bei JX, Sun L, Jia WH, Li T, Zhang F, Seielstad M, Zeng YX, Zhang X, Liu J. (2009) Genetic structure of the Han Chinese population revealed by genome-wide SNP variation. Am J Hum Genet. 85:775-85.

34. Raychaudhuri S, Thomson BP, Remmers EF, Eyre S, Hinks A, Guiducci C, Catanese JJ, Xie G, Stahl EA, Chen R, Alfredsson L, Amos CI, Ardlie KG; BIRAC Consortium, Barton A, Bowes J, Burtt NP, Chang M, Coblyn J, Costenbader KH, Criswell LA, Crusius JB, Cui J, De Jager PL, Ding B, Emery P, Flynn E, Harrison P, Hocking LJ, Huizinga TW, Kastner DL, Ke X, Kurreeman FA, Lee AT, Liu X, Li Y, Martin P, Morgan AW, Padyukov L, Reid DM, Seielstad M, Seldin MF, Shadick NA, Steer S, Tak PP, Thomson W, van der Helm-van Mil AH, van der Horst-Bruinsma IE, Weinblatt ME, Wilson AG, Wolbink GJ, Wordsworth P; YEAR Consortium, Altshuler D, Karlson EW, Toes RE, de Vries N, Begovich AB, Siminovitch KA, Worthington J, Klareskog L, Gregersen PK, Daly MJ, Plenge RM. (2009) Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. Nat Genet. 41:1313-8.

35. Teo YY, Sim X, Ong RT, Tan AK, Chen J, Tantoso E, Small KS, Ku CS, Lee EJ, Seielstad M, Chia KS. (2009) Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. Genome Res. 19:2154-62.

36. **HUGO Pan-Asian SNP Consortium, Abdulla MA, Ahmed I, Assawamakin A, Bhak J, Brahmachari SK, Calacal GC, Chaurasia A, Chen CH, Chen J, Chen YT, Chu J, Cutiongco-de la Paz EM, De Ungria MC, Delfin FC, Edo J, Fuchareon S, Ghang H, Gojobori T, Han J, Ho SF, Hoh BP, Huang W, Inoko H, Jha P, Jinam TA, Jin L, Jung J, Kangwanpong D, Kampuansai J, Kennedy GC, Khurana P, Kim HL, Kim K, Kim S, Kim WY, Kimm K, Kimura R, Koike T, Kulawonganunchai S, Kumar V, Lai PS, Lee JY, Lee S, Liu ET, Majumder PP, Mandapati KK, Marzuki S, Mitchell W, Mukerji M, Naritomi K, Ngamphiw C, Niikawa N, Nishida N, Oh B, Oh S, Ohashi J, Oka A, Ong R, Padilla CD, Palittapongarnpim P, Perdigon HB, Phipps ME, Png E, Sakaki Y, Salvador JM, Sandraling Y, Scaria V, Seielstad** M, Sidek MR, Sinha A, Srikummool M, Sudoyo H, Sugano S, Suryadi H, Suzuki Y, Tabbada KA, Tan A, Tokunaga K, Tongsima S, Villamor LP, Wang E, Wang Y, Wang H, Wu JY, Xiao H, Xu S, Yang JO, Shugart YY, Yoo HS, Yuan W, Zhao G, Zilfalil BA; Indian Genome Variation Consortium. (2009) Mapping human genetic diversity in Asia. Science. 326:1541-5.
** corresponding author

37. Törkvist L, Halfvarson J, Ong RT, Lördal M, Sjöqvist U, Bresso F, Björk J, Befrits R, Löfberg R, Blom J, Carlson M, Padyukov L, D'Amato M, Seielstad M, Pettersson S. (2010) Analysis of 39 Crohn's disease risk loci in Swedish inflammatory bowel disease patients. Inflamm Bowel Dis 16:907-9.

38. Shu XO, Long J, Cai Q, Qi L, Xiang YB, Cho YS, Tai ES, Li X, Lin X, Chow WH, Go MJ, Seielstad M, Bao W, Li H, Cornelis MC, Yu K, Wen W, Shi J, Han BG, Sim XL, Liu L, Qi Q, Kim HL, Ng DP, Lee JY, Kim YJ, Li C, Gao YT, Zheng W, Hu FB. Identification of new genetic risk variants for type 2 diabetes. PLoS Genet. 2010 Sep; 6(9).

39. Stahl EA, Raychaudhuri S, Remmers EF, Xie G, Eyre S, Thomson BP, Li Y, Kurreeman FA, Zhernakova A, Hinks A, Guiducci C, Chen R, Alfredsson L, Amos CI, Ardlie KG; BIRAC Consortium, Barton A, Bowes J, Brouwer E, Burtt NP, Catanese JJ, Coblyn J, Coenen MJ, Costenbader KH, Criswell LA, Crusius JB, Cui J, de Bakker PI, De Jager PL, Ding B, Emery P, Flynn E, Harrison P, Hocking LJ, Huizinga TW, Kastner DL, Ke X, Lee AT, Liu X, Martin P, Morgan AW, Padyukov L, Posthumus MD, Radstake TR, Reid DM, Seielstad M, Seldin MF, Shadick NA, Steer S, Tak PP, Thomson W, van der Helm-van Mil AH, van der Horst-Bruinsma IE, van der Schoot CE, van Riel PL, Weinblatt ME, Wilson AG, Wolbink GJ, Wordsworth BP; YEAR Consortium, Wijmenga C, Karlson EW, Toes RE, de Vries N, Begovich AB, Worthington J, Siminovitch KA, Gregersen PK, Klareskog L,

Plenge RM. (2010) Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nat Genet. 42:508-14.

40. Ku CS, Pawitan Y, Sim X, Ong RT, Seielstad M, Lee EJ, Teo YY, Chia KS, Salim A. (2010) Genomic copy number variations in three Southeast Asian populations. Hum Mutat. 31:851-857.

41. Dellinger AE, Saw SM, Goh LK, Seielstad M, Young TL, Li YJ. (2010) Comparative analyses of seven algorithms for copy number variant identification from single nucleotide polymorphism arrays. Nucleic Acids Res. 38:e105.

42. Khor CC, Fan Q, Goh LK, Wong TY, Li YJ, Cheung N, Seielstad M, Goh DL, Young TL, Tai ES, Saw SM. (2010) Hepatocyte growth factor and retinal arteriolar diameter in Singapore Chinese. Ophthalmology 117:939-45.

43. Davila S, Froeling FE, Tan A, Bonnard C, Boland GJ, Snippe H, Hibberd ML, Seielstad M. (2010) New genetic associations detected in a host response study to hepatitis B vaccine. Genes Immun. 11:232-8.

44. Xu S, Kangwanpong D, Seielstad M, Srikummool M, Kampuansai J, Jin L; HUGO Pan-Asian SNP Consortium. (2010) Genetic evidence supports linguistic affinity of Mlabri--a hunter-gatherer group in Thailand. BMC Genet. 11:18.

45. Tan JT, Ng DP, Nurbaya S, Ye S, Lim XL, Leong H, Seet LT, Siew WF, Kon W, Wong TY, Saw SM, Aung T, Chia KS, Lee J, Chew SK, Seielstad M, Tai ES. (2010) Polymorphisms identified through genome-wide association studies and their associations with type 2 diabetes in Chinese, Malays, and Asian-Indians in Singapore. J Clin Endocrinol Metab. 95:390-7.

46. Teslovich TM, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Ripatti S, Chasman DI, Willer CJ, Johansen CT, Fouchier SW, Isaacs A, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Aulchenko YS, Thorleifsson G, Feitosa MF, Chambers J, Orho-Melander M, Melander O, Johnson T, Li X, Guo X, Li M, Shin Cho Y, Jin Go M, Jin Kim Y, Lee JY, Park T, Kim K, Sim X, Twee-Hee Ong R, Croteau-Chonka DC, Lange LA, Smith JD, Song K, Hua Zhao J, Yuan X, Luan J, Lamina C, Ziegler A, Zhang W, Zee RY, Wright AF, Witteman JC, Wilson JF, Willemsen G, Wichmann HE, Whitfield JB, Waterworth DM, Wareham NJ, Waeber G, Vollenweider P, Voight BF, Vitart V, Uitterlinden AG, Uda M, Tuomilehto J, Thompson JR, Tanaka T, Surakka I, Stringham HM, Spector TD, Soranzo N, Smit JH, Sinisalo J, Silander K, Sijbrands EJ, Scuteri A, Scott J, Schlessinger D, Sanna S, Salomaa V, Saharinen J, Sabatti C, Ruokonen A, Rudan I, Rose LM, Roberts R, Rieder M, Psaty BM, Pramstaller PP, Pichler I, Perola M, Penninx BW, Pedersen NL, Pattaro C, Parker AN, Pare G, Oostra BA, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, Meitinger T, McPherson R, McCarthy MI, McArdle W, Masson D, Martin NG, Marroni F, Mangino M, Magnusson PK, Lucas G, Luben R, Loos RJ, Lokki ML, Lettre G, Langenberg C, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, Kronenberg F, König IR, Khaw KT, Kaprio J, Kaplan LM, Johansson A, Jarvelin MR, Cecile J W Janssens A, Ingelsson E, Igl W, Kees Hovingh G, Hottenga JJ, Hofman A, Hicks AA, Hengstenberg C, Heid IM, Hayward C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Gyllensten U, Guiducci C, Groop LC, Gonzalez E, Gieger C, Freimer NB, Ferrucci L, Erdmann J, Elliott P, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Geus EJ, de Faire U, Crawford G, Collins FS, Chen YD, Caulfield MJ, Campbell H, Burtt NP, Bonnycastle LL, Boomsma DI, Boekholdt SM, Bergman RN, Barroso I, Bandinelli S, Ballantyne CM, Assimes TL, Quertermous T, Altshuler D, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Adair LS, Taylor HA Jr, Borecki IB, Gabriel SB, Wilson JG, Holm

H, Thorsteinsdottir U, Gudnason V, Krauss RM, Mohlke KL, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Rotter JI, Boerwinkle E, Strachan DP, Mooser V, Stefansson K, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, van Duijn CM, Peltonen L, Abecasis GR, Boehnke M, Kathiresan S. (2010) Biological, clinical and population relevance of 95 loci for blood lipids. Nature. 466:707-13.

47. McGovern DP, Gardet A, Törkvist L, Goyette P, Essers J, Taylor KD, Neale BM, Ong RT, Lagacé C, Li C, Green T, Stevens CR, Beauchamp C, Fleshner PR, Carlson M, D'Amato M, Halfvarson J, Hibberd ML, Lördal M, Padyukov L, Andriulli A, Colombo E, Latiano A, Palmieri O, Bernard EJ, Deslandres C, Hommes DW, de Jong DJ, Stokkers PC, Weersma RK; NIDDK IBD Genetics Consortium, Sharma Y, Silverberg MS, Cho JH, Wu J, Roeder K, Brant SR, Schumm LP, Duerr RH, Dubinsky MC, Glazer NL, Haritunians T, Ippoliti A, Melmed GY, Siscovick DS, Vasiliauskas EA, Targan SR, Annese V, Wijmenga C, Pettersson S, Rotter JI, Xavier RJ, Daly MJ, Rioux JD, Seielstad M. (2010) Genome-wide association identifies multiple ulcerative colitis susceptibility loci. Nat Genet. 42:332-7.

48. Khor CC, Fan Q, Goh L, Tan D, Young TL, Li YJ, **Seielstad** M, Goh DL, Saw SM. (2010) Support for TGFB1 as a susceptibility gene for high myopia in individuals of Chinese descent. Arch Ophthalmol. **128**(8):1081-4.
PMID: 20697017

49. Li YJ, Goh L, Khor CC, Fan Q, Yu M, Han S, Sim X, Ong RT, Wong TY, Vithana EN, Yap E, Nakanishi H, Matsuda F, Ohno-Matsui K, Yoshimura N, **Seielstad** M, Tai ES, Young TL, Saw SM. (2011) Genome-wide association studies reveal genetic variants in CTNND2 for high myopia in Singapore Chinese. Ophthalmology. **118**(2):368-75.

50. Kutanan W, Kampuansai J, Fuselli S, Nakbunlung S, **Seielstad** M, Bertorelle G, Kangwanpong D. (2011) Genetic structure of the Mon-Khmer speaking groups and their affinity to the neighbouring Tai populations in Northern Thailand. BMC Genet. **12**:56.
PMID: 21672265

51. Han S, Chen P, Fan Q, Khor CC, Sim X, Tay WT, Ong RT, Suo C, Goh LK, Lavanya R, Zheng Y, Wu R, **Seielstad** M, Vithana E, Liu J, Chia KS, Lee JJ, Tai ES, Wong TY, Aung T, Teo YY, Saw SM. (2011) Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. Hum Mol Genet **20**(18):3693-8.
PMID: 21665993

52. 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. (2011) Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nat Genet. **43**(6):531-8
PMID: 21572416

53. Khor CC, Ramdas WD, Vithana EN, Cornes BK, Sim X, Tay WT, Saw SM, Zheng Y, Lavanya R, Wu R, Wang JJ, Mitchell P, Uitterlinden AG, Rivadeneira F, Teo YY, Chia KS, Seielstad M, Hibberd M, Vingerling JR, Klaver CC, Jansonius NM, Tai ES, Wong TY, van Duijn CM, Aung T. Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Hum Mol Genet. 2011 May 1; 20(9):1864-72.

54. Hatin WI, Nur-Shafawati AR, Zahri MK, Xu S, Jin L, Tan SG, Rizman-Idid M, Zilfalil BA; HUGO Pan-Asian SNP Consortium. (2011) Population genetic structure of peninsular Malaysia Malay sub-ethnic groups. PLoS One.**6**(4):e18312.
PMID: 21483678

55. Teo SM, Pawitan Y, Kumar V, Thalamuthu A, **Seielstad** M, Chia KS, Salim A. (2011) Multi-platform segmentation for joint detection of copy number variants. Bioinformatics. (2011) **27**(11):1555-61.
PMID: 21471018

56. Fox ER, Young JH, Li Y, Dreisbach AW, Keating BJ, Musani SK, Liu K, Morrison AC, Ganesh S, Kutlar A, Ramachandran VS, Polak JF, Fabsitz RR, Dries DL, Farlow DN, Redline S, Adeyemo A, Hirschorn JN, Sun YV, Wyatt SB, Penman AD, Palmas W, Rotter JI, Townsend RR, Doumatey AP, Tayo BO, Mosley TH Jr, Lyon HN, Kang SJ, Rotimi CN, Cooper RS, Franceschini N, Curb JD, Martin LW, Eaton CB, Kardia SL, Taylor HA, Caulfield MJ, Ehret GB, Johnson T; International Consortium for Blood Pressure Genome-wide Association Studies (ICBP-GWAS), Chakravarti A, Zhu X, Levy D, Munroe PB, Rice KM, Bochud M, Johnson AD, Chasman DI, Smith AV, Tobin MD, Verwoert GC, Hwang SJ, Pihur V, Vollenweider P, O'Reilly PF, Amin N, Bragg-Gresham JL, Teumer A, Glazer NL, Launer L, Zhao JH, Aulchenko Y, Heath S, Sõber S, Parsa A, Luan J, Arora P, Dehghan A, Zhang F, Lucas G, Hicks AA, Jackson AU, Peden JF, Tanaka T, Wild SH, Rudan I, Igl W, Milaneschi Y, Parker AN, Fava C, Chambers JC, Kumari M, Go MJ, van der Harst P, Kao WH, Sjögren M, Vinay DG, Alexander M, Tabara Y, Shaw-Hawkins S, Whincup PH, Liu Y, Shi G, Kuusisto J, **Seielstad** M, Sim X, Nguyen KD, Lehtimäki T, Matullo G, Wu Y, Gaunt TR, Onland-Moret NC, Cooper MN, Platou CG, Org E, Hardy R, Dahgam S, Palmen J, Vitart V, Braund PS, Kuznetsova T, Uiterwaal CS, Campbell H, Ludwig B, Tomaszewski M, Tzoulaki I, Palmer ND; CARDIoGRAM consortium; CKDGen consortium; KidneyGen consortium; EchoGen consortium; CHARGE-HF consortium, Aspelund T, Garcia M, Chang YP, O'Connell JR, Steinle NI, Grobbee DE, Arking DE, Hernandez D, Najjar S, McArdle WL, Hadley D, Brown MJ, Connell JM, Hingorani AD, Day IN, Lawlor DA, Beilby JP, Lawrence RW, Clarke R, Collins R, Hopewell JC, Ongen H, Bis JC, Kähönen M, Viikari J, Adair LS, Lee NR, Chen MH, Olden M, Pattaro C, Hoffman Bolton JA, Köttgen A, Bergmann S, Mooser V, Chaturvedi N, Frayling TM, Islam M, Jafar TH, Erdmann J, Kulkarni SR, Bornstein SR, Grässler J, Groop L, Voight BF, Kettunen J, Howard P, Taylor A, Guarrera S, Ricceri F, Emilsson V, Plump A, Barroso I, Khaw KT, Weder AB, Hunt SC, Bergman RN, Collins FS, Bonnycastle LL, Scott LJ, Stringham HM, Peltonen L, Perola M, Vartiainen E, Brand SM, Staessen JA, Wang TJ, Burton PR, Artigas MS, Dong Y, Snieder H, Wang X, Zhu H, Lohman KK, Rudock ME, Heckbert SR, Smith NL, Wiggins KL, Shriner D, Veldre G, Viigimaa M, Kinra S, Prabhakaran D, Tripathy V, Langefeld CD, Rosengren A, Thelle DS, Corsi AM, Singleton A, Forrester T, Hilton G, McKenzie CA, Salako T, Iwai N, Kita Y, Ogihara T, Ohkubo T, Okamura T, Ueshima H, Umemura S, Eyheramendy S, Meitinger T, Wichmann HE, Cho YS, Kim HL, Lee JY, Scott J, Sehmi JS, Zhang W, Hedblad B, Nilsson P, Smith GD, Wong A, Narisu N, Stancáková A, Raffel LJ, Yao J, Kathiresan S, O'Donnell C, Schwartz SM, Ikram MA, Longstreth WT Jr, Seshadri S, Shrine NR, Wain LV, Morken MA, Swift AJ, Laitinen J, Prokopenko I, Zitting P, Cooper JA, Humphries SE, Danesh J, Rasheed A, Goel A, Hamsten A, Watkins H, Bakker SJ, van Gilst WH, Janipalli C, Mani KR, Yajnik CS, Hofman A, Mattace-Raso FU, Oostra BA, Demirkan A, Isaacs A, Rivadeneira F, Lakatta EG, Orru M, Scuteri A, Ala-Korpela M, Kangas AJ, Lyytikäinen LP, Soininen P, Tukiainen T, Würz P, Ong RT, Dörr M, Kroemer HK, Völker U, Völzke H, Galan P, Hercberg S, Lathrop M, Zelenika D, Deloukas P, Mangino M, Spector TD, Zhai G, Meschia JF, Nalls MA, Sharma P, Terzic J, Kumar MJ, Denniff M, Zukowska-Szczechowska E, Wagenknecht LE, Fowkes FG, Charchar FJ,

Schwarz PE, Hayward C, Guo X, Bots ML, Brand E, Samani N, Polasek O, Talmud PJ, Nyberg F, Kuh D, Laan M, Hveem K, Palmer LJ, van der Schouw YT, Casas JP, Mohlke KL, Vineis P, Raitakari O, Wong TY, Tai ES, Laakso M, Rao DC, Harris TB, Morris RW, Dominiczak AF, Kivimaki M, Marmot MG, Miki T, Saleheen D, Chandak GR, Coresh J, Navis G, Salomaa V, Han BG, Kooner JS, Melander O, Ridker PM, Bandinelli S, Gyllensten UB, Wright AF, Wilson JF, Ferrucci L, Farrall M, Tuomilehto J, Pramstaller PP, Elosua R, Soranzo N, Sijbrands EJ, Altshuler D, Loos RJ, Shuldiner AR, Gieger C, Meneton P, Uitterlinden AG, Wareham NJ, Gudnason V, Rettig R, Uda M, Strachan DP, Witteman JC, Hartikainen AL, Beckmann JS, Boerwinkle E, Boehnke M, Larson MG, Järvelin MR, Psaty BM, Abecasis GR, Elliott P, van Duijn CM, Newton-Cheh C. (2011) Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Hum Mol Genet. **20**(11):2273-84.
PMID: 21378095

57. Sim X, Ong RT, Suo C, Tay WT, Liu J, Ng DP, Boehnke M, Chia KS, Wong TY, **Seielstad** M, Teo YY, Tai ES. (2011) Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. PLoS Genet. Apr; 7(4):e1001363.

58. Khor CC, Ramdas WD, Vithana EN, Cornes BK, Sim X, Tay WT, Saw SM, Zheng Y, Lavanya R, Wu R, Wang JJ, Mitchell P, Uitterlinden AG, Rivadeneira F, Teo YY, Chia KS, **Seielstad** M, Hibberd M, Vingerling JR, Klaver CC, Jansonius NM, Tai ES, Wong TY, van Duijn CM, Aung T. (2011) Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Hum Mol Genet. **20**(9):1864-72.
PMID: 21307088

59. Anderson CA, Boucher G, Lees CW, Franke A, D'Amato M, Taylor KD, Lee JC, Goyette P, Imielinski M, Latiano A, Lagacé C, Scott R, Amininejad L, Bumpstead S, Baidoo L, Baldassano RN, Barclay M, Bayless TM, Brand S, Büning C, Colombel JF, Denson LA, De Vos M, Dubinsky M, Edwards C, Ellinghaus D, Fehrmann RS, Floyd JA, Florin T, Franchimont D, Franke L, Georges M, Glas J, Glazer NL, Guthery SL, Haritunians T, Hayward NK, Hugot JP, Jobin G, Laukens D, Lawrance I, Lémann M, Levine A, Libioulle C, Louis E, McGovern DP, Milla M, Montgomery GW, Morley KI, Mowat C, Ng A, Newman W, Ophoff RA, Papi L, Palmieri O, Peyrin-Biroulet L, Panés J, Phillips A, Prescott NJ, Proctor DD, Roberts R, Russell R, Rutgeerts P, Sanderson J, Sans M, Schumm P, Seibold F, Sharma Y, Simms LA, **Seielstad** M, Steinhart AH, Targan SR, van den Berg LH, Vatn M, Verspaget H, Walters T, Wijmenga C, Wilson DC, Westra HJ, Xavier RJ, Zhao ZZ, Ponsioen CY, Andersen V, Torkvist L, Gazouli M, Anagnou NP, Karlsen TH, Kupcinskas L, Sventoraityte J, Mansfield JC, Kugathasan S, Silverberg MS, Halfvarson J, Rotter JI, Mathew CG, Griffiths AM, Gearry R, Ahmad T, Brant SR, Chamaillard M, Satsangi J, Cho JH, Schreiber S, Daly MJ, Barrett JC, Parkes M, Annese V, Hakonarson H, Radford-Smith G, Duerr RH, Vermeire S, Weersma RK, Rioux JD. (2011) Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nat Genet. **43**(3):246-52.
PMID: 21297633

60. Zimring JC, Welniak L, Semple JW, Ness PM, Slichter SJ, Spitalnik SL; NHLBI Alloimmunization Working Group. (2011) Current problems and future directions of transfusion-induced alloimmunization: summary of an NHLBI working group. Transfusion. **51**(2):435-41.
PMID: 21251006

61. Zhao J, Gupta S, **Seielstad** M, Liu J, Thalamuthu A. (2011) Pathway-based analysis using reduced gene subsets in genome-wide association studies. BMC Bioinformatics.**12**:17. PMID: 21226955

62. Ku CS, Teo SM, Naidoo N, Sim X, Teo YY, Pawitan Y, **Seielstad** M, Chia KS, Salim A. (2011) Copy number polymorphisms in new HapMap III and Singapore populations. J Hum Genet. **56**(8):552-60.

63. Padyukov L, **Seielstad** M, Ong RT, Ding B, Rönnelid J, Seddighzadeh M, Alfredsson L, Klareskog L; Epidemiological Investigation of Rheumatoid Arthritis (EIRA) study group. (2011) A genome-wide association study suggests contrasting associations in ACPA-positive versus ACPA-negative rheumatoid arthritis. Ann Rheum Dis. **70**(2):259-65. PMID: 21156761

64. Png E, Thalamuthu A, Ong RT, Snippe H, Boland GJ, **Seielstad** M. (2011) A genome-wide association study of hepatitis B vaccine response in an Indonesian population reveals multiple independent risk variants in the HLA region. Hum Mol Genet. **20**(19):3893-8.

65. Kutanan W, Kampuansai J, Colonna V, Nakbunlung S, Lertvicha P, **Seielstad** M, Bertorelle G, Kangwanpong D. (2011) Genetic affinity and admixture of northern Thai people along their migration route in northern Thailand: evidence from autosomal STR loci. J Hum Genet. **56**(2):130-7. PMID: 21107341

66. Vithana EN, Aung T, Khor CC, Cornes BK, Tay WT, Sim X, Lavanya R, Wu R, Zheng Y, Hibberd ML, Chia KS, **Seielstad** M, Goh LK, Saw SM, Tai ES, Wong TY. (2011) Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Hum Mol Genet. **20**(4):649-58. PMID: 21098505

67. Thuong NT, Hawn TR, Chau TT, Bang ND, Yen NT, Thwaites GE, Teo YY, **Seielstad** M, Hibberd M, Lan NT, Caws M, Farrar JJ, Dunstan SJ. (2011) Epiregulin (EREG) variation is associated with susceptibility to tuberculosis. Genes Immun. doi: 10.1038/gene.2011.83. PMID:22170233

68. International Consortium for Blood Pressure Genome-Wide Association Studies, Ehret GB, Munroe PB, Rice KM, Bochud M, Johnson AD, Chasman DI, Smith AV, Tobin MD, Verwoert GC, Hwang SJ, Pihur V, Vollenweider P, O'Reilly PF, Amin N, Bragg-Gresham JL, Teumer A, Glazer NL, Launer L, Zhao JH, Aulchenko Y, Heath S, Sõber S, Parsa A, Luan J, Arora P, Dehghan A, Zhang F, Lucas G, Hicks AA, Jackson AU, Peden JF, Tanaka T, Wild SH, Rudan I, Igl W, Milaneschi Y, Parker AN, Fava C, Chambers JC, Fox ER, Kumari M, Go MJ, van der Harst P, Kao WH, Sjögren M, Vinay DG, Alexander M, Tabara Y, Shaw-Hawkins S, Whincup PH, Liu Y, Shi G, Kuusisto J, Tayo B, **Seielstad** M, Sim X, Nguyen KD, Lehtimäki T, Matullo G, Wu Y, Gaunt TR, Onland-Moret NC, Cooper MN, Platou CG, Org E, Hardy R, Dahgam S, Palmen J, Vitart V, Braund PS, Kuznetsova T, Uiterwaal CS, Adeyemo A, Palmas W, Campbell H, Ludwig B, Tomaszewski M, Tzoulaki I, Palmer ND; CARDIoGRAM consortium; CKDGen Consortium; KidneyGen Consortium; EchoGen consortium; CHARGE-HF consortium, Aspelund T, Garcia M, Chang YP, O'Connell JR, Steinle NI, Grobbee DE, Arking DE, Kardia SL, Morrison AC, Hernandez D, Najjar S, McArdle WL, Hadley D, Brown MJ, Connell JM, Hingorani AD, Day IN, Lawlor DA, Beilby JP, Lawrence RW, Clarke R, Hopewell JC, Ongen H, Dreisbach AW, Li Y, Young JH, Bis JC, Kähönen M, Viikari J, Adair LS, Lee NR, Chen MH, Olden M, Pattaro C, Bolton JA, Köttgen A, Bergmann S, Mooser V, Chaturvedi N, Frayling TM, Islam M, Jafar TH, Erdmann J, Kulkarni SR, Bornstein SR, Grässler J, Groop L, Voight BF, Kettunen J,

Howard P, Taylor A, Guarrera S, Ricceri F, Emilsson V, Plump A, Barroso I, Khaw KT, Weder AB, Hunt SC, Sun YV, Bergman RN, Collins FS, Bonnycastle LL, Scott LJ, Stringham HM, Peltonen L, Perola M, Vartiainen E, Brand SM, Staessen JA, Wang TJ, Burton PR, Artigas MS, Dong Y, Snieder H, Wang X, Zhu H, Lohman KK, Rudock ME, Heckbert SR, Smith NL, Wiggins KL, Doumatey A, Shriner D, Veldre G, Viigimaa M, Kinra S, Prabhakaran D, Tripathy V, Langefeld CD, Rosengren A, Thelle DS, Corsi AM, Singleton A, Forrester T, Hilton G, McKenzie CA, Salako T, Iwai N, Kita Y, Ogihara T, Ohkubo T, Okamura T, Ueshima H, Umemura S, Eyheramendy S, Meitinger T, Wichmann HE, Cho YS, Kim HL, Lee JY, Scott J, Sehmi JS, Zhang W, Hedblad B, Nilsson P, Smith GD, Wong A, Narisu N, Stančáková A, Raffel LJ, Yao J, Kathiresan S, O'Donnell CJ, Schwartz SM, Ikram MA, Longstreth WT Jr, Mosley TH, Seshadri S, Shrine NR, Wain LV, Morken MA, Swift AJ, Laitinen J, Prokopenko I, Zitting P, Cooper JA, Humphries SE, Danesh J, Rasheed A, Goel A, Hamsten A, Watkins H, Bakker SJ, van Gilst WH, Janipalli CS, Mani KR, Yajnik CS, Hofman A, Mattace-Raso FU, Oostra BA, Demirkan A, Isaacs A, Rivadeneira F, Lakatta EG, Orru M, Scuteri A, Ala-Korpela M, Kangas AJ, Lyytikäinen LP, Soininen P, Tukiainen T, Würtz P, Ong RT, Dörr M, Kroemer HK, Völker U, Völzke H, Galan P, Hercberg S, Lathrop M, Zelenika D, Deloukas P, Mangino M, Spector TD, Zhai G, Meschia JF, Nalls MA, Sharma P, Terzic J, Kumar MV, Denniff M, Zukowska-Szczechowska E, Wagenknecht LE, Fowkes FG, Charchar FJ, Schwarz PE, Hayward C, Guo X, Rotimi C, Bots ML, Brand E, Samani NJ, Polasek O, Talmud PJ, Nyberg F, Kuh D, Laan M, Hveem K, Palmer LJ, van der Schouw YT, Casas JP, Mohlke KL, Vineis P, Raitakari O, Ganesh SK, Wong TY, Tai ES, Cooper RS, Laakso M, Rao DC, Harris TB, Morris RW, Dominiczak AF, Kivimaki M, Marmot MG, Miki T, Saleheen D, Chandak GR, Coresh J, Navis G, Salomaa V, Han BG, Zhu X, Kooner JS, Melander O, Ridker PM, Bandinelli S, Gyllensten UB, Wright AF, Wilson JF, Ferrucci L, Farrall M, Tuomilehto J, Pramstaller PP, Elosua R, Soranzo N, Sijbrands EJ, Altshuler D, Loos RJ, Shuldiner AR, Gieger C, Meneton P, Uitterlinden AG, Wareham NJ, Gudnason V, Rotter JI, Rettig R, Uda M, Strachan DP, Witteman JC, Hartikainen AL, Beckmann JS, Boerwinkle E, Vasan RS, Boehnke M, Larson MG, Järvelin MR, Psaty BM, Abecasis GR, Chakravarti A, Elliott P, van Duijn CM, Newton-Cheh C, Levy D, Caulfield MJ, Johnson T, Tang H, Knowles J, Hlatky M, Fortmann S, Assimes TL, Quertermous T, Go A, Iribarren C, Absher D, Risch N, Myers R, Sidney S, Ziegler A, Schillert A, Bickel C, Sinning C, Rupprecht HJ, Lackner K, Wild P, Schnabel R, Blankenberg S, Zeller T, Münzel T, Perret C, Cambien F, Tiret L, Nicaud V, Proust C, Dehghan A, Hofman A, Uitterlinden A, van Duijn C, Levy D, Whitteman J, Cupples LA, Demissie-Banjaw S, Ramachandran V, Smith A, Gudnason V, Boerwinkle E, Folsom A, Morrison A, Psaty BM, Chen IY, Rotter JI, Bis J, Volcik K, Rice K, Taylor KD, Marciante K, Smith N, Glazer N, Heckbert S, Harris T, Lumley T, Kong A, Thorleifsson G, Thorgeirsson G, Holm H, Gulcher JR, Stefansson K, Andersen K, Gretarsdottir S, Thorsteinsdottir U, Preuss M, Schreiber S, Meitinger T, König IR, Lieb W, Hengstenberg C, Schunkert H, Erdmann J, Fischer M, Grosshennig A, Medack A, Stark K, Linsel-Nitschke P, Bruse P, Aherrahrou Z, Peters A, Loley C, Willenborg C, Nahrstedt J, Freyer J, Gulde S, Doering A, Meisinger C, Wichmann HE, Klopp N, Illig T, Meinitzer A, Tomaschitz A, Halperin E, Dobnig H, Scharnagl H, Kleber M, Laaksonen R, Pilz S, Grammer TB, Stojakovic T, Renner W, März W, Böhm BO, Winkelmann BR, Winkler K, Hoffmann MM, O'Donnell CJ, Voight BF, Altshuler D, Siscovick DS, Musunuru K, Peltonen L, Barbalic M, Melander O, Elosua R, Kathiresan S, Schwartz SM, Salomaa V, Guiducci C, Burtt N, Gabriel SB, Stewart AF, Wells GA, Chen L, Jarinova O, Roberts R, McPherson R, Dandona S, Pichard AD, Rader DJ, Devaney J, Lindsay JM, Kent KM, Qu L, Satler L, Burnett MS, Li M, Reilly MP, Wilensky R, Waksman R, Epstein S, Matthai W, Knouff CW, Waterworth DM, Hakonarson HH, Walker MC, Mooser V, Hall AS, Balmforth AJ, Wright BJ, Nelson C, Thompson JR, Samani NJ, Braund PS, Ball SG, Smith NL, Felix JF, Morrison

AC, Demissie S, Glazer NL, Loehr LR, Cupples LA, Dehghan A, Lumley T, Rosamond WD, Lieb W, Rivadeneira F, Bis JC, Folsom AR, Benjamin E, Aulchenko YS, Haritunians T, Couper D, Murabito J, Wang YA, Stricker BH, Gottdiener JS, Chang PP, Wang TJ, Rice KM, Hofman A, Heckbert SR, Fox ER, O'Donnell CJ, Uitterlinden AG, Rotter JI, Willerson JT, Levy D, van Duijn CM, Psaty BM, Witteman JC, Boerwinkle E, Vasan RS, Köttgen A, Pattaro C, Böger CA, Fuchsberger C, Olden M, Glazer NL, Parsa A, Gao X, Yang Q, Smith AV, O'Connell JR, Li M, Schmidt H, Tanaka T, Isaacs A, Ketkar S, Hwang SJ, Johnson AD, Dehghan A, Teumer A, Paré G, Atkinson EJ, Zeller T, Lohman K, Cornelis MC, Probst-Hensch NM, Kronenberg F, Tönjes A, Hayward C, Aspelund T, Eiriksdottir G, Launer LJ, Harris TB, Rampersaud E, Mitchell BD, Arking DE, Boerwinkle E, Struchalin M, Cavalieri M, Singleton A, Giallauria F, Metter J, de Boer J, Haritunians T, Lumley T, Siscovick D, Psaty BM, Zillikens MC, Oostra BA, Feitosa M, Province M, de Andrade M, Turner ST, Schillert A, Ziegler A, Wild PS, Schnabel RB, Wilde S, Munzel TF, Leak TS, Illig T, Klopp N, Meisinger C, Wichmann HE, Koenig W, Zgaga L, Zemunik T, Kolcic I, Minelli C, Hu FB, Johansson A, Igl W, Zaboli G, Wild SH, Wright AF, Campbell H, Ellinghaus D, Schreiber S, Aulchenko YS, Felix JF, Rivadeneira F, Uitterlinden AG, Hofman A, Imboden M, Nitsch D, Brandstätter A, Kollerits B, Kedenko L, Mägi R, Stumvoll M, Kovacs P, Boban M, Campbell S, Endlich K, Völzke H, Kroemer HK, Nauck M, Völker U, Polasek O, Vitart V, Badola S, Parker AN, Ridker PM, Kardia SL, Blankenberg S, Liu Y, Curhan GC, Franke A, Rochat T, Paulweber B, Prokopenko I, Wang W, Gudnason V, Shuldiner AR, Coresh J, Schmidt R, Ferrucci L, Shlipak MG, van Duijn CM, Borecki I, Krämer BK, Rudan I, Gyllensten U, Wilson JF, Witteman JC, Pramstaller PP, Rettig R, Hastie N, Chasman DI, Kao WH, Heid IM, Fox CS, Vasan RS, Glazer NL, Felix JF, Lieb W, Wild PS, Felix SB, Watzinger N, Larson MG, Smith NL, Dehghan A, Grosshennig A, Schillert A, Teumer A, Schmidt R, Kathiresan S, Lumley T, Aulchenko YS, König IR, Zeller T, Homuth G, Struchalin M, Aragam J, Bis JC, Rivadeneira F, Erdmann J, Schnabel RB, Dörr M, Zweiker R, Lind L, Rodeheffer RJ, Greiser KH, Levy D, Haritunians T, Deckers JW, Stritzke J, Lackner KJ, Völker U, Ingelsson E, Kullo I, Haerting J, O'Donnell CJ, Heckbert SR, Stricker BH, Ziegler A, Reffelmann T, Redfield MM, Werdan K, Mitchell GF, Rice K, Arnett DK, Hofman A, Gottdiener JS, Uitterlinden AG, Meitinger T, Blettner M, Friedrich N, Wang TJ, Psaty BM, van Duijn CM, Wichmann HE, Munzel TF, Kroemer HK, Benjamin EJ, Rotter JI, Witteman JC, Schunkert H, Schmidt H, Völzke H, Blankenberg S, Chambers JC, Zhang W, Lord GM, van der Harst P, Lawlor DA, Sehmi JS, Gale DP, Wass MN, Ahmadi KR, Bakker SJ, Beckmann J, Bilo HJ, Bochud M, Brown MJ, Caulfield MJ, Connell JM, Cook HT, Cotlarciuc I, Davey Smith G, de Silva R, Deng G, Devuyst O, Dikkeschei LD, Dimkovic N, Dockrell M, Dominiczak A, Ebrahim S, Eggermann T, Farrall M, Ferrucci L, Floege J, Forouhi NG, Gansevoort RT, Han X, Hedblad B, Homan van der Heide JJ, Hepkema BG, Hernandez-Fuentes M, Hypponen E, Johnson T, de Jong PE, Kleefstra N, Lagou V, Lapsley M, Li Y, Loos RJ, Luan J, Luttropp K, Maréchal C, Melander O, Munroe PB, Nordfors L, Parsa A, Peltonen L, Penninx BW, Perucha E, Pouta A, Prokopenko I, Roderick PJ, Ruokonen A, Samani NJ, Sanna S, Schalling M, Schlessinger D, Schlieper G, Seelen MA, Shuldiner AR, Sjögren M, Smit JH, Snieder H, Soranzo N, Spector TD, Stenvinkel P, Sternberg MJ, Swaminathan R, Tanaka T, Ubink-Veltmaat LJ, Uda M, Vollenweider P, Wallace C, Waterworth D, Zerres K, Waeber G, Wareham NJ, Maxwell PH, McCarthy MI, Jarvelin MR, Mooser V, Abecasis GR, Lightstone L, Scott J, Navis G, Elliott P, Kooner JS. (2011) Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature **478**(7367):103-9.
PMID: 21909115

69. Xu H, Poh WT, Sim X, Twee-Hee Ong R, Suo C, Tay WT, Khor CC, **Seielstad** M, Liu J, Aung T, Tai ES, Wong TY, Chia KS, Teo YY. (2011) SgD-CNV, a database for common

and rare copy number variants in three Asian populations. Hum Mutat. **32**(12):1341-9 PMID:21882294

70. Dorajoo R, Blakemore AI, Sim X, Ong RT, Ng DP, **Seielstad** M, Wong TY, Saw SM, Froguel P, Liu J, Tai ES. (2011) Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. Int J Obes (Lond). **36**(1):159-63 PMID:21544081

71. Chambers JC, Zhang W, Sehmi J, Li X, Wass MN, Van der Harst P, Holm H, Sanna S, Kavousi M, Baumeister SE, Coin LJ, Deng G, Gieger C, Heard-Costa NL, Hottenga JJ, Kühnel B, Kumar V, Lagou V, Liang L, Luan J, Vidal PM, Mateo Leach I, O'Reilly PF, Peden JF, Rahmioglu N, Soininen P, Speliotes EK, Yuan X, Thorleifsson G, Alizadeh BZ, Atwood LD, Borecki IB, Brown MJ, Charoen P, Cucca F, Das D, de Geus EJ, Dixon AL, Döring A, Ehret G, Eyjolfsson GI, Farrall M, Forouhi NG, Friedrich N, Goessling W, Gudbjartsson DF, Harris TB, Hartikainen AL, Heath S, Hirschfield GM, Hofman A, Homuth G, Hyppönen E, Janssen HL, Johnson T, Kangas AJ, Kema IP, Kühn JP, Lai S, Lathrop M, Lerch MM, Li Y, Liang TJ, Lin JP, Loos RJ, Martin NG, Moffatt MF, Montgomery GW, Munroe PB, Musunuru K, Nakamura Y, O'Donnell CJ, Olafsson I, Penninx BW, Pouta A, Prins BP, Prokopenko I, Puls R, Ruokonen A, Savolainen MJ, Schlessinger D, Schouten JN, Seedorf U, Sen-Chowdhry S, Siminovitch KA, Smit JH, Spector TD, Tan W, Teslovich TM, Tukiainen T, Uitterlinden AG, Van der Klauw MM, Vasan RS, Wallace C, Wallaschofski H, Wichmann HE, Willemsen G, Würtz P, Xu C, Yerges-Armstrong LM; Alcohol Genome-wide Association (AlcGen) Consortium; Diabetes Genetics Replication and Meta-analyses (DIAGRAM+) Study; Genetic Investigation of Anthropometric Traits (GIANT) Consortium; Global Lipids Genetics Consortium; Genetics of Liver Disease (GOLD) Consortium; International Consortium for Blood Pressure (ICBP-GWAS); Meta-analyses of Glucose and Insulin-Related Traits Consortium (MAGIC), Abecasis GR, Ahmadi KR, Boomsma DI, Caulfield M, Cookson WO, van Duijn CM, Froguel P, Matsuda K, McCarthy MI, Meisinger C, Mooser V, Pietiläinen KH, Schumann G, Snieder H, Sternberg MJ, Stolk RP, Thomas HC, Thorsteinsdottir U, Uda M, Waeber G, Wareham NJ, Waterworth DM, Watkins H, Whitfield JB, Witteman JC, Wolffenbuttel BH, Fox CS, Ala-Korpela M, Stefansson K, Vollenweider P, Völzke H, Schadt EE, Scott J, Järvelin MR, Elliott P, Kooner JS. (2011) Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nat Genet. **43**(11):1131-8. PMID: 22001757

72. Kooner JS, Saleheen D, Sim X, Sehmi J, Zhang W, Frossard P, Been LF, Chia KS, Dimas AS, Hassanali N, Jafar T, Jowett JB, Li X, Radha V, Rees SD, Takeuchi F, Young R, Aung T, Basit A, Chidambaram M, Das D, Grunberg E, Hedman AK, Hydrie ZI, Islam M, Khor CC, Kowlessur S, Kristensen MM, Liju S, Lim WY, Matthews DR, Liu J, Morris AP, Nica AC, Pinidiyapathirage JM, Prokopenko I, Rasheed A, Samuel M, Shah N, Shera AS, Small KS, Suo C, Wickremasinghe AR, Wong TY, Yang M, Zhang F; DIAGRAM; MuTHER, Abecasis GR, Barnett AH, Caulfield M, Deloukas P, Frayling TM, Froguel P, Kato N, Katulanda P, Kelly MA, Liang J, Mohan V, Sanghera DK, Scott J, **Seielstad** M, Zimmet PZ, Elliott P, Teo YY, McCarthy MI, Danesh J, Tai ES, Chambers JC. (2011) Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nat Genet. **43**(10):984-9 PMID:21874001

73. Sivakumaran TA, Igo RP, Kidd JM, Itsara A, Kopplin LJ, Chen W, Hagstrom SA, Peachey NS, Francis PJ, Klein ML, Chew EY, Ramprasad VL, Tay WT, Mitchell P, **Seielstad** M, Stambolian DE, Edwards AO, Lee KE, Leontiev DV, Jun G, Wang Y, Tian L, Qiu F,

Henning AK, LaFramboise T, Sen P, Aarthi M, George R, Raman R, Das MK, Vijaya L, Kumaramanickavel G, Wong TY, Swaroop A, Abecasis GR, Klein R, Klein BE, Nickerson DA, Eichler EE, Iyengar SK. (2011) A 32 kb critical region excluding Y402H in CFH mediates risk for age-related macular degeneration. PLoS One. **6**(10):e25598.

74. Fan Q, Zhou X, Khor CC, Cheng CY, Goh LK, Sim X, Tay WT, Li YJ, Ong RT, Suo C, Cornes B, Ikram MK, Chia KS, **Seielstad** M, Liu J, Vithana E, Young TL, Tai ES, Wong TY, Aung T, Teo YY, Saw SM. (2011) Genome-Wide Meta-Analysis of Five Asian Cohorts Identifies PDGFRA as a Susceptibility Locus for Corneal Astigmatism. PLoS Genet. **7**(12):e1002402.

75. Yang X, Xu S; HUGO Pan-Asian SNP Consortium; Indian Genome Variation Consortium. (2011) Identification of close relatives in the HUGO Pan-Asian SNP database. PLoS One.**6**(12):e29502.
PMID: 22242128

76. Cho YS, Chen CH, Hu C, Long J, Hee Ong RT, Sim X, Takeuchi F, Wu Y, Go MJ, Yamauchi T, Chang YC, Kwak SH, Ma RC, Yamamoto K, Adair LS, Aung T, Cai Q, Chang LC, Chen YT, Gao Y, Hu FB, Kim HL, Kim S, Kim YJ, Lee JJ, Lee NR, Li Y, Liu JJ, Lu W, Nakamura J, Nakashima E, Ng DP, Tay WT, Tsai FJ, Wong TY, Yokota M, Zheng W, Zhang R, Wang C, So WY, Ohnaka K, Ikegami H, Hara K, Cho YM, Cho NH, Chang TJ, Bao Y, Hedman AK, Morris AP, McCarthy MI, DIAGRAM Consortium; MuTHER Consortium, Takayanagi R, Park KS, Jia W, Chuang LM, Chan JC, Maeda S, Kadowaki T, Lee JY, Wu JY, Teo YY, Tai ES, Shu XO, Mohlke KL, Kato N, Han BG, **Seielstad** M. (2011) Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nat Genet. **44**(1):67-72.

77. Png E, Alisjahbana B, Sahiratmadja E, Marzuki S, Nelwan R, Balabanova Y, Nikolayevskyy V, Drobniewski F, Nejentsev S, Adnan I, van de Vosse E, Hibberd ML, van Crevel R, Ottenhoff TH, **Seielstad** M. (2012) A genome wide association study of pulmonary tuberculosis susceptibility in Indonesians. BMC Med Genet. **13**:5.

78. Png E, Alisjahbana B, Sahiratmadja E, Marzuki S, Nelwan R, Adnan I, van de Vosse E, Hibberd M, van Crevel R, Ottenhoff TH, **Seielstad** M. Polymorphisms in SP110 are not associated with pulmonary tuberculosis in Indonesians. Infect Genet Evol. 2012 Aug; 12(6):1319-23.

79. Fan Q, Barathi VA, Cheng CY, Zhou X, Meguro A, Nakata I, Khor CC, Goh LK, Li YJ, Lim W, Ho CE, Hawthorne F, Zheng Y, Chua D, Inoko H, Yamashiro K, Ohno-Matsui K, Matsuo K, Matsuda F, Vithana E, **Seielstad** M, Mizuki N, Beuerman RW, Tai ES, Yoshimura N, Aung T, Young TL, Wong TY, Teo YY, Saw SM. Genetic variants on chromosome 1q41 influence ocular axial length and high myopia. PLoS Genet. 2012 Jun; 8(6):e1002753.

80. Cornes BK, Khor CC, Nongpiur ME, Xu L, Tay WT, Zheng Y, Lavanya R, Li Y, Wu R, Sim X, Wang YX, Chen P, Teo YY, Chia KS, **Seielstad** M, Liu J, Hibberd ML, Cheng CY, Saw SM, Tai ES, Jonas JB, Vithana EN, Wong TY, Aung T. (2012) Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Hum Mol Genet. **21**(2):437-45.

81. 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. Meta-

analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. Nat Genet. 2012 Aug; 44(8):904-9.

82. Wen W, Cho YS, Zheng W, Dorajoo R, Kato N, Qi L, Chen CH, Delahanty RJ, Okada Y, Tabara Y, Gu D, Zhu D, Haiman CA, Mo Z, Gao YT, Saw SM, Go MJ, Takeuchi F, Chang LC, Kokubo Y, Liang J, Hao M, Le Marchand L, Zhang Y, Hu Y, Wong TY, Long J, Han BG, Kubo M, Yamamoto K, Su MH, Miki T, Henderson BE, Song H, Tan A, He J, Ng DP, Cai Q, Tsunoda T, Tsai FJ, Iwai N, Chen GK, Shi J, Xu J, Sim X, Xiang YB, Maeda S, Ong RT, Li C, Nakamura Y, Aung T, Kamatani N, Liu JJ, Lu W, Yokota M, **Seielstad** M, Fann CS; The Genetic Investigation of ANthropometric Traits (GIANT) Consortium, Wu JY, Lee JY, Hu FB, Tanaka T, Tai ES, Shu XO. (2012) Meta-analysis identifies common variants associated with body mass index in east Asians. Nat Genet.;**44**(3):307-311. PMID: 22344219

83. Ottenhoff TH, Dass RH, Yang N, Zhang MM, Wong HE, Sahiratmadja E, Khor CC, Alisjahbana B, van Crevel R, Marzuki S, **Seielstad** M, van de Vosse E, Hibberd ML. Genome-wide expression profiling identifies type 1 interferon response pathways in active tuberculosis. PLoS One. 2012; 7(9):e45839.

84. Xu S, Pugach I, Stoneking M, Kayser M, Jin L; HUGO Pan-Asian SNP Consortium. Indonesia corresponds to the Austronesian expansion. Proc Natl Acad Sci U S A.;**109**(12):4574-9.

85. Dastani Z, Hivert MF, Timpson N, Perry JR, Yuan X, Scott RA, Henneman P, Heid IM, Kizer JR, Lyytikäinen LP, Fuchsberger C, Tanaka T, Morris AP, Small K, Isaacs A, Beekman M, Coassin S, Lohman K, Qi L, Kanoni S, Pankow JS, Uh HW, Wu Y, Bidulescu A, Rasmussen-Torvik LJ, Greenwood CM, Ladouceur M, Grimsby J, Manning AK, Liu CT, Kooner J, Mooser VE, Vollenweider P, Kapur KA, Chambers J, Wareham NJ, Langenberg C, Frants R, Willems-Vandijk K, Oostra BA, Willems SM, Lamina C, Winkler TW, Psaty BM, Tracy RP, Brody J, Chen I, Viikari J, Kähönen M, Pramstaller PP, Evans DM, St Pourcain B, Sattar N, Wood AR, Bandinelli S, Carlson OD, Egan JM, Böhringer S, van Heemst D, Kedenko L, Kristiansson K, Nuotio ML, Loo BM, Harris T, Garcia M, Kanaya A, Haun M, Klopp N, Wichmann HE, Deloukas P, Katsareli E, Couper DJ, Duncan BB, Kloppenburg M, Adair LS, Borja JB; DIAGRAM+ Consortium; MAGIC Consortium; GLGC Investigators; MuTHER Consortium, Wilson JG, Musani S, Guo X, Johnson T, Semple R, Teslovich TM, Allison MA, Redline S, Buxbaum SG, Mohlke KL, Meulenbelt I, Ballantyne CM, Dedoussis GV, Hu FB, Liu Y, Paulweber B, Spector TD, Slagboom PE, Ferrucci L, Jula A, Perola M, Raitakari O, Florez JC, Salomaa V, Eriksson JG, Frayling TM, Hicks AA, Lehtimäki T, Smith GD, Siscovick DS, Kronenberg F, van Duijn C, Loos RJ, Waterworth DM, Meigs JB, Dupuis J, Richards JB, Voight BF, Scott LJ, Steinthorsdottir V, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Hofmann OM, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B,

Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Morris AD, Palmer CN, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Pedersen O, Barroso I, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, Boehnke M, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Elliott P, Rybin D, Dehghan A, Hottenga JJ, Song K, Goel A, Lajunen T, Doney A, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hillman DR, Hingorani AD, Hui J, Hung J, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S, Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Orrù M, Pakyz R, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sigurðsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global B Pgen Consortium, Borecki IB, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Serrano-Ríos M, Lind L, Palmer LJ, Hu FB 1st, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A; Procardis Consortium, Buchanan TA, Valle TT, Rotter JI, Penninx BW, Boomsma DI, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Peltonen L, Mooser V, Sladek R; MAGIC investigators; GLGC Consortium, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Chasman DI, Johansen CT, Fouchier SW, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Feitosa MF, Orho-Melander M, Melander O, Li X, Li M, Cho YS, Go MJ, Kim YJ, Lee JY, Park T, Kim K, Sim X, Ong RT, Croteau-Chonka DC, Lange LA, Smith JD, Ziegler A, Zhang W, Zee RY, Whitfield JB, Thompson JR, Surakka I, Spector TD, Smit JH, Sinisalo J, Scott J, Saharinen J, Sabatti C, Rose LM, Roberts R, Rieder M, Parker AN, Pare G, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, McArdle W, Masson D, Martin NG, Marroni F, Lucas G, Luben R, Lokki ML, Lettre G, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, König IR, Khaw KT, Kaplan LM, Johansson Å, Janssens AC, Igl W, Hovingh GK, Hengstenberg C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Groop LC, Gonzalez E, Freimer NB, Erdmann J, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Faire U, Crawford G, Chen YD, Caulfield MJ, Boekholdt SM, Assimes TL, Quertermous T, **Seielstad** M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Taylor HA Jr, Gabriel SB, Holm H, Gudnason V, Krauss RM, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Strachan DP, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, Kathiresan S. Novel loci for adiponectin levels and their

influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. PLoS Genet.;**8**(3):e1002607.

86. Kelly MA, Rees SD, Hydrie MZ, Shera AS, Bellary S, O'Hare JP, Kumar S, Taheri S, Basit A, Barnett AH; DIAGRAM Consortium; SAT2D Consortium. Circadian gene variants and susceptibility to type 2 diabetes: a pilot study. PLoS One.;**7**(4):e32670.

87. Xi B, Takeuchi F, Chandak GR, Kato N, Pan HW; AGEN-T2D Consortium, Zhou DH, Pan HY, Mi J. Common polymorphism near the MC4R gene is associated with type 2 diabetes: data from a meta-analysis of 123,373 individuals. Diabetologia;**55**(10):2660-6.

88. Lu Y, Chen H, Nikamo P, Qi Low H, Helms C, **Seielstad** M, Liu J, Bowcock AM, Stahle M, Liao W. Association of Cardiovascular and Metabolic Disease Genes with Psoriasis. J Invest Dermatoldoi: 10.1038/jid.2012.366.

89. Li H, Gan W, Lu L, Dong X, Han X, Hu C, Yang Z, Sun L, Bao W, Li P, He M, Sun L, Wang Y, Zhu J, Ning Q, Tang Y, Zhang R, Wen J, Wang D, Zhu X, Guo K, Zuo X, Guo X, Yang H, Zhou X; DIAGRAM Consortium; AGEN-T2D Consortium, Zhang X, Qi L, Loos RJ, Hu FB, Wu T, Liu Y, Liu L, Yang Z, Hu R, Jia W, Ji L, Li Y, Lin X. A genome-wide association study identifies GRK5 and RASGRP1 as type 2 diabetes loci in Chinese Hans. Diabetes. 2013 62(1):291-8. doi: 10.2337/db12-0454. PubMed Central PMCID: PMC3526061.

90. Saxena R, Saleheen D, Been LF, Garavito ML, Braun T, Bjonnes A, Young R, Ho WK, Rasheed A, Frossard P, Sim X, Hassanali N, Radha V, Chidambaram M, Liju S, Rees SD, Ng DP, Wong TY, Yamauchi T, Hara K, Tanaka Y, Hirose H, McCarthy MI, Morris AP; DIAGRAM; MuTHER; AGEN, Basit A, Barnett AH, Katulanda P, Matthews D, Mohan V, Wander GS, Singh JR, Mehra NK, Ralhan S, Kamboh MI, Mulvihill JJ, Maegawa H, Tobe K, Maeda S, Cho YS, Tai ES, Kelly MA, Chambers JC, Kooner JS, Kadowaki T, Deloukas P, Rader DJ, Danesh J, Sanghera DK. Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. Diabetes. 2013; 62(5):1746-55. doi: 10.2337/db12-1077. PubMed Central PMCID: PMC3636649.

91. Franceschini N, Fox E, Zhang Z, Edwards TL, Nalls MA, Sung YJ, Tayo BO, Sun YV, Gottesman O, Adeyemo A, Johnson AD, Young JH, Rice K, Duan Q, Chen F, Li Y, Tang H, Fornage M, Keene KL, Andrews JS, Smith JA, Faul JD, Guangfa Z, Guo W, Liu Y, Murray SS, Musani SK, Srinivasan S, Velez Edwards DR, Wang H, Becker LC, Bovet P, Bochud M, Broeckel U, Burnier M, Carty C, Chasman DI, Ehret G, Chen WM, Chen G, Chen W, Ding J, Dreisbach AW, Evans MK, Guo X, Garcia ME, Jensen R, Keller MF, Lettre G, Lotay V, Martin LW, Moore JH, Morrison AC, Mosley TH, Ogunniyi A, Palmas W, Papanicolaou G, Penman A, Polak JF, Ridker PM, Salako B, Singleton AB, Shriner D, Taylor KD, Vasan R, Wiggins K, Williams SM, Yanek LR, Zhao W, Zonderman AB, Becker DM, Berenson G, Boerwinkle E, Bottinger E, Cushman M, Eaton C, Nyberg F, Heiss G, Hirschhron JN, Howard VJ, Karczewsk KJ, Lanktree MB, Liu K, Liu Y, Loos R, Margolis K, Snyder M; Asian Genetic Epidemiology Network Consortium, Psaty BM, Schork NJ, Weir DR, Rotimi CN, Sale MM, Harris T, Kardia SL, Hunt SC, Arnett D, Redline S, Cooper RS, Risch NJ, Rao DC, Rotter JI, Chakravarti A, Reiner AP, Levy D, Keating BJ, Zhu X. Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. Am J Hum Genet. 2013;93(3):545-54. doi: 10.1016/j.ajhg.2013.07.010. PubMed Central PMCID: PMC3769920.

92. Jensen RA, Sim X, Li X, Cotch MF, Ikram MK, Holliday EG, Eiriksdottir G, Harris TB, Jonasson F, Klein BE, Launer LJ, Smith AV, Boerwinkle E, Cheung N, Hewitt AW, Liew G, Mitchell P, Wang JJ, Attia J, Scott R, Glazer NL, Lumley T, McKnight B, Psaty BM, Taylor K, Hofman A, de Jong PT, Rivadeneira F, Uitterlinden AG, Tay WT, Teo YY, **Seielstad** M, Liu J, Cheng CY, Saw SM, Aung T, Ganesh SK, O'Donnell CJ, Nalls MA, Wiggins KL, Kuo JZ; Blue Mountains Eye Study GWAS Team; CKDGen Consortium, van Duijn CM, Gudnason V, Klein R, Siscovick DS, Rotter JI, Tai ES, Vingerling J, Wong TY. Genome-wide association study of retinopathy in individuals without diabetes. PLoS One. 2013;8(2):e54232. doi: 10.1371/journal.pone.0054232. PubMed Central PMCID: PMC3564946.

93. Deng X, Sabino EC, Cunha-Neto E, Ribeiro AL, Ianni B, Mady C, Busch MP, **Seielstad** M; REDSII Chagas Study Group from the NHLBI Retrovirus Epidemiology Donor Study-II Component International. Genome wide association study (GWAS) of Chagas cardiomyopathy in Trypanosoma cruzi seropositive subjects. PLoS One. 2013;8(11):e79629. doi: 10.1371/journal.pone.0079629.; PubMed Central PMCID: PMC3854669.

94. SIGMA Type 2 Diabetes Consortium, Williams AL, Jacobs SB, Moreno-Macías H, Huerta-Chagoya A, Churchhouse C, Márquez-Luna C, García-Ortíz H, Gómez-Vázquez MJ, Burtt NP, Aguilar-Salinas CA, González-Villalpando C, Florez JC, Orozco L, Haiman CA, Tusié-Luna T, Altshuler D. Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. Nature. 2014;506(7486):97-101. doi: 10.1038/nature12828.

95. Chen Z, Pereira MA, **Seielstad** M, Koh WP, Tai ES, Teo YY, Liu J, Hsu C, Wang R, Odegaard AO, Thyagarajan B, Koratkar R, Yuan JM, Gross MD, Stram DO. Joint effects of known type 2 diabetes susceptibility loci in genome-wide association study of Singapore Chinese: the Singapore Chinese health study. PLoS One. 2014;9(2):e87762. doi: 10.1371/journal.pone.0087762.; PubMed Central PMCID: PMC3919750.

96. Wen W, Zheng W, Okada Y, Takeuchi F, Tabara Y, Hwang JY, Dorajoo R, Li H, Tsai FJ, Yang X, He J, Wu Y, He M, Zhang Y, Liang J, Guo X, Sheu WH, Delahanty R, Guo X, Kubo M, Yamamoto K, Ohkubo T, Go MJ, Liu JJ, Gan W, Chen CC, Gao Y, Li S, Lee NR, Wu C, Zhou X, Song H, Yao J, Lee IT, Long J, Tsunoda T, Akiyama K, Takashima N, Cho YS, Ong RT, Lu L, Chen CH, Tan A, Rice TK, Adair LS, Gui L, Allison M, Lee WJ, Cai Q, Isomura M, Umemura S, Kim YJ, **Seielstad** M, Hixson J, Xiang YB, Isono M, Kim BJ, Sim X, Lu W, Nabika T, Lee J, Lim WY, Gao YT, Takayanagi R, Kang DH, Wong TY, Hsiung CA, Wu IC, Juang JM, Shi J, Choi BY, Aung T, Hu F, Kim MK, Lim WY, Wang TD, Shin MH, Lee J, Ji BT, Lee YH, Young TL, Shin DH, Chun BY, Cho MC, Han BG, Hwu CM, Assimes TL, Absher D, Yan X, Kim E, Kuo JZ, Kwon S, Taylor KD, Chen YD, Rotter JI, Qi L, Zhu D, Wu T, Mohlke KL, Gu D, Mo Z, Wu JY, Lin X, Miki T, Tai ES, Lee JY, Kato N, Shu XO, Tanaka T. Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Hum Mol Genet. 2014 May 26. pii: ddu248. [Epub ahead of print] PubMed PMID: 24861553.

97. DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium; Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium; South Asian Type 2 Diabetes (SAT2D) Consortium; Mexican American Type 2 Diabetes (MAT2D) Consortium; Type 2 Diabetes Genetic Exploration by Nex-generation sequencing in muylti-Ethnic Samples (T2D-GENES) Consortium, Mahajan A, Go MJ, Zhang W, Below JE, Gaulton KJ, Ferreira T, Horikoshi M, Johnson AD, Ng MC, Prokopenko I, Saleheen D, Wang X, Zeggini E, Abecasis GR, Adair LS, Almgren P, Atalay M, Aung T, Baldassarre D, Balkau B, Bao Y, Barnett AH, Barroso I, Basit A, Been LF, Beilby J, Bell GI, Benediktsson R, Bergman RN,

Boehm BO, Boerwinkle E, Bonnycastle LL, Burtt N, Cai Q, Campbell H, Carey J, Cauchi S, Caulfield M, Chan JC, Chang LC, Chang TJ, Chang YC, Charpentier G, Chen CH, Chen H, Chen YT, Chia KS, Chidambaram M, Chines PS, Cho NH, Cho YM, Chuang LM, Collins FS, Cornelis MC, Couper DJ, Crenshaw AT, van Dam RM, Danesh J, Das D, de Faire U, Dedoussis G, Deloukas P, Dimas AS, Dina C, Doney AS, Donnelly PJ, Dorkhan M, van Duijn C, Dupuis J, Edkins S, Elliott P, Emilsson V, Erbel R, Eriksson JG, Escobedo J, Esko T, Eury E, Florez JC, Fontanillas P, Forouhi NG, Forsen T, Fox C, Fraser RM, Frayling TM, Froguel P, Frossard P, Gao Y, Gertow K, Gieger C, Gigante B, Grallert H, Grant GB, Grrop LC, Groves CJ, Grundberg E, Guiducci C, Hamsten A, Han BG, Hara K, Hassanali N, Hattersley AT, Hayward C, Hedman AK, Herder C, Hofman A, Holmen OL, Hovingh K, Hreidarsson AB, Hu C, Hu FB, Hui J, Humphries SE, Hunt SE, Hunter DJ, Hveem K, Hydrie ZI, Ikegami H, Illig T, Ingelsson E, Islam M, Isomaa B, Jackson AU, Jafar T, James A, Jia W, Jöckel KH, Jonsson A, Jowett JB, Kadowaki T, Kang HM, Kanoni S, Kao WH, Kathiresan S, Kato N, Katulanda P, Keinanen-Kiukaanniemi KM, Kelly AM, Khan H, Khaw KT, Khor CC, Kim HL, Kim S, Kim YJ, Kinnunen L, Klopp N, Kong A, Korpi-Hyövälti E, Kowlessur S, Kraft P, Kravic J, Kristensen MM, Krithika S, Kumar A, Kumate J, Kuusisto J, Kwak SH, Laakso M, Lagou V, Lakka TA, Langenberg C, Langford C, Lawrence R, Leander K, Lee JM, Lee NR, Li M, Li X, Li Y, Liang J, Liju S, Lim WY, Lind L, Lindgren CM, Lindholm E, Liu CT, Liu JJ, Lobbens S, Long J, Loos RJ, Lu W, Luan J, Lyssenko V, Ma RC, Maeda S, Mägi R, Männisto S, Matthews DR, Meigs JB, Melander O, Metspalu A, Meyer J, Mirza G, Mihailov E, Moebus S, Mohan V, Mohlke KL, Morris AD, Mühleisen TW, Müller-Nurasyid M, Musk B, Nakamura J, Nakashima E, Navarro P, Ng PK, Nica AC, Nilsson PM, Njølstad I, Nöthen MM, Ohnaka K, Ong TH, Owen KR, Palmer CN, Pankow JS, Park KS, Parkin M, Pechlivanis S, Pedersen NL, Peltonen L, Perry JR, Peters A, Pinidiyapathirage JM, Platou CG, Potter S, Price JF, Qi L, Radha V, Rallidis L, Rasheed A, Rathman W, Rauramaa R, Raychaudhuri S, Rayner NW, Rees SD, Rehnberg E, Ripatti S, Robertson N, Roden M, Rossin EJ, Rudan I, Rybin D, Saaristo TE, Salomaa V, Saltevo J, Samuel M, Sanghera DK, Saramies J, Scott J, Scott LJ, Scott RA, Segrè AV, Sehmi J, Sennblad B, Shah N, Shah S, Shera AS, Shu XO, Shuldiner AR, Sigurđsson G, Sijbrands E, Silveira A, Sim X, Sivapalaratnam S, Small KS, So WY, Stančáková A, Stefansson K, Steinbach G, Steinthorsdottir V, Stirrups K, Strawbridge RJ, Stringham HM, Sun Q, Suo C, Syvänen AC, Takayanagi R, Takeuchi F, Tay WT, Teslovich TM, Thorand B, Thorleifsson G, Thorsteinsdottir U, Tikkanen E, Trakalo J, Tremoli E, Trip MD, Tsai FJ, Tuomi T, Tuomilehto J, Uitterlinden AG, Valladares-Salgado A, Vedantam S, Veglia F, Voight BF, Wang C, Wareham NJ, Wennauer R, Wickremasinghe AR, Wilsgaard T, Wilson JF, Wiltshire S, Winckler W, Wong TY, Wood AR, Wu JY, Wu Y, Yamamoto K, Yamauchi T, Yang M, Yengo L, Yokota M, Young R, Zabaneh D, Zhang F, Zhang R, Zheng W, Zimmet PZ, Altshuler D, Bowden DW, Cho YS, Cox NJ, Cruz M, Hanis CL, Kooner J, Lee JY, **Seielstad** M, Teo YY, Boehnke M, Parra EJ, Chambers JC, Tai ES, McCarthy MI, Morris AP. Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nat Genet. 2014;46(3):234-44. doi: 10.1038/ng.2897.; PubMed Central PMCID: PMC3969612.

98. Long D, Fix OK, Deng X, **Seielstad** M, Lauring AS. The Acute Liver Failure Study Group. Whole genome sequencing to identify host genetic risk factors for severe outcomes of hepatitis a virus infection. J Med Virol. 2014 Jun 30. doi: 10.1002/jmv.24007. PubMed PMID: 24978929.

99. Majithia AR, Flannick J, Shahinian P, Guo M, Bray MA, Fontanillas P, Gabriel SB; GoT2D Consortium; NHGRI JHS/FHS Allelic Spectrum Project; SIGMA T2D Consortium; T2D-GENES Consortium, Rosen ED, Altshuler D; GoT2D Consortium. Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of

type 2 diabetes. Proc Natl Acad Sci U S A. 2014 Aug 25. pii: 201410428. [Epub ahead of print]

100. Joo-Yeon Hwang, Xueling Sim, Ying Wu, Jun Liang, Yasuharu Tabara, Cheng Hu, Kazuo Hara, Claudia H.T. Tam, Qiuyin Cai, Qi Zhao, Sunha Jee, Fumihiko Takeuchi, Min Jin Go, Rick Twee Hee Ong, Takayoshi Ohkubo, Young Jin Kim, Rong Zhang, Toshimasa Yamauchi, Wing Yee So, Jirong Long, Dongfeng Gu, Nanette R. Lee, Soriul Kim, Katsuya Tomohiro, JiHee Oh, JianJun Liu, Satoshi Umemura, Yeon-Jung Kim, Feng Jiang, Shiro Maeda, Juliana C.N. Chan, Wei Lu, James E. Hixson, Linda S. Adair, KeumJi Jung, Toru Nabika, Jae-Bum Bae, MiHee Lee, Mark **Seielstad**, Terri L Young, Yik Ying Teo, Yoshikuni Kita, Naoyuki Takashima, Haruhiko Osawa, So-Hyun Lee, Min-Ho Shin, Dong Hoon Shin, Bo Youl Choi, Jiajun Shi, Yu-Tang Gao, Yong-Bing Xiang, Wei Zheng, Norihiro Kato, Miwuk Yoon, Jiang He, Xiao Ou Shu, Ronald C.W. Ma, Takashi Kadowaki, Weiping Jia, Tetsuro Miki, Lu Qi, E Shyong Tai, Karen L. Mohlke, Bok-Ghee Han, Yoon Shin Cho, and Bong-Jo Kim. Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. Diabetes published ahead of print September 3, 2014, doi:10.2337/db14-0563

101. Yin X, Low H, Wang L, Li Y, Ellinghaus E, Han J, Estivill X, Sun L, Zuo X, Shen C, Zhu C, Zhang A, Sanchez F, Padyukov L, Catanese JJ, Krueger GG, Callis-Duffin KP, Mucha S, Weichenthal M, Weidinger S, Lieb W, Foo JN, Li Y, Sim K, Liany H, Irwan I, Teo YY, Theng CTS, Gupta R, Bowcock A, De Jager PL, Qureshi AA, de Bakker PIW, **Seielstad M****, Liao W, Ståhle M, Franke A, Zhang X, and Jianjun Liu JJ. (2015) Trans-ethnic genome-wide meta-analysis identifies multiple novel associations and reveals ethnic heterogeneity of psoriasis susceptibility. Nat Commun. **6** :6916. doi: 10.1038/ncomms7916.
****corresponding author**

102. He M, Xu M, Zhang B, Liang J, Chen P, Lee JY, Johnson TA, Li H, Yang X, Dai J, Liang L, Gui L, Qi Q, Huang J, Li Y, Adair LS, Aung T, Cai Q, Cheng CY, Cho MC, Cho YS, Chu M, Cui B, Gao YT, Go MJ, Gu D, Gu W, Guo H, Hao Y, Hong J, Hu Z, Hu Y, Huang J, Hwang JY, Ikram MK, Jin G, Kang DH, Khor CC, Kim BJ, Kim HT, Kubo M, Lee J, Lee J, Lee NR, Li R, Li J, Liu J, Longe J, Lu W, Lu X, Miao X, Okada Y, Ong RT, Qiu G, **Seielstad** M, Sim X, Song H, Takeuchi F, Tanaka T, Taylor PR, Wang L, Wang W, Wang Y, Wu C, Wu Y, Xiang YB, Yamamoto K, Yang H, Liao M, Yokota M, Young T, Zhang X, Kato N, Wang QK, Zheng W, Hu FB, Lin D, Shen H, Teo YY, Mo Z, Wong TY, Lin X, Mohlke KL, Ning G, Tsunoda T, Han BG, Shu XO, Tai ES, Wu T, Qi L. (2014) Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Hum Mol Genet. **24**(6):1791-800. doi: 10.1093/hmg/ddu583. Epub 2014 Nov 26.

103. Nititham J, Taylor KE, Gupta R, Chen H, Ahn R, Liu J, **Seielstad** M, Ma A, Bowcock AM, Criswell LA, Stahle M, Liao W. (2014) Meta-analysis of the TNFAIP3 region in psoriasis reveals a risk haplotype that is distinct from other autoimmune diseases. Genes Immun. **16**(2):120-6. doi: 10.1038/gene.

104. Goyette P, Boucher G, Mallon D, Ellinghaus E, Jostins L, Huang H, Ripke S, Gusareva ES, Annese V, Hauser SL, Oksenberg JR, Thomsen I, Leslie S; International Inflammatory Bowel Disease Genetics Consortium; Australia and New Zealand IBDGC; Belgium IBD Genetics Consortium; Italian Group for IBD Genetic Consortium; NIDDK Inflammatory Bowel Disease Genetics Consortium; United Kingdom IBDGC; Wellcome Trust Case Control Consortium; Quebec IBD Genetics Consortium, Daly MJ, Van Steen K, Duerr RH, Barrett JC, McGovern DP, Schumm LP, Traherne JA, Carrington MN, Kosmoliaptsis V, Karlsen TH, Franke A, Rioux JD. (2015) High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous

advantage in ulcerative colitis. Nat Genet. **47**(2):172-9. doi: 10.1038/ng.3176. Epub 2015 Jan 5.

105. Kutanan W, Srikummool M, Pittayaporn P, **Seielstad** M, Kangwanpong D, Kumar V, Prombanchachai T, Chantawannakul P. (2015) Admixed origin of the Kayah (Red Karen) in Northern Thailand revealed by biparental and paternal markers. Ann Hum Genet. **79**(2):108-21. doi: 10.1111/ahg.12100. Epub 2015 Jan 15.

106. Mahajan A, Sim X, Ng HJ, Manning A, Rivas MA, Highland HM, Locke AE, Grarup N, Im HK, Cingolani P, Flannick J, Fontanillas P, Fuchsberger C, Gaulton KJ, Teslovich TM, Rayner NW, Robertson NR, Beer NL, Rundle JK, Bork-Jensen J, Ladenvall C, Blancher C, Buck D, Buck G, Burtt NP, Gabriel S, Gjesing AP, Groves CJ, Hollensted M, Huyghe JR, Jackson AU, Jun G, Justesen JM, Mangino M, Murphy J, Neville M, Onofrio R, Small KS, Stringham HM, Syvänen AC, Trakalo J, Abecasis G, Bell GI, Blangero J, Cox NJ, Duggirala R, Hanis CL, **Seielstad** M, Wilson JG, Christensen C, Brandslund I, Rauramaa R, Surdulescu GL, Doney AS, Lannfelt L, Linneberg A, Isomaa B, Tuomi T, Jørgensen ME, Jørgensen T, Kuusisto J, Uusitupa M, Salomaa V, Spector TD, Morris AD, Palmer CN, Collins FS, Mohlke KL, Bergman RN, Ingelsson E, Lind L, Tuomilehto J, Hansen T, Watanabe RM, Prokopenko I, Dupuis J, Karpe F, Groop L, Laakso M, Pedersen O, Florez JC, Morris AP, Altshuler D, Meigs JB, Boehnke M, McCarthy MI, Lindgren CM, Gloyn AL; T2D-GENES consortium and GoT2D consortium. (2015) Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. PLoS Genet. **11**(1):e1004876. doi: 10.1371/journal.pgen.1004876. />

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

McKnight AJ, McPherson R, Metspalu A, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Olsson C, Perry JR, Reinmaa E, Salem RM, Sandholm N, Schadt EE, Scott RA, Stolk L, Vallejo EE, Westra HJ, Zondervan KT; ADIPOGen Consortium; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GEFOS Consortium; GENIE Consortium; GLGC; ICBP; International Endogene Consortium; LifeLines Cohort Study; MAGIC Investigators; MuTHER Consortium; PAGE Consortium; ReproGen Consortium, Amouyel P, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Brown MJ, Burnier M, Campbell H, Chakravarti A, Chines PS, Claudi-Boehm S, Collins FS, Crawford DC, Danesh J, de Faire U, de Geus EJ, Dörr M, Erbel R, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gieger C, Gudnason V, Haiman CA, Harris TB, Hattersley AT, Heliövaara M, Hicks AA, Hingorani AD, Hoffmann W, Hofman A, Homuth G, Humphries SE, Hyppönen E, Illig T, Jarvelin MR, Johansen B, Jousilahti P, Jula AM, Kaprio J, Kee F, Keinanen-Kiukaanniemi SM, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Musk AW, Möhlenkamp S, Morris AD, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Palmer LJ, Penninx BW, Peters A, Pramstaller PP, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Shuldiner AR, Staessen JA, Steinthorsdottir V, Stolk RP, Strauch K, Tönjes A, Tremblay A, Tremoli E, Vohl MC, Völker U, Vollenweider P, Wilson JF, Witteman JC, Adair LS, Bochud M, Boehm BO, Bornstein SR, Bouchard C, Cauchi S, Caulfield MJ, Chambers JC, Chasman DI, Cooper RS, Dedoussis G, Ferrucci L, Froguel P, Grabe HJ, Hamsten A, Hui J, Hveem K, Jöckel KH, Kivimaki M, Kuh D, Laakso M, Liu Y, März W, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sinisalo J, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Veronesi G, Walker M, Wareham NJ, Watkins H, Wichmann HE, Abecasis GR, Assimes TL, Berndt SI, Boehnke M, Borecki IB, Deloukas P, Franke L, Frayling TM, Groop LC, Hunter DJ, Kaplan RC, O'Connell JR, Qi L, Schlessinger D, Strachan DP, Stefansson K, van Duijn CM, Willer CJ, Visscher PM, Yang J, Hirschhorn JN, Zillikens MC, McCarthy MI, Speliotes EK, North KE, Fox CS, Barroso I, Franks PW, Ingelsson E, Heid IM, Loos RJ, Cupples LA, Morris AP, Lindgren CM, Mohlke KL. (2015) New genetic loci link adipose and insulin biology to body fat distribution. Nature. **518**(7538):187-96. doi: 10.1038/nature14132.

108. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR, Powell C, Vedantam S, Buchkovich ML, Yang J, Croteau-Chonka DC, Esko T, Fall T, Ferreira T, Gustafsson S, Kutalik Z, Luan J, Mägi R, Randall JC, Winkler TW, Wood AR, Workalemahu T, Faul JD, Smith JA, Hua Zhao J, Zhao W, Chen J, Fehrmann R, Hedman ÅK, Karjalainen J, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bolton JL, Bragg-Gresham JL, Buyske S, Demirkan A, Deng G, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Goel A, Gong J, Jackson AU, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Mangino M, Mateo Leach I, Medina-Gomez C, Medland SE, Nalls MA, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Shungin D, Stančáková A, Strawbridge RJ, Ju Sung Y, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Isaacs A, Albrecht E, Ärnlöv J, Arscott GM, Attwood AP, Bandinelli S, Barrett A, Bas IN, Bellis C, Bennett AJ, Berne C, Blagieva R, Blüher M, Böhringer S, Bonnycastle LL, Böttcher Y, Boyd HA, Bruinenberg M, Caspersen IH, Ida Chen YD, Clarke R, Daw EW, de Craen AJ, Delgado G, Dimitriou M, Doney AS, Eklund N, Estrada K, Eury E, Folkersen L, Fraser RM, Garcia ME, Geller F, Giedraitis V, Gigante B, Go AS, Golay A,

Goodall AH, Gordon SD, Gorski M, Grabe HJ, Grallert H, Grammer TB, Gräßler J, Grönberg H, Groves CJ, Gusto G, Haessler J, Hall P, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hengstenberg C, Holmen O, Hottenga JJ, James AL, Jeff JM, Johansson Å, Jolley J, Juliusdottir T, Kinnunen L, Koenig W, Koskenvuo M, Kratzer W, Laitinen J, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Sin Lo K, Lobbens S, Lorbeer R, Lu Y, Mach F, Magnusson PK, Mahajan A, McArdle WL, McLachlan S, Menni C, Merger S, Mihailov E, Milani L, Moayyeri A, Monda KL, Morken MA, Mulas A, Müller G, Müller-Nurasyid M, Musk AW, Nagaraja R, Nöthen MM, Nolte IM, Pilz S, Rayner NW, Renstrom F, Rettig R, Ried JS, Ripke S, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Scott WR, Seufferlein T, Shi J, Vernon Smith A, Smolonska J, Stanton AV, Steinthorsdottir V, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tan ST, Tayo BO, Thorand B, Thorleifsson G, Tyrer JP, Uh HW, Vandenput L, Verhulst FC, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Warren HR, Waterworth D, Weedon MN, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q; LifeLines Cohort Study, Brennan EP, Choi M, Dastani Z, Drong AW, Eriksson P, Franco-Cereceda A, Gådin JR, Gharavi AG, Goddard ME, Handsaker RE, Huang J, Karpe F, Kathiresan S, Keildson S, Kiryluk K, Kubo M, Lee JY, Liang L, Lifton RP, Ma B, McCarroll SA, McKnight AJ, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Okada Y, Perry JR, Dorajoo R, Reinmaa E, Salem RM, Sandholm N, Scott RA, Stolk L, Takahashi A, Tanaka T, Van't Hooft FM, Vinkhuyzen AA, Westra HJ, Zheng W, Zondervan KT; ADIPOGen Consortium; AGEN-BMI Working Group; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GLGC; ICBP; MAGIC Investigators; MuTHER Consortium; MIGen Consortium; PAGE Consortium; ReproGen Consortium; GENIE Consortium; International Endogene Consortium, Heath AC, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Bovet P, Campbell H, Caulfield MJ, Cesana G, Chakravarti A, Chasman DI, Chines PS, Collins FS, Crawford DC, Cupples LA, Cusi D, Danesh J, de Faire U, den Ruijter HM, Dominiczak AF, Erbel R, Erdmann J, Eriksson JG, Farrall M, Felix SB, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gejman PV, Gieger C, Gottesman O, Gudnason V, Gyllensten U, Hall AS, Harris TB, Hattersley AT, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Homuth G, Hovingh GK, Humphries SE, Hunt SC, Hyppönen E, Illig T, Jacobs KB, Jarvelin MR, Jöckel KH, Johansen B, Jousilahti P, Jukema JW, Jula AM, Kaprio J, Kastelein JJ, Keinanen-Kiukaanniemi SM, Kiemeney LA, Knekt P, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Moll FL, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Madden PA, Pasterkamp G, Peden JF, Peters A, Postma DS, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Rioux JD, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schunkert H, Schwarz PE, Sever P, Shuldiner AR, Sinisalo J, Stolk RP, Strauch K, Tönjes A, Trégouët DA, Tremblay A, Tremoli E, Virtamo J, Vohl MC, Völker U, Waeber G, Willemsen G, Witteman JC, Zillikens MC, Adair LS, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bornstein SR, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hui J, Hunter DJ, Hveem K, Kaplan RC, Kivimaki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Metspalu A, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sattar N, Schadt EE, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Walker M, Wallaschofski H, Wareham NJ, Watkins H, Weir DR, Wichmann HE, Wilson

JF, Zanen P, Borecki IB, Deloukas P, Fox CS, Heid IM, O'Connell JR, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, Franke L, Frayling TM, McCarthy MI, Visscher PM, Scherag A, Willer CJ, Boehnke M, Mohlke KL, Lindgren CM, Beckmann JS, Barroso I, North KE, Ingelsson E, Hirschhorn JN, Loos RJ, Speliotes EK. (2015) Genetic studies of body mass index yield new insights for obesity biology. Nature. **518**(7538):197-206. doi: 10.1038/nature14177.

109. Liu JZ, van Sommeren S, Huang H, Ng SC, Alberts R, Takahashi A, Ripke S, Lee JC, Jostins L, Shah T, Abedian S, Cheon JH, Cho J, Daryani NE, Franke L, Fuyuno Y, Hart A, Juyal RC, Juyal G, Kim WH, Morris AP, Poustchi H, Newman WG, Midha V, Orchard TR, Vahedi H, Sood A, Sung JJ, Malekzadeh R, Westra HJ, Yamazaki K, Yang SK; International Multiple Sclerosis Genetics Consortium; International IBD Genetics Consortium, Barrett JC, Franke A, Alizadeh BZ, Parkes M, B K T, Daly MJ, Kubo M, Anderson CA, Weersma RK. (2015) Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nat Genet. **47**(9):979-86. doi: 10.1038/ng.3359.

110. Keating SM, Deng X, Fernandes F, Cunha-Neto E, Ribeiro AL, Adesina B, Beyer AI, Contestable P, Custer B, Busch MP, Sabino EC; NHLBI Retrovirus Epidemiology Donor Study-II (REDS-II), International Component. (2015) Inflammatory and cardiac biomarkers are differentially expressed in clinical stages of Chagas disease. Int J Cardiol. **199**:451-9. doi: 10.1016/j.ijcard.2015.07.040.

111. Cleynen I, Boucher G, Jostins L, Schumm LP, Zeissig S, Ahmad T, Andersen V, Andrews JM, Annese V, Brand S, Brant SR, Cho JH, Daly MJ, Dubinsky M, Duerr RH, Ferguson LR, Franke A, Gearry RB, Goyette P, Hakonarson H, Halfvarson J, Hov JR, Huang H, Kennedy NA, Kupcinskas L, Lawrance IC, Lee JC, Satsangi J, Schreiber S, Théâtre E, van der Meulen-de Jong AE, Weersma RK, Wilson DC; International Inflammatory Bowel Disease Genetics Consortium, Parkes M, Vermeire S, Rioux JD, Mansfield J, Silverberg MS, Radford-Smith G, McGovern DP, Barrett JC, Lees CW. (2015) Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet. **387**(10014):156-67. doi: 10.1016/S0140-6736(15)00465-1. Epub 2015 Oct 18.

112. Kim YJ, Lee J, Kim BJ; T2D-Genes Consortium, Park T. (2015) A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. BMC Genomics. **16**(1):1109. doi: 10.1186/s12864-015-2192-y.

113. Pattaro C, Teumer A, Gorski M, Chu AY, Li M, Mijatovic V, Garnaas M, Tin A, Sorice R, Li Y, Taliun D, Olden M, Foster M, Yang Q, Chen MH, Pers TH, Johnson AD, Ko YA, Fuchsberger C, Tayo B, Nalls M, Feitosa MF, Isaacs A, Dehghan A, d'Adamo P, Adeyemo A, Dieffenbach AK, Zonderman AB, Nolte IM, van der Most PJ, Wright AF, Shuldiner AR, Morrison AC, Hofman A, Smith AV, Dreisbach AW, Franke A, Uitterlinden AG, Metspalu A, Tonjes A, Lupo A, Robino A, Johansson Å, Demirkan A, Kollerits B, Freedman BI, Ponte B, Oostra BA, Paulweber B, Krämer BK, Mitchell BD, Buckley BM, Peralta CA, Hayward C, Helmer C, Rotimi CN, Shaffer CM, Müller C, Sala C, van Duijn CM, Saint-Pierre A, Ackermann D, Shriner D, Ruggiero D, Toniolo D, Lu Y, Cusi D, Czamara D, Ellinghaus D, Siscovick DS, Ruderfer D, Gieger C, Grallert H, Rochtchina E, Atkinson EJ, Holliday EG, Boerwinkle E, Salvi E, Bottinger EP, Murgia F, Rivadeneira F, Ernst F, Kronenberg F, Hu FB, Navis GJ, Curhan GC, Ehret GB, Homuth G, Coassin S, Thun GA, Pistis G, Gambaro G, Malerba G, Montgomery GW, Eiriksdottir G, Jacobs G, Li G, Wichmann HE, Campbell H, Schmidt H, Wallaschofski H, Völzke H, Brenner H, Kroemer HK, Kramer H, Lin H, Mateo Leach I, Ford I, Guessous I, Rudan I, Prokopenko I, Borecki I, Heid IM, Kolcic I, Persico I,

Jukema JW, Wilson JF, Felix JF, Divers J, Lambert JC, Stafford JM, Gaspoz JM, Smith JA, Faul JD, Wang JJ, Ding J, Hirschhorn JN, Attia J, Whitfield JB, Chalmers J, Viikari J, Coresh J, Denny JC, Karjalainen J, Fernandes JK, Endlich K, Butterbach K, Keene KL, Lohman K, Portas L, Launer LJ, Lyytikäinen LP, Yengo L, Franke L, Ferrucci L, Rose LM, Kedenko L, Rao M, Struchalin M, Kleber ME, Cavalieri M, Haun M, Cornelis MC, Ciullo M, Pirastu M, de Andrade M, McEvoy MA, Woodward M, Adam M, Cocca M, Nauck M, Imboden M, Waldenberger M, Pruijm M, Metzger M, Stumvoll M, Evans MK, Sale MM, Kähönen M, Boban M, Bochud M, Rheinberger M, Verweij N, Bouatia-Naji N, Martin NG, Hastie N, Probst-Hensch N, Soranzo N, Devuyst O, Raitakari O, Gottesman O, Franco OH, Polasek O, Gasparini P, Munroe PB, Ridker PM, Mitchell P, Muntner P, Meisinger C, Smit JH; ICBP Consortium; AGEN Consortium; CARDIOGRAM; CHARGe-Heart Failure Group; ECHOGen Consortium, Kovacs P, Wild PS, Froguel P, Rettig R, Mägi R, Biffar R, Schmidt R, Middelberg RP, Carroll RJ, Penninx BW, Scott RJ, Katz R, Sedaghat S, Wild SH, Kardia SL, Ulivi S, Hwang SJ, Enroth S, Kloiber S, Trompet S, Stengel B, Hancock SJ, Turner ST, Rosas SE, Stracke S, Harris TB, Zeller T, Zemunik T, Lehtimäki T, Illig T, Aspelund T, Nikopensius T, Esko T, Tanaka T, Gyllensten U, Völker U, Emilsson V, Vitart V, Aalto V, Gudnason V, Chouraki V, Chen WM, Igl W, März W, Koenig W, Lieb W, Loos RJ, Liu Y, Snieder H, Pramstaller PP, Parsa A, O'Connell JR, Susztak K, Hamet P, Tremblay J, de Boer IH, Böger CA, Goessling W, Chasman DI, Köttgen A, Kao WH, Fox CS. (2016) Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nat Commun. **7**:10023. doi: 10.1038/ncomms10023.

114. Horikoshi M, Pasquali L, Wiltshire S, Huyghe JR, Mahajan A, Asimit JL, Ferreira T, Locke AE, Robertson NR, Wang X, Sim X, Fujita H, Hara K, Young R, Zhang W, Choi S, Chen H, Kaur I, Takeuchi F, Fontanillas P, Thuillier D, Yengo L, Below JE, Tam CH, Wu Y, Abecasis G, Altshuler D, Bell GI, Blangero J, Burtt NP, Duggirala R, Florez JC, Hanis CL, **Seielstad** M, Atzmon G, Chan JC, Ma RC, Froguel P, Wilson JG, Bharadwaj D, Dupuis J, Meigs JB, Cho YS, Park T, Kooner JS, Chambers JC, Saleheen D, Kadowaki T, Tai ES, Mohlke KL, Cox NJ, Ferrer J, Zeggini E, Kato N, Teo YY, Boehnke M, McCarthy MI, Morris AP; T2D-GENES Consortium. (2016) Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Hum Mol Genet. 25(10):2070-2081. Epub 2016 Feb 23.

115. Khor CC, Do T, Jia H, Nakano M, George R, Abu-Amero K, Duvesh R, Chen LJ, Li Z, Nongpiur ME, Perera SA, Qiao C, Wong HT, Sakai H, Barbosa de Melo M, Lee MC, Chan AS, Azhany Y, Dao TL, Ikeda Y, Perez-Grossmann RA, Zarnowski T, Day AC, Jonas JB, Tam PO, Tran TA, Ayub H, Akhtar F, Micheal S, Chew PT, Aljasim LA, Dada T, Luu TT, Awadalla MS, Kitnarong N, Wanichwecharungruang B, Aung YY, Mohamed-Noor J, Vijayan S, Sarangapani S, Husain R, Jap A, Baskaran M, Goh D, Su DH, Wang H, Yong VK, Yip LW, Trinh TB, Makornwattana M, Nguyen TT, Leuenberger EU, Park KH, Wiyogo WA, Kumar RS, Tello C, Kurimoto Y, Thapa SS, Pathanapitoon K, Salmon JF, Sohn YH, Fea A, Ozaki M, Lai JS, Tantisevi V, Khaing CC, Mizoguchi T, Nakano S, Kim CY, Tang G, Fan S, Wu R, Meng H, Nguyen TT, Tran TD, Ueno M, Martinez JM, Ramli N, Aung YM, Reyes RD, Vernon SA, Fang SK, Xie Z, Chen XY, Foo JN, Sim KS, Wong TT, Quek DT, Venkatesh R, Kavitha S, Krishnadas SR, Soumittra N, Shantha B, Lim BA, Ogle J, de Vasconcellos JP, Costa VP, Abe RY, de Souza BB, Sng CC, Aquino MC, Kosior-Jarecka E, Fong GB, Tamanaja VC, Fujita R, Jiang Y, Waseem N, Low S, Pham HN, Al-Shahwan S, Craven ER, Khan MI, Dada R, Mohanty K, Faiq MA, Hewitt AW, Burdon KP, Gan EH, Prutthipongsit A, Patthanathamrongkasem T, Catacutan MA, Felarca IR, Liao CS, Rusmayani E, Istiantoro VW, Consolandi G, Pignata G, Lavia C, Rojanapongpun P, Mangkornkanokpong L, Chansangpetch S, Chan JC, Choy BN, Shum JW, Than HM, Oo KT, Han AT, Yong VH, Ng XY, Goh SR, Chong YF, Hibberd ML, **Seielstad** M, Png E,

Dunstan SJ, Chau NV, Bei J, Zeng YX, Karkey A, Basnyat B, Pasutto F, Paoli D, Frezzotti P, Wang JJ, Mitchell P, Fingert JH, Allingham RR, Hauser MA, Lim ST, Chew SH, Ebstein RP, Sakuntabhai A, Park KH, Ahn J, Boland G, Snippe H, Stead R, Quino R, Zaw SN, Lukasik U, Shetty R, Zahari M, Bae HW, Oo NL, Kubota T, Manassakorn A, Ho WL, Dallorto L, Hwang YH, Kiire CA, Kuroda M, Djamal ZE, Peregrino JI, Ghosh A, Jeoung JW, Hoan TS, Srisamran N, Sandragasu T, Set SH, Doan VH, Bhattacharya SS, Ho CL, Tan DT, Sihota R, Loon SC, Mori K, Kinoshita S, Hollander AI, Qamar R, Wang YX, Teo YY, Tai ES, Hartleben-Matkin C, Lozano-Giral D, Saw SM, Cheng CY, Zenteno JC, Pang CP, Bui HT, Hee O, Craig JE, Edward DP, Yonahara M, Neto JM, Guevara-Fujita ML, Xu L, Ritch R, Liza-Sharmini AT, Wong TY, Al-Obeidan S, Do NH, Sundaresan P, Tham CC, Foster PJ, Vijaya L, Tashiro K, Vithana EN, Wang N, Aung T. Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. (2016) Nat Genet. May; **48**(5):556-62. PMID: 27064256

116. Long D, Deng X, Singh P, Loeb M, Lauring AS, **Seielstad** M. (2016) Identification of genetic variants associated with susceptibility to West Nile virus neuroinvasive disease. Genes Immun. 17(5):298-304. PMID: 27170560. PMCID: PMC5215919

117. Lek M, Karczewski KJ, Minikel EV, Samocha KE, Banks E, Fennell T, O'Donnell-Luria AH, Ware JS, Hill AJ, Cummings BB, Tukiainen T, Birnbaum DP, Kosmicki JA, Duncan LE, Estrada K, Zhao F, Zou J, Pierce-Hoffman E, Berghout J, Cooper DN, Deflaux N, DePristo M, Do R, Flannick J, Fromer M, Gauthier L, Goldstein J, Gupta N, Howrigan D, Kiezun A, Kurki MI, Moonshine AL, Natarajan P, Orozco L, Peloso GM, Poplin R, Rivas MA, Ruano-Rubio V, Rose SA, Ruderfer DM, Shakir K, Stenson PD, Stevens C, Thomas BP, Tiao G, Tusie-Luna MT, Weisburd B, Won HH, Yu D, Altshuler DM, Ardissino D, Boehnke M, Danesh J, Donnelly S, Elosua R, Florez JC, Gabriel SB, Getz G, Glatt SJ, Hultman CM, Kathiresan S, Laakso M, McCarroll S, McCarthy MI, McGovern D, McPherson R, Neale BM, Palotie A, Purcell SM, Saleheen D, Scharf JM, Sklar P, Sullivan PF, Tuomilehto J, Tsuang MT, Watkins HC, Wilson JG, Daly MJ, MacArthur DG; Exome Aggregation Consortium. (2016) Analysis of protein-coding genetic variation in 60,706 humans. Nature. **536**(7616):285-91.

118. Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JR, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Fernandez Tajes J, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SC, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, Voight BF, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MC, Palmer ND, Balkau B, Stancáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VK, Park KS, Saleheen D, So WY, Tam CH, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, van der Schouw YT, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney AS, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic

J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, Hrabé de Angelis M, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CN, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JC, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RC, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJ, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, **Seielstad** M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Burtt NP, Mohlke KL, Meitinger T, Groop L, Abecasis G, Florez JC, Scott LJ, Morris AP, Kang HM, Boehnke M, Altshuler D, McCarthy MI. (2016) The genetic architecture of type 2 diabetes. Nature. **536**(7614):41-7. PMID: 27398621. PMCID: PMC5034897

119. Ferreira LR, Ferreira FM, Nakaya HI, Deng X, Cândido DD, de Oliveira LC, Billaud JN, Lanteri MC, Rigaud VO, **Seielstad** M, Kalil J, Fernandes F, Ribeiro AL, Sabino EC, Cunha-Neto E. (2016) Blood Gene Signatures of Chagas disease Cardiomyopathy with or without ventricular dysfunction. J Infect Dis. **215**(3):387-395. PMID: 28003350

120. Manning A, Highland HM, Gasser J, Sim X, Tukiainen T, Fontanillas P, Grarup N, Rivas MA, Mahajan A, Locke AE, Cingolani P, Pers TH, Viñuela A, Brown AA, Wu Y, Flannick J, Fuchsberger C, Gamazon ER, Gaulton KJ, Im HK, Teslovich TM, Blackwell TW, Bork-Jensen J, Burtt NP, Chen Y, Green T, Hartl C, Kang HM, Kumar A, Ladenvall C, Ma C, Moutsianas L, Pearson RD, Perry JR, Rayner NW, Robertson NR, Scott LJ, van de Bunt M, Eriksson JG, Jula A, Koskinen S, Lehtimäki T, Palotie A, Raitakari OT, Jacobs SB, Wessel J, Chu AY, Scott RA, Goodarzi MO, Blancher C, Buck G, Buck D, Chines PS, Gabriel S, Gjesing AP, Groves CJ, Hollensted M, Huyghe JR, Jackson AU, Jun G, Justesen JM, Mangino M, Murphy J, Neville M, Onofrio R, Small KS, Stringham HM, Trakalo J, Banks E, Carey J, Carneiro MO, DePristo M, Farjoun Y, Fennell T, Goldstein JI, Grant G, Hrabé de Angelis M, Maguire J, Neale BM, Poplin R, Purcell S, Schwarzmayr T, Shakir K, Smith JD, Strom TM, Wieland T, Lindstrom J, Brandslund I, Christensen C, Surdulescu GL, Lakka TA, Doney AS, Nilsson P, Wareham NJ, Langenberg C, Varga TV, Franks PW, Rolandsson O, Rosengren AH, Farook VS, Thameem F, Puppala S, Kumar S, Lehman DM, Jenkinson CP, Curran JE, Hale DE, Fowler SP, Arya R, DeFronzo RA, Abboud HE, Syvänen AC, Hicks PJ, Palmer ND, Ng MC, Bowden DW, Freedman BI, Esko T, Mägi R, Milani L, Mihailov E, Metspalu A, Narisu N, Kinnunen L, Bonnycastle LL, Swift A, Pasko D, Wood AR, Fadista J, Pollin TI, Barzilai N, Atzmon G, Glaser B, Thorand B, Strauch K, Peters A, Roden M, Müller-Nurasyid M, Liang L, Kriebel J, Illig T, Grallert H, Gieger C, Meisinger C, Lannfelt L, Musani SK, Griswold M, Taylor HA Jr, Wilson G Sr, Correa A, Oksa H, Scott WR, Afzal U, Tan ST, Loh M, Chambers JC, Sehmi J, Kooner JS, Lehne B, Cho YS, Lee JY, Han BG, Käräjämäki A, Qi Q, Qi L, Huang J, Hu FB, Melander O, Orho-Melander M, Below JE, Aguilar D, Wong TY, Liu J, Khor CC, Chia KS, Lim WY, Cheng CY, Chan E, Tai ES, Aung T, Linneberg A, Isomaa B, Meitinger T, Tuomi T, Hakaste L, Kravic J, Jørgensen ME, Lauritzen T, Deloukas P, Stirrups KE, Owen KR,

Farmer AJ, Frayling TM, O'Rahilly SP, Walker M, Levy JC, Hodgkiss D, Hattersley AT, Kuulasmaa T, Stančáková A, Barroso I, Bharadwaj D, Chan J, Chandak GR, Daly MJ, Donnelly PJ, Ebrahim SB, Elliott P, Fingerlin T, Froguel P, Hu C, Jia W, Ma RC, McVean G, Park T, Prabhakaran D, Sandhu M, Scott J, Sladek R, Tandon N, Teo YY, Zeggini E, Watanabe RM, Koistinen HA, Kesaniemi YA, Uusitupa M, Spector TD, Salomaa V, Rauramaa R, Palmer CN, Prokopenko I, Morris AD, Bergman RN, Collins FS, Lind L, Ingelsson E, Tuomilehto J, Karpe F, Groop L, Jørgensen T, Hansen T, Pedersen O, Kuusisto J, Abecasis G, Bell GI, Blangero J, Cox NJ, Duggirala R, **Seielstad** M, Wilson JG, Dupuis J, Ripatti S, Hanis CL, Florez JC, Mohlke KL, Meigs JB, Laakso M, Morris AP, Boehnke M, Altshuler D, McCarthy MI, Gloyn AL, Lindgren CM. (2017) A Low-Frequency Inactivating Akt2 Variant Enriched in the Finnish Population is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes. Mar 24. pii: db161329. doi: 10.2337/db16-1329.

121. Brunelli A, Kampuansai J, **Seielstad** M, Lomthaisong K, Kangwanpong D, Ghirotto S, Kutanan W. (2017) Y chromosomal evidence on the origin of northern Thai people. PLoS One. Jul 24;12(7):e0181935. doi: 10.1371/journal.pone.0181935. eCollection 2017

122. **Seielstad** M, Page GP, Gaddis N, Lanteri M, Lee TH, Kakaiya R, Barcellos LF, Criswell LA, Triulzi D, Norris PJ, and Busch MP, for the NHLBI REDSIII Study Investigators. Genome-wide association study of HLA alloimmunization in previously pregnant women Transfusion (submitted)

123. Kumar V, Ong RTH, Soo HM, Phipps ME, Teo YY, and **Seielstad** M. Deep Resequencing of Human Y Chromosome Haplogroups. Ann Hum Genet (submitted)

124. Flannick J, Fuchsberger C, Mahajan A, Teslovich TM, Agarwala V, Gaulton KJ, Caulkins L, Koesterer R, Ma C, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SCJ, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, Voight BF, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MCY, Palmer ND, Balkau B, Stancáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JMM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VKL, Park KS, Saleheen D, So WY, Tam CHT, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney ASF, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, de Angelis MH, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L,

Peters A, Huth C, O'Rahilly SP, Palmer CNA, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JC, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RCW, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJF, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, **Seielstad** M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Mohlke KL, Meitinger T, Groop L, Abecasis G, Scott LJ, Morris AP, Kang HM, Altshuler D, Burtt NP, Florez JC, Boehnke M, McCarthy MI. Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Sci Data. 2017 12 19; 4:170179. PMID: 29257133. PMCID: PMC5735917

125. Jun G, Manning A, Almeida M, Zawistowski M, Wood AR, Teslovich TM, Fuchsberger C, Feng S, Cingolani P, Gaulton KJ, Dyer T, Blackwell TW, Chen H, Chines PS, Choi S, Churchhouse C, Fontanillas P, King R, Lee S, Lincoln SE, Trubetskoy V, DePristo M, Fingerlin T, Grossman R, Grundstad J, Heath A, Kim J, Kim YJ, Laramie J, Lee J, Li H, Liu X, Livne O, Locke AE, Maller J, Mazur A, Morris AP, Pollin TI, Ragona D, Reich D, Rivas MA, Scott LJ, Sim X, Tearle RG, Teo YY, Williams AL, Zöllner S, Curran JE, Peralta J, Akolkar B, Bell GI, Burtt NP, Cox NJ, Florez JC, Hanis CL, McKeon C, Mohlke KL, **Seielstad** M, Wilson JG, Atzmon G, Below JE, Dupuis J, Nicolae DL, Lehman D, Park T, Won S, Sladek R, Altshuler D, McCarthy MI, Duggirala R, Boehnke M, Frayling TM, Abecasis GR, Blangero J. Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proc Natl Acad Sci U S A. 2018 Jan 09; 115(2):379-384. PMID: 29279374. PMCID: PMC5777025

126. Flannick J, Fuchsberger C, Mahajan A, Teslovich TM, Agarwala V, Gaulton KJ, Caulkins L, Koesterer R, Ma C, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SCJ, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, Voight BF, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MCY, Palmer ND, Balkau B, Stancáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JMM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VKL, Park KS, Saleheen D, So WY, Tam CHT, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney ASF, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH,

Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, de Angelis MH, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CNA, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JCN, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RCW, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJF, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, **Seielstad** M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Mohlke KL, Meitinger T, Groop L, Abecasis G, Scott LJ, Morris AP, Kang HM, Altshuler D, Burtt NP, Florez JC, Boehnke M, McCarthy MI. Erratum: Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Sci Data. 2018 Jan 23; 5:180002. PMID: 29360107. PMCID: PMC5779067

127. Momozawa Y, Dmitrieva J, Théâtre E, Deffontaine V, Rahmouni S, Charloteaux B, Crins F, Docampo E, Elansary M, Gori AS, Lecut C, Mariman R, Mni M, Oury C, Altukhov I, Alexeev D, Aulchenko Y, Amininejad L, Bouma G, Hoentjen F, Löwenberg M, Oldenburg B, Pierik MJ, Vander Meulen-de Jong AE, Janneke van der Woude C, Visschedijk MC; International IBD Genetics Consortium, Lathrop M, Hugot JP, Weersma RK, De Vos M, Franchimont D, Vermeire S, Kubo M, Louis E, Georges M. IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. Nat Commun. 2018 Jun 21;9(1):2427. doi: 10.1038/s41467-018-04365-8.

128. **Seielstad** M, Page GP, Gaddis N, Lanteri M, Lee TH, Kakaiya R, Barcellos LF, Criswell LA, Triulzi D, Norris PJ, Busch MP. Genomewide association study of HLA alloimmunization in previously pregnant blood donors. Transfusion. 2018 Feb; 58(2):402-412. PMID: 29168253. PMCID: PMC5803399

129. Guo Y, Busch MP, **Seielstad** M, Endres-Dighe S, Westhoff CM, Keating B, Hoppe C, Bordbar A, Custer B, Butterworth AS, Kanias T, Mast AE, Kleinman S, Lu Y, Page GP; National Heart, Lung, and Blood Institute Recipient Epidemiology Donor Evaluation Study (REDS)-III. Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion. 2019 Jan;59(1):101-111.

130. Rajan JV, Semitala FC, Mehta T, **Seielstad** M, Montalvo L, Andama A, Asege L, Nakaye M, Katende J, Mwebe S, Kamya MR, Yoon C, Cattamanchi A. A Novel, 5-Transcript, Whole-blood Gene-expression Signature for Tuberculosis Screening Among People Living With Human Immunodeficiency Virus. Clin Infect Dis. 2019 Jun 18;69(1):77-83.

131. Flannick J, Mercader JM, Fuchsberger C, Udler MS, Mahajan A, Wessel J, Teslovich TM, Caulkins L, Koesterer R, Barajas-Olmos F, Blackwell TW, Boerwinkle E, Brody JA, Centeno-Cruz F, Chen L, Chen S, Contreras-Cubas C, Córdova E, Correa A, Cortes M, DeFronzo RA, Dolan L, Drews KL, Elliott A, Floyd JS, Gabriel S, Garay-Sevilla ME, García-Ortiz H, Gross M, Han S, Heard-Costa NL, Jackson AU, Jørgensen ME, Kang HM, Kelsey M, Kim BJ, Koistinen HA, Kuusisto J, Leader JB, Linneberg A, Liu CT, Liu J, Lyssenko V, Manning AK, Marcketta A, Malacara-Hernandez JM, Martínez-Hernández A, Matsuo K, Mayer-Davis E, Mendoza-Caamal E, Mohlke KL, Morrison AC, Ndungu A, Ng MCY, O'Dushlaine C, Payne AJ, Pihoker C; Broad Genomics Platform, Post WS, Preuss M,

Psaty BM, Vasan RS, Rayner NW, Reiner AP, Revilla-Monsalve C, Robertson NR, Santoro N, Schurmann C, So WY, Soberón X, Stringham HM, Strom TM, Tam CHT, Thameem F, Tomlinson B, Torres JM, Tracy RP, van Dam RM, Vujkovic M, Wang S, Welch RP, Witte DR, Wong TY, Atzmon G, Barzilai N, Blangero J, Bonnycastle LL, Bowden DW, Chambers JC, Chan E, Cheng CY, Cho YS, Collins FS, de Vries PS, Duggirala R, Glaser B, Gonzalez C, Gonzalez ME, Groop L, Kooner JS, Kwak SH, Laakso M, Lehman DM, Nilsson P, Spector TD, Tai ES, Tuomi T, Tuomilehto J, Wilson JG, Aguilar-Salinas CA, Bottinger E, Burke B, Carey DJ, Chan JCN, Dupuis J, Frossard P, Heckbert SR, Hwang MY, Kim YJ, Kirchner HL, Lee JY, Lee J, Loos RJF, Ma RCW, Morris AD, O'Donnell CJ, Palmer CNA, Pankow J, Park KS, Rasheed A, Saleheen D, Sim X, Small KS, Teo YY, Haiman C, Hanis CL, Henderson BE, Orozco L, Tusié-Luna T, Dewey FE, Baras A, Gieger C, Meitinger T, Strauch K, Lange L, Grarup N, Hansen T, Pedersen O, Zeitler P, Dabelea D, Abecasis G, Bell GI, Cox NJ, **Seielstad** M, Sladek R, Meigs JB, Rich SS, Rotter JI; DiscovEHR Collaboration; CHARGE; LuCamp; ProDiGY; GoT2D; ESP; SIGMA-T2D; T2D-GENES; AMP-T2D-GENES, Altshuler D, Burtt NP, Scott LJ, Morris AP, Florez JC, McCarthy MI, Boehnke M. Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. Nature. 2019 Jun;570(7759):71-76.

132. Albao DS, Cutiongco-de la Paz EM, Mercado ME, Lirio A, Mariano M, Kim S, Yangco A, Melegrito J, Wad-Asen K, Gauran II, Francisco MA, Santos-Acuin C, David-Padilla C, Murphy EJ, Paz-Pacheco E, Seielstad M. Methylation changes in the peripheral blood of Filipinos with type 2 diabetes suggest spurious transcription initiation at TXNIP. Hum Mol Genet. 2019 Dec 15;28(24):4208-4218.

REVIEW ARTICLES

1. Whiffs of selection', (2000) *Nature Genetics* **26**:131-2 (News & Views).
2. Asymmetries in the maternal and paternal genetic histories of Colombian populations (2000) *American Journal of Human Genetics,* **67**:1062-1066 (Invited Editorial).
3. Review of *Microsatellites: evolution and applications*. Goldstein D and Schloetterer C, eds. for *Quarterly Review of Biology* (2001) **76:**74-5.
4. Ardlie K, Kruglyak L & **Seielstad** M (2002) Patterns of linkage disequilibrium in the human genome. *Nature Reviews Genetics,* **3:**299-309.

BOOKS AND CHAPTERS

1. **Seielstad** M Some effects of culture on genetic variation. in *Proceedings of the trinational workshop on molecular evolution.* M. Uyenoyama and A. von Haeseler, eds. Duke University Publications Group, Durham (1998).
2. Ruvolo M and **Seielstad** M. The apportionment of human diversity 25 years later. In *Thinking about evolution: historical, philosophical and political perspectives.* Singh, Krimbas, Paul and Beatty, eds. Cambridge University Press. (2001)
3. Srikummool M, Kangwanpong D, Singh N and **Seielstad** M Y-chromosomal variation in uxorilocal and patrilocal populations in Thailand. in *Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia,* Jin L, Seielstad M, & Xiao C, eds. World Scientific Press, Singapore. (2001)
4. *Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia,* Jin L, **Seielstad** M, and Xiao C, eds. World Scientific Publishing, Singapore. (2001)

OTHER PUBLICATIONS

1. Cavalli-Sforza, LL *(2000) Genes, Peoples, and Languages*, Farrar, Straus & Giroux, New York. M. **Seielstad**, trans. (from the Italian).

SIGNIFICANT PUBLICATIONS

1. Yin X, Low H, Wang L, Li Y, Ellinghaus E, Han J, Estivill X, Sun L, Zuo X, Shen C, Zhu C, Zhang A, Sanchez F, Padyukov L, Catanese JJ, Krueger GG, Callis-Duffin KP, Mucha S, Weichenthal M, Weidinger S, Lieb W, Foo JN, Li Y, Sim K, Liany H, Irwan I, Teo YY, Theng CTS, Gupta R, Bowcock A, De Jager PL, Qureshi AA, de Bakker PIW, **Seielstad M****, Liao W, Ståhle M, Franke A, Zhang X, and Jianjun Liu JJ. Trans-ethnic genome-wide meta-analysis identifies multiple novel associations and reveals ethnic heterogeneity of psoriasis susceptibility. Nat Commun. (2015) 6 :6916. doi: 10.1038/ncomms7916.
   ****corresponding author**

   I was PI of and led, designed and funded the GWAS of Chinese psoriasis patients that comprised a major component of this multi-ethnic study. This included developing the study design, enrolling patients and controls from the National Skin Centre in Singapore, directing the genome-wide SNP genotyping and primary association analysis. Also, I was instrumental in bringing together and leading the collaborating groups, directing the meta-analysis, as well as the publication describing results.

2. Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JR, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Fernandez Tajes J, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SC, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, Voight BF, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MC, Palmer ND, Balkau B, Stancáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VK, Park KS, Saleheen D, So WY, Tam CH, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, van der Schouw YT, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney AS, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, Hrabé de Angelis M, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CN, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JC, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RC, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJ, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, **Seielstad** M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Burtt NP, Mohlke KL, Meitinger T, Groop L, Abecasis G, Florez JC, Scott LJ, Morris AP, Kang HM, Boehnke M, Altshuler D, McCarthy MI. The genetic architecture of type 2 diabetes. Nature. 2016 Aug 4; 536(7614):41-7. PMID: 27398621. PMCID: PMC5034897

   I was PI of and one of ten members of the Steering Committee that planned, directed, and conducted this landmark study appearing in Nature. As Steering Committee member I made several seminars contributions to the design of the study, chiefly in adopting a whole exome (vs. more limited target region) sequencing approach. The paper results from the fusion of two jointly submitted papers with partially overlapping authors that the editors directed us to combine into a single publication. As a result, there was considerable jostling of co-authorsips. My ultimate position amongst the senior authors ultimately is not commensurate with the numerous substantive contributions I made to the design, conduct, and analysis of the study data.

3. Long D, Deng X, Singh P, Loeb M, Lauring AS, **Seielstad** M. Identification of genetic variants associated with susceptibility to West Nile virus neuroinvasive disease. Genes Immun. 2016 Jul; 17(5):298-304. PMID: 27170560. PMCID: PMC5215919

   I designed, funded, and led this study of whole exome sequencing applied to the outcomes to an infectious disease (West Nile Virus Infection). This is the first and most comprehensive application published to date, and the study highlights the potential and the pitfalls for whole exome and whole genome sequencing studies.

4. Flannick J, Mercader JM, Fuchsberger C, Udler MS, Mahajan A, Wessel J, Teslovich TM, Caulkins L, Koesterer R, Barajas-Olmos F, Blackwell TW, Boerwinkle E, Brody JA, Centeno-Cruz F, Chen L, Chen S, Contreras-Cubas C, Córdova E, Correa A, Cortes M, DeFronzo RA, Dolan L, Drews KL, Elliott A, Floyd JS, Gabriel S, Garay-Sevilla ME, García-Ortiz H, Gross M, Han S, Heard-Costa NL, Jackson AU, Jørgensen ME, Kang HM, Kelsey M, Kim BJ, Koistinen HA, Kuusisto J, Leader JB, Linneberg A, Liu CT, Liu J, Lyssenko V, Manning AK, Marcketta A, Malacara-Hernandez JM, Martínez-Hernández A, Matsuo K, Mayer-Davis E, Mendoza-Caamal E, Mohlke KL, Morrison AC, Ndungu A, Ng MCY, O'Dushlaine C, Payne AJ, Pihoker C; Broad Genomics Platform, Post WS, Preuss M, Psaty BM, Vasan RS, Rayner NW, Reiner AP, Revilla-Monsalve C, Robertson NR, Santoro N, Schurmann C, So WY, Soberón X, Stringham HM, Strom TM, Tam CHT, Thameem F, Tomlinson B, Torres JM, Tracy RP, van Dam RM, Vujkovic M, Wang S, Welch RP, Witte DR, Wong TY, Atzmon G, Barzilai N, Blangero J, Bonnycastle LL, Bowden DW, Chambers JC, Chan E, Cheng CY, Cho YS, Collins FS, de Vries PS, Duggirala R, Glaser B, Gonzalez C, Gonzalez ME, Groop L, Kooner JS, Kwak SH, Laakso M, Lehman DM, Nilsson P, Spector TD, Tai ES, Tuomi T, Tuomilehto J, Wilson JG, Aguilar-Salinas CA, Bottinger E, Burke B, Carey DJ, Chan JCN, Dupuis J, Frossard P, Heckbert SR, Hwang MY, Kim YJ, Kirchner HL, Lee JY, Lee J, Loos RJF, Ma RCW, Morris AD, O'Donnell CJ, Palmer CNA, Pankow J, Park KS, Rasheed A, Saleheen D, Sim X, Small KS, Teo YY, Haiman C, Hanis CL, Henderson BE, Orozco L, Tusié-Luna T, Dewey FE, Baras A, Gieger C, Meitinger T, Strauch K, Lange L, Grarup N, Hansen T, Pedersen O, Zeitler P, Dabelea D, Abecasis G, Bell GI, Cox NJ, Seielstad M, Sladek R, Meigs JB, Rich SS, Rotter JI; DiscovEHR Collaboration; CHARGE; LuCamp; ProDiGY; GoT2D; ESP; SIGMA-T2D; T2D-GENES; AMP-T2D-GENES, Altshuler D, Burtt NP, Scott LJ, Morris AP, Florez JC, McCarthy MI, Boehnke M. Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. Nature. 2019 Jun;570(7759):71-76.

   I was PI of and one of ten members of the Steering Committee that planned, directed, and conducted this landmark study appearing in Nature. As Steering Committee member I made several seminars contributions to the design of the study, chiefly in adopting a whole exome (vs. more limited target region) sequencing approach. The paper results from the fusion of two jointly submitted papers with partially overlapping authors that the editors directed us to combine into a single publication. As a result, there was considerable jostling of co-authorsips. My ultimate position amongst the senior authors ultimately is not commensurate with the numerous substantive contributions I made to the design, conduct, and analysis of the study data.

5. Albao DS, Cutiongco-de la Paz EM, Mercado ME, Lirio A, Mariano M, Kim S, Yangco A, Melegrito J, Wad-Asen K, Gauran II, Francisco MA, Santos-Acuin C, David-Padilla C, Murphy EJ, Paz-Pacheco E, Seielstad M. Methylation changes in the peripheral blood of Filipinos with type 2 diabetes suggest spurious transcription initiation at TXNIP. Hum Mol Genet. 2019 Dec 15;28(24):4208-4218.

   I was PI for this project. I wrote the proposal that funded the research, and I designed and oversaw every aspect of the work, through and including publication. This move into epigenetic also marks a significant new innovation for my lab, and highlights a significant and fruitful new avenue for future research.

CONFERENCE ABSTRACTS

1. Seielstad, MT; Pritchard, JK; and Cavalli-Sforza, LL (1996) Analysis of Y chromosome microsatellites in a geographically diverse sample. Am. Soc. Hum. Genet., Annual Meetings (poster).
2. Seielstad, M, Minch, E, and Cavalli-Sforza, LL (1997) The apportionment of Y chromosome diversity. Cold Spring Harbor Laboratory Meetings on Human Evolution (talk).
3. Conference on the Genetics of the Populations of the Sudan, University of Khartoum, Sudan (March 1, 1998) (talk).
4. Xiao C, Seielstad M, Kangwanpong D, Schork N, and Xu X (1999) X and Y-chromosomal variation in populations of Southeast Asia. Cold Spring Harbor Laboratory Meetings on Human Evolution (poster).
5. Seielstad M, Xu X, and Xu X (1999) Direct observations of microsatellite mutations. Cold Spring Harbor Laboratory Meetings on Human Evolution (talk).
6. Seielstad M, Miller A, and Schork N (1999) The effects of population history on linkage disequilibrium among SNPs. American Society of Human Genetics, Annual Meetings October 1999 (platform presentation).
7. Seielstad M, Ardlie K, Miller A, and Schork N (1999) Linkage Disequilibrium Among SNPs. Gordon Conference on Molecular Evolution, Hayama, Japan (poster) November 1999.
8. Srikummool M, Kangwanpong D, Singh N and Seielstad M (2000) Origins and migrations of Southeast Asians. International Symposium on Human Genomic Diversity in Southeast Asia. Kunming, China. (invited talk) June 2000.
9. Seielstad M (2000) The effects of population history on linkage disequilibrium among SNPs. 3rd HUGO Pacific Meeting and 4th Asia-Pacific Conference on Human Genetics. Shangahi, China (poster) October 2000.
10. Seielstad M, Singh N, Ardlie K, Miller A, Schork N (2000) Some effects of recombination and population history on linkage disequilibrium and nucleotide diversity. Cold Spring Harbor Laboratory Meetings on Human Evolution.
11. Seielstad M, Yuldasheva N, Sing N, Underhill P, Oefner P, Shen P, and Wells R (2002) A novel Y chromosome variant puts a firm upper limit on the timing of the first entry to the Americas. Cold Spring Harbor Laboratory Meetings on Human Origins & Disease.

12. J. Tan, M.L. Hibberd, R. Ong, E. Png & M Seielstad (2006) Elevated level of common non-synonymous variationis in human EMR1 gene is consistent with balancing selection. 56th Annual Meetings of the American Society of Human Genetics.
13. Seielstad M, L. Padyukov, B. Ding, L. Alfredsson, L. Klareskog & the EIRA Study Group (2007). Genomics of Common Diseases Conference, Hinxton, UK.
14. Y. J. Li, A. Dellinger, M. Seielstad, L. K. Goh, T. L. Young, S. M. Saw. Evaluation of seven CNV detection methods using whole genome SNP arrays from myopia samples. American Society of Human Genetics Annual Meetings 2008.
15. A. Dellinger, T. L. Young, M. Seielstad, L. K. Goh, S. M. Saw, Y. J. Li. Significant Results of CNV Analysis of Myopia in Schoolchildren. American Society of Human Genetics Annual Meetings 2008.
16. V. Kumar, J. H. H. Tan, Y. Zhu, F. Yao, Y. Ruan, M. Seielstad Genome-wide analysis of structural variation by pair-end mapping. American Society of Human Genetics Annual Meetings 2008.
17. R. M. Plenge, S. Raychaudhuri, E. F. Remmers, A. T. Lee, L. Gianniny, L. Padyukov, L. A. Criswell, C. I. Amos, M. F. Seldin, D. L. Kastner, T. W. J. Huizinga, N. de Vries, J. Worthington, M. Seielstad, R. E. M. Toes, E. W. Karlson, A. B. Begovich, L. Klareskog, P. K. Gregersen, M. J. Daly, BRASS, EIRA, GENRA, NARAC, WTCCC. Meta-analysis of rheumatoid arthritis genome-wide association studies identifies common variants at CD40 and five other gene loci. American Society of Human Genetics Annual Meetings 2008.
18. Trans-ethnic fine-mapping of Type 2 Diabetes susceptibility loci using a □Cosmopolitan□ reference panel for imputation. T2D-GENES, American Society of Human Genetics Annual Meetings 2011.
19. Deep Sequencing in Extended Pedigrees Reveals both Common and Rare Non-Synonymous Variants Influencing Free Triiodothyronine Levels. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
20. Identification of genes influencing serum levels of brain-derived neurotrophic factor in large Mexican American pedigrees. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
21. Whole-exome sequencing of 10,000 type 2 diabetes cases and controls from five major ancestry groups. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
22. Deep whole genome sequencing in pedigrees illuminates the contribution of low frequency and private mutations to the genetic architecture of metabolic quantitative traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
23. Analyzing Deep Whole Genome Sequence and Genotype Data of >1,000 Individuals from Large Mexican-American Pedigrees in the T2D-GENES Study. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
24. The impact of genetic variation on diabetes-related quantitative traits from whole exome sequences: The T2D-GENES Consortium. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.

25. Large-scale exome chip association analysis identifies rare and low-frequency coding variants associated with glycemic traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
26. Fine-mapping of Type 2 Diabetes susceptibility loci via trans-ethnic meta-analysis. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
27. Gene-set test for rare variants. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
28. Meiotic gene conversion in humans: rate, sex ratio and GC bias. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
29. Statistical dissection of genetic factors influencing antibodies against Epstein-Barr virus nuclear antigen 1 (EBNA-1) using whole-genome sequence data.T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
30. Gene pathway burden test application to cardiovascular disease using whole genome sequencing data. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
31. Deep Sequencing in Extended Pedigrees Reveals a Major Rare Non-Synonymous Variant Influencing the De Novo Ceramide Synthesis Pathway. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
32. A test of association of genome-wide coding variation with type 2 diabetes in 13,000 individuals from five ancestry groups. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
33. Loss of function mutations in SLC30A8 protect against type 2 diabetes. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
34. Deep whole-genome sequencing in pedigrees to quantify the contribution of private variants to type 2 diabetes and related metabolic traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
35. Esensten JH, Cheng MH, Anderson MS, Chehab F.F, Gundling K, **Seielstad** M. A Case of Good Syndrome with a Full Genome Analysis of the Patient and Family. Academy of Clinical Laboratory Physicians and Scientists (ACLPS) Annual Meeting, 2014.
36. Genome wide association and exome sequence data analysis for more than 100 traits in Mexican Americans. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
37. A low frequency AKT2 coding variant enriched in the Finnish population is associated with fasting insulin levels. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
38. Gene-centric association tests applied to cardiovascular disease using whole genome sequencing. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
39. An exome-wide sequencing study for type 2 diabetes-associated kidney disease in African Americans. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
40. Yin, X ; Low, H; Seielstad, M ; Liao, W ; Stahle, M ; Franke, A; Zhang, X ; Liu, J. Trans-ethnic genome-wide meta-analysis identifies multiple novel associations and reveals

ethnic heterogeneity of psoriasis susceptibility. Annual Meeting of the Society-for-Investigative-Dermatology. 2015

41. Nititham, J; Taylor, KE ; Gupta, R ; Ahn, R ; Lee, KM ; Chen, H ; Liu, J ; Seielstad, M ; Ma, A ; Bowcock, AM ; Criswell, LA ; Stahle, M ; Liao, W. Meta-analysis of the TNIP1 region in psoriasis identifies two independent association signals. Annual Meeting of the Society-for-Investigative-Dermatology. 2015
42. Page, GP ; Guo, Y ; Seielstad, M ; Keating, B ; Westhoff, CM; Hoppe, C ; Bordbar, A ; Custer, B ; Lu, Y; Busch, M ; Lu, Y ; Busch, M. Development and Evaluation of a Transfusion Medicine Genome-wide SNP Array. AABB Annual Meeting. 2016
43. Rajan, J ; Deng, X ; Seielstad, M ; Semitala, F ; Kamya, M ; Yoon, C; Cattamanchi, A. Performance Of Gene Expression Signatures In The Context Of Intensified Tuberculosis Case Finding Among People Living With Hiv (plhiv). International Conference of the American-Thoracic-Society (ATS) 2017
44. MARIA ELIZABETH P. MERCADO, SARAH KIM, EVA MARIA C. CUTIONGCO DE LA PAZ, MARK SEIELSTAD, ELIZABETH PAZ-PACHECO, ELIZABETH MURPHY. Discordance between A1C and Glucose for the Diagnosis of Prediabetes in a Filipino-American Population. American Diabetes Association Annual Meeting. 2019

OTHER CREATIVE ACTIVITIES

1. Led and managed an effort to describe haplotype variation in three ethnic populations inhabiting Singapore (Chinese, Malays and Indians) and helped develop a website to distribute the data: http://www.nus-cme.org.sg/SGVP username: Reviewer; password: sgvp

ADDITIONAL RELEVANT INFORMATION

LANGUAGES

French, Italian (primarily reading), Latin (reading only, limited), and Attic Greek (reading only, very limited).