

Stanford




Erik Ingelsson

Professor of Medicine (Cardiovascular Medicine) and, by courtesy, of Health Research and Policy (Epidemiology)

Medicine - Cardiovascular Medicine

 NIH Biosketch available Online

 Curriculum Vitae available Online

CONTACT INFORMATION

• Administrative Contact

Alyssa Sacro - Administrative Assistant

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Bio

BIO

Dr. Ingelsson obtained his MD (2000) and PhD (2005) at Uppsala University, Sweden. After internship, he did a residency in general medicine (2003-2006) and took up a postdoctoral research fellowship at the Framingham Heart Study (2006-2007). He moved to Karolinska Institutet (Stockholm, Sweden) in 2007 and was appointed Professor of Cardiovascular Epidemiology in 2010. From 2013-2016, he was a Professor of Molecular Epidemiology at Uppsala University. He was also a Visiting Professor at the Wellcome Trust Centre for Human Genetics at University of Oxford in 2012-2015. Since May 2016, he is Professor of Medicine at Stanford University.

His main area of interest is the link between metabolic disturbances, such as obesity and insulin resistance, and the development of subclinical and clinical cardiovascular disease. His research is translational and interdisciplinary, combining methods from the molecular epidemiology field - such as genomic, metabolomic, transcriptomic, epigenomic and proteomic profiling in large population-based studies - with molecular biology methods using in vivo and in vitro models to reach new insights into the pathophysiology of cardiovascular disease and related conditions, identification of new biomarkers for improved risk prediction, and discovery of novel targets for drug development.

He has had a leading role in many of the large efforts identifying new loci associated with cardiovascular and metabolic traits, and has extensive experience from research on biomarkers and -omics methods, including development and use of prediction metrics and Mendelian randomization. He has served as PI of numerous -omics efforts in several Swedish cohort studies, including ULSAM, PIVUS, TwinGene and EpiHealth. Since 2014 and on, he has also built a team using molecular biology methods to characterize of loci established in GWAS using different functional model systems. He has published over 270 peer-reviewed original articles, of which >50 in journals with impact factor over 30. Before relocating to the U.S, he received many European research grants, and now after joining the Stanford faculty in May 2016, he has received his first NIH grants. He has won several prestigious awards and grants, such as the AHA Trudy Bush Fellowship for Cardiovascular Research in Women's Health, ERC starting grant, Wallenberg Academy Fellow and the Göran Gustafsson Prize in Medicine in 2015 (to the most successful medical researcher in Sweden under age 45).

ACADEMIC APPOINTMENTS

- Professor, Medicine - Cardiovascular Medicine
- Professor (By courtesy), Health Research & Policy
- Member, Bio-X

- Member, Cardiovascular Institute

ADMINISTRATIVE APPOINTMENTS

- Committee Member, Department of Medicine's Professoriate Appointments and Promotions Committee, (2018- present)
- National Director, EATRIS.se (Swedish node of the European Infrastructure for Translational Medicine), (2015-2016)
- Board Member, Faculty Board of the Disciplinary Domain of Medicine and Pharmacy, Uppsala University, (2014-2015)
- Executive Group Member, Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, (2010-2012)

HONORS AND AWARDS

- Göran Gustafsson Prize in Medicine, Göran Gustafsson Foundation (2015)
- Wallenberg Academy Fellow, Knut och Alice Wallenberg Foundation (2013)
- ERC Starting Grant Award, European Research Council (2013)
- Fellow of the American Heart Association (FAHA), American Heart Association (2010)
- Ingvar Carlsson Award, Swedish Foundation for Strategic Research (2009)
- Trudy Bush Fellowship for Cardiovascular Research in Women's Health, American Heart Association (2009)
- Young Investigator Award, EuroPREvent 2008, European Association of Cardiovascular Prevention and Rehabilitation (2008)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Scientific advisor, Precision Wellness (2016 - present)
- Scientific advisor, Olink Proteomics (2017 - present)

PROFESSIONAL EDUCATION

- PhD, Uppsala University , Epidemiology (2005)
- MD, Uppsala University , Medicine (2000)

PATENTS

- Lindholm D, Fukaya E, Leeper NJ, Ingelsson E. "United States Patent 62/522,601 Systems and Methods for Predicting Heart Failure Using Leg Bioimpedance", Leland Stanford Junior University, Jun 20, 2017

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our research area is cardiovascular medicine with a special focus on metabolic disturbances, such as obesity and insulin resistance and their role in the development of subclinical and clinical cardiovascular disease. The methods used are from the molecular epidemiology field where we use -omics studies of how cardiovascular disease and related conditions varies with DNA variation, RNA expression, and circulating biomarkers such as proteins and metabolites; but also functional characterization of candidate genes using CRISPR-Cas9 gene editing in cell and animal models. Our research is translational, trying to bridge population studies with molecular biology to reach new important insights into the pathophysiology of cardiovascular diseases, identification of new biomarkers for improved risk prediction, and discovery of novel targets for drug development.

Population-based studies

We are performing many population-based projects in the UK Biobank, which is an excellent example of science in the new era of open science initiatives and big data analytics. In 2006-2010, the UK Biobank recruited 502,650 participants aged 37-73 years to undergo physical measurements, detailed assessments about risk factors and future disease events, and sampling of blood, urine and saliva. Genome-wide genotyping on the UK Biobank Axiom Array and imputation to ~80 million variants has been performed in all participants. They have also been extensively examined, and outcome events are recorded in a longitudinal fashion.

We are working on a wide range of projects using this excellent cohort, including traditional epidemiological studies and GWAS addressing important, but understudied conditions, such as peripheral vascular disease and heart failure – including risk prediction studies to improve patient stratification, as well as studies of environmental risk factors, genetic determinants and their interactions; but also more novel approaches which aims at addressing causality of risk factors and biomarkers and importantly, at finding druggable targets using genomic approaches. The statistical power, as well as the opportunities to study new research questions, are unprecedented given the very large sample size (ten- to hundred-fold larger than all previous studies) and the extreme richness of the data.

In addition to UK Biobank, we are also working with several other datasets. I am still the PI for a range of –omics projects in several Swedish cohorts – ULSAM, PIVUS, TwinGene and EpiHealth. These include genomics, transcriptomics, epigenomics, proteomics and metabolomics, often used in combination - aiming at increasing the biological knowledge of obesity, insulin resistance and CVD, and to identify new biomarkers for risk prediction and novel drug targets.

Wet-lab approaches

To further characterize gene function after various –omics studies and use of in silico data on gene regulation and transcription from public resources, we proceed to studies of gene function in model systems. We use CRISPR-Cas9 techniques for gene editing in human SGBS adipocytes, HepG2 hepatocytes, HMCL-7304 skeletal myocytes, and murine 3T3-L1 adipocytes to study phenotypes related to obesity and insulin resistance. We transfect cells using our custom-built lentivirus CRISPR-Cas9 constructs, and assess the effect of knockdown or overexpression of candidate genes on basal and insulin-stimulated glucose uptake (using ¹⁴C-labeled deoxyglucose) and lipolysis (measuring glycerol after insulin and isoprenaline exposure), as well as insulin signaling proteins and adipogenesis. We address downstream effects of gene knockdown using transcriptomic and metabolomic profiling on cell lysates.

Teaching

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Sylwia Figarska, Jiehan Li

Postdoctoral Research Mentor

Sylwia Figarska, Joanna Lankester, Jiehan Li

Publications

PUBLICATIONS

- **Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation.** *Nature genetics*
Christophersen, I. E., Rienstra, M., Roselli, C., Yin, X., Geelhoed, B., Barnard, J., Lin, H., Arking, D. E., Smith, A. V., Albert, C. M., Chaffin, M., Tucker, N. R., Li, et al
2017; 49 (6): 946-952
- **An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans.** *Diabetes*
Scott, R. A., Scott, L. J., Mägi, R., Marullo, L., Gaulton, K. J., Kaakinen, M., Pervjakova, N., Pers, T. H., Johnson, A. D., Eicher, J. D., Jackson, A. U., Ferreira, T., Lee, et al
2017
- **Leveraging Human Genetics to Understand the Relation of LDL Cholesterol with Type 2 Diabetes.** *Clinical chemistry*
Ingelsson, E., Knowles, J. W.
2017
- **Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function** *JOURNAL OF CLINICAL INVESTIGATION*
Wild, P. S., Felix, J. F., Schillert, A., Teumer, A., Chen, M., Leening, M. J., Voelker, U., Grossmann, V., Brody, J. A., Irvin, M. R., Shah, S. J., Pramana, S., Lieb, et al

2017; 127 (5): 1798-1812

- **Locus Due to Gene-Smoking Interactions.** *Circulation*
Saleheen, D., Zhao, W., Young, R., Nelson, C. P., Ho, W. K., Ferguson, J. F., Rasheed, A., Ou, K., Nurnberg, S. T., Bauer, R. C., Goel, A., Do, R., Stewart, et al
2017
- **Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits** *NATURE COMMUNICATIONS*
Justice, A. E., Winkler, T. W., Feitosa, M. F., Graff, M., Fisher, V. A., Young, K., Barata, L., Deng, X., Czajkowski, J., Hadley, D., Ngwa, J. S., Ahluwalia, T. S., Chu, et al
2017; 8
- **Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease.** *PLoS genetics*
Folkersen, L., Fauman, E., Sabater-Lleal, M., Strawbridge, R. J., Fränberg, M., Sennblad, B., Baldassarre, D., Veglia, F., Humphries, S. E., Rauramaa, R., de Faire, U., Smit, A. J., Giral, et al
2017; 13 (4)
- **Alterations in Multiple Lifestyle Factors in Subjects with the Metabolic Syndrome Independently of Obesity** *METABOLIC SYNDROME AND RELATED DISORDERS*
Roos, V., Elmstahl, S., Ingelsson, E., Sundstrom, J., Arnlov, J., Lind, L.
2017; 15 (3): 118-123
- **Variant Enriched in the Finnish Population is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk.** *Diabetes*
Manning, A., Highland, H. M., Gasser, J., Sim, X., Tukiainen, T., Fontanillas, P., Grarup, N., Rivas, M. A., Mahajan, A., Locke, A. E., Cingolani, P., Pers, T. H., Viñuela, et al
2017
- **Association of Pregnancy Complications and Characteristics With Future Risk of Elevated Blood Pressure: The Västerbotten Intervention Program.** *Hypertension*
Parikh, N. I., Norberg, M., Ingelsson, E., Cnattingius, S., Vasan, R. S., Domellöf, M., Jansson, J. H., Edstedt Bonamy, A.
2017; 69 (3): 475-483
- **Association of Pregnancy Complications and Characteristics With Future Risk of Elevated Blood Pressure The Vasterbotten Intervention Program** *HYPERTENSION*
Parikh, N. I., Norberg, M., Ingelsson, E., Cnattingius, S., Vasan, R. S., Domellof, M., Jansson, J. H., Bonamy, A. E.
2017; 69 (3): 475-483
- **Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk** *NATURE GENETICS*
Warren, H. R., Evangelou, E., Cabrera, C. P., Gao, H., Ren, M., Mifsud, B., Ntalla, I., Surendran, P., Liu, C., Cook, J. P., Kraja, A. T., Drenos, F., Loh, et al
2017; 49 (3): 403-415
- **Rare and low-frequency coding variants alter human adult height.** *Nature*
Marouli, E., Graff, M., Medina-Gomez, C., Lo, K. S., Wood, A. R., Kjaer, T. R., Fine, R. S., Lu, Y., Schurmann, C., Highland, H. M., Rieger, S., Thorleifsson, G., Justice, et al
2017; 542 (7640): 186-190
- **PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study.** *The lancet. Diabetes & endocrinology*
Schmidt, A. F., Swerdlow, D. I., Holmes, M. V., Patel, R. S., Fairhurst-Hunter, Z., Lyall, D. M., Hartwig, F. P., Horta, B. L., Hyppönen, E., Power, C., Moldovan, M., van Iperen, E., Hovingh, et al
2017; 5 (2): 97-105
- **Metabolic Syndrome Development During Aging with Special Reference to Obesity Without the Metabolic Syndrome** *METABOLIC SYNDROME AND RELATED DISORDERS*
Roos, V., Elmstahl, S., Ingelsson, E., Sundstrom, J., Arnlov, J., Lind, L.
2017; 15 (1): 36-43
- **Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution** *DIABETES*
Ehrlund, A., Mejhert, N., Bjork, C., Andersson, R., Kulyte, A., Astrom, G., Itoh, M., Kawaji, H., Lassmann, T., Daub, C. O., Carninci, P., Forrest, A. R., Hayashizaki, et al
2017; 66 (1): 218-230
- **Genetic and methylation variation in the CYP2B6 gene is related to circulating p,p'-dde levels in a population-based sample** *ENVIRONMENT INTERNATIONAL*

- Lind, L., Ng, E., Ingelsson, E., Lindgren, C., Salihovic, S., van Bavel, B., Mahajan, A., Lampa, E., Morris, A. P., Lind, P. M.
2017; 98: 212-218
- **Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation** *NATURE GENETICS*
Chu, A. Y., Deng, X., Fisher, V. A., Drong, A., Zhang, Y., Feitosa, M. F., Liu, C., Weeks, O., Choh, A. C., Duan, Q., Dyer, T. D., Eicher, J. D., Guo, et al
2017; 49 (1): 125-130
 - **Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach.** *PLoS medicine*
Mendelson, M. M., Marioni, R. E., Joehanes, R., Liu, C., Hedman, Å. K., Aslibekyan, S., Demerath, E. W., Guan, W., Zhi, D., Yao, C., Huan, T., Willinger, C., Chen, et al
2017; 14 (1)
 - **Sensitivity Analyses for Robust Causal Inference from Mendelian Randomization Analyses with Multiple Genetic Variants** *EPIDEMIOLOGY*
Burgess, S., Bowden, J., Fall, T., Ingelsson, E., Thompson, S. G.
2017; 28 (1): 30-42
 - **Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies.** *Circulation. Cardiovascular genetics*
Hedman, Å. K., Mendelson, M. M., Marioni, R. E., Gustafsson, S., Joehanes, R., Irvin, M. R., Zhi, D., Sandling, J. K., Yao, C., Liu, C., Liang, L., Huan, T., McRae, et al
2017; 10 (1)
 - **Statistical power considerations in genotype-based recall randomized controlled trials** *SCIENTIFIC REPORTS*
Atabaki-Pasdar, N., Ohlsson, M., Shungin, D., Kurbasic, A., Ingelsson, E., Pearson, E. R., Ali, A., Franks, P. W.
2016; 6
 - **DNA methylation patterns associated with oxidative stress in an ageing population** *BMC MEDICAL GENOMICS*
Hedman, A. K., Zilmer, M., Sundstrom, J., Lind, L., Ingelsson, E.
2016; 9
 - **Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults.** *International journal of epidemiology*
Varga, T. V., Kurbasic, A., Aine, M., Eriksson, P., Ali, A., Hindy, G., Gustafsson, S., Luan, J., Shungin, D., Chen, Y., Schulz, C., Nilsson, P. M., Hallmans, et al
2016
 - **A DNA methylation biomarker of alcohol consumption.** *Molecular psychiatry*
Liu, C., Marioni, R. E., Hedman, Å. K., Pfeiffer, L., Tsai, P., Reynolds, L. M., JUST, A. C., Duan, Q., Boer, C. G., Tanaka, T., Elks, C. E., Aslibekyan, S., Brody, et al
2016
 - **Effects of cigarette smoking on cardiovascular-related protein profiles in two community-based cohort studies.** *Atherosclerosis*
Huang, B., Svensson, P., Ärnlöv, J., Sundström, J., Lind, L., Ingelsson, E.
2016; 254: 52-58
 - **Transcriptional Dynamics During Human Adipogenesis and its Link to Adipose Morphology and Distribution.** *Diabetes*
Ehrlund, A., Mejhert, N., Björk, C., Andersson, R., Kulyté, A., Åström, G., Itoh, M., Kawaji, H., Lassmann, T., Daub, C. O., Carninci, P., Forrest, A. R., Hayashizaki, et al
2016
 - **Metabolic Syndrome Development During Aging with Special Reference to Obesity Without the Metabolic Syndrome.** *Metabolic syndrome and related disorders*
Roos, V., Elmståhl, S., Ingelsson, E., Sundström, J., Ärnlöv, J., Lind, L.
2016: -?
 - **No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis** *SCIENTIFIC REPORTS*
Loley, C., Alver, M., Assimes, T. L., Bjonnes, A., Goel, A., Gustafsson, S., Hernesniemi, J., Hopewell, J. C., Kanoni, S., Kleber, M. E., Lau, K. W., Lu, Y., Lyytikäinen, et al
2016; 6
 - **Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior.** *Human molecular genetics*

Cornelis, M. C., Kacprowski, T., Menni, C., Gustafsson, S., Pivin, E., Adamski, J., Artati, A., Eap, C. B., Ehret, G., Friedrich, N., Ganna, A., Guessous, I., Homuth, et al

2016

- **Non-targeted metabolomics combined with genetic analyses identifies bile acid synthesis and phospholipid metabolism as being associated with incident type 2 diabetes.** *Diabetologia*
Fall, T., Salihovic, S., Brandmaier, S., Nowak, C., Ganna, A., Gustafsson, S., Broeckling, C. D., Prezzi, J. E., Kastenmüller, G., Peters, A., Magnusson, P. K., Wang-Sattler, R., Giedraitis, et al
2016; 59 (10): 2114-2124
- **Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension** *NATURE GENETICS*
Surendran, P., Drenos, F., Young, R., Warren, H., Cook, J. P., Manning, A. K., Grarup, N., Sim, X., Barnes, D. R., Witkowska, K., Staley, J. R., Tragante, V., Tukiainen, et al
2016; 48 (10): 1151-1161
- **Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci.** *Diabetes*
Walford, G. A., Gustafsson, S., Rybin, D., Stancáková, A., Chen, H., Liu, C., Hong, J., Jensen, R. A., Rice, K., Morris, A. P., Mägi, R., Tönjes, A., Prokopenko, et al
2016; 65 (10): 3200-3211
- **Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study.** *PLoS genetics*
Nowak, C., Salihovic, S., Ganna, A., Brandmaier, S., Tukiainen, T., Broeckling, C. D., Magnusson, P. K., Prezzi, J. E., Wang-Sattler, R., Peters, A., Strauch, K., Meitinger, T., Giedraitis, et al
2016; 12 (10)
- **The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals** *NATURE GENETICS*
Ehret, G. B., Ferreira, T., Chasman, D. I., Jackson, A. U., Schmidt, E. M., Johnson, T., Thorleifsson, G., Luan, J., Donnelly, L. A., Kanoni, S., Petersen, A. -, Pihur, V., Strawbridge, et al
2016; 48 (10): 1171-1184
- **The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals.** *Nature genetics*
Ehret, G. B., Ferreira, T., Chasman, D. I., Jackson, A. U., Schmidt, E. M., Johnson, T., Thorleifsson, G., Luan, J., Donnelly, L. A., Kanoni, S., Petersen, A., Pihur, V., Strawbridge, et al
2016; 48 (10): 1171-1184
- **Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction** *ANALYTICAL CHEMISTRY*
Broeckling, C. D., Ganna, A., Layer, M., Brown, K., Sutton, B., Ingelsson, E., Peers, G., Prezzi, J. E.
2016; 88 (18): 9226-9234
- **Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity.** *American journal of human genetics*
Mahajan, A., Rodan, A. R., Le, T. H., Gaulton, K. J., Haessler, J., Stilp, A. M., Kamatani, Y., Zhu, G., Sofer, T., Puri, S., Schellinger, J. N., Chu, P., Cechova, et al
2016; 99 (3): 636-646
- **Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study.** *Journal of the American College of Cardiology*
van der Laan, S. W., Fall, T., Soumaré, A., Teumer, A., Sedaghat, S., Baumert, J., Zabaneh, D., van Setten, J., Isgum, I., Galesloot, T. E., Arpegård, J., Amouyel, P., Trompet, et al
2016; 68 (9): 934-945
- **The genetic architecture of type 2 diabetes** *NATURE*
Fuchsberger, C., Flannick, J., Teslovich, T. M., Mahajan, A., Agarwala, V., Gaulton, K. J., Ma, C., Fontanillas, P., Moutsianas, L., McCarthy, D. J., Rivas, M. A., Perry, J. R., Sim, et al
2016; 536 (7614): 41-?
- **?-3 Polyunsaturated Fatty Acid Biomarkers and Coronary Heart Disease: Pooling Project of 19 Cohort Studies.** *JAMA internal medicine*
Del Gobbo, L. C., Imamura, F., Aslibekyan, S., Marklund, M., Virtanen, J. K., Wennberg, M., Yakoob, M. Y., Chiuve, S. E., Dela Cruz, L., Frazier-Wood, A. C., Fretts, A. M., Guallar, E., Matsumoto, et al
2016; 176 (8): 1155-1166
- **Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies** *LANCET NEUROLOGY*

- Chauhan, G., Arnold, C. R., Chu, A. Y., Fornage, M., Reyahi, A., Bis, J. C., Havulinna, A. S., Sargurupremraj, M., Smith, A. V., Adams, H. H., Choi, S. H., Pulit, S. L., Trompet, et al
2016; 15 (7): 695-707
- **The metabolic fingerprint of p,p'-DDE and HCB exposure in humans** *ENVIRONMENT INTERNATIONAL*
Salihovic, S., Ganna, A., Fall, T., Broeckling, C. D., Prenni, J. E., van Bavel, B., Lind, P. M., Ingelsson, E., Lind, L.
2016; 88: 60-66
 - **Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies** *PLOS GENETICS*
Choi, S. H., Ruggiero, D., Sorice, R., Song, C., Nutile, T., Smith, A. V., Concas, M. P., Traglia, M., Barbieri, C., Ndiaye, N. C., Stathopoulou, M. G., Lagou, V., Maestrale, et al
2016; 12 (2)
 - **Prediction impact curve is a new measure integrating intervention effects in the evaluation of risk models** *JOURNAL OF CLINICAL EPIDEMIOLOGY*
Campbell, W., Ganna, A., Ingelsson, E., Janssens, A. C.
2016; 69: 89-95
 - **Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels.** *Nature communications*
Kilpeläinen, T. O., Carli, J. F., Skowronski, A. A., Sun, Q., Kriebel, J., Feitosa, M. F., Hedman, Å. K., Drong, A. W., Hayes, J. E., Zhao, J., Pers, T. H., Schick, U., Grarup, et al
2016; 7: 10494-?
 - **New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk.** *Nature communications*
Lu, Y., Day, F. R., Gustafsson, S., Buchkovich, M. L., Na, J., Bataille, V., Cousminer, D. L., Dastani, Z., Drong, A. W., Esko, T., Evans, D. M., Falchi, M., Feitosa, et al
2016; 7: 10495-?
 - **Large-scale non-targeted metabolomic profiling in three human population-based studies** *METABOLOMICS*
Ganna, A., Fall, T., Salihovic, S., Lee, W., Broeckling, C. D., Kumar, J., Hagg, S., Stenemo, M., Magnusson, P. K., Prenni, J. E., Lind, L., Pawitan, Y., Ingelsson, et al
2016; 12 (1)
 - **Protein Biomarkers for Insulin Resistance and Type 2 Diabetes Risk in Two Large Community Cohorts** *DIABETES*
Nowak, C., Sundstrom, J., Gustafsson, S., Giedraitis, V., Lind, L., Ingelsson, E., Fall, T.
2016; 65 (1): 276-284
 - **Genome-wide genetic homogeneity between sexes and populations for human height and body mass index** *HUMAN MOLECULAR GENETICS*
Yang, J., Bakshi, A., Zhu, Z., Hemani, G., Vinkhuyzen, A. A., Nolte, I. M., van Vliet-Ostapchouk, J. V., Snieder, H., Study, L. C., Esko, T., Milani, L., Maegi, R., Metspalu, et al
2015; 24 (25): 7445-7449
 - **Genome-wide genetic homogeneity between sexes and populations for human height and body mass index.** *Human molecular genetics*
Yang, J., Bakshi, A., Zhu, Z., Hemani, G., Vinkhuyzen, A. A., Nolte, I. M., van Vliet-Ostapchouk, J. V., Snieder, H., Esko, T., Milani, L., Mägi, R., Metspalu, A., Hamsten, et al
2015; 24 (25): 7445-7449
 - **Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci** *NATURE GENETICS*
Gaulton, K. J., Ferreira, T., Lee, Y., Raimondo, A., Maegi, R., Reschen, M. E., Mahajan, A., Locke, A., Rayner, N. W., Robertson, N., Scott, R. A., Prokopenko, I., Scott, et al
2015; 47 (12): 1415-?
 - **Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation** *NATURE COMMUNICATIONS*
Artigas, M. S., Wain, L. V., Miller, S., Kheirallah, A. K., Huffman, J. E., Ntalla, I., Shrine, N., Obeidat, M., Trochet, H., McArdle, W. L., Alves, A. C., Hui, J., Zhao, et al
2015; 6
 - **Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity** *HUMAN MOLECULAR GENETICS*
Hagg, S., Ganna, A., van der Laan, S. W., Esko, T., Pers, T. H., Locke, A. E., Berndt, S. I., Justice, A. E., Kahali, B., Siemelink, M. A., Pasterkamp, G., Strachan, D. P., Speliotes, et al
2015; 24 (23): 6849-6860

- **Population genetic differentiation of height and body mass index across Europe** *NATURE GENETICS*
Robinson, M. R., Hemani, G., Medina-Gomez, C., Mezzavilla, M., Esko, T., Shakhbazov, K., Powell, J. E., Vinkhuyzen, A., Berndt, S. I., Gustafsson, S., Justice, A. E., Kahali, B., Locke, et al
2015; 47 (11): 1357-?
- **Early Exposure to Dogs and Farm Animals and the Risk of Childhood Asthma** *JAMA PEDIATRICS*
Fall, T., Lundholm, C., Orqvist, A. K., Fall, K., Fang, F., Hedhammar, A., Kampe, O., Ingelsson, E., Almqvist, C.
2015; 169 (11)
- **A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease** *NATURE GENETICS*
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