Curriculum vitae: Lude Franke

Personal details

Name:	Prof. L.H. (Lude) Franke, PhD
Gender:	Male
Date and place of birth:	14-01-1980, Oldenzaal, the Netherlands
Nationality:	Dutch
Civil status:	Living together with Madelien van de Beek Father of two daughters (Suzan and Dorien)
E-mail address:	lude@ludesign.nl
URLs:	http://www.rug.nl/research/genetics/staff/lude-franke http://ludesign.nl/frankelab/ and http://www.systemsgenetics.nl
Google Scholar profile	http://scholar.google.nl/citations?user=--4kM8cAAAAJ&hl

Education

Doctorate degree

University:	**Utrecht University (*cum laude*)**
Starting date:	01/01/2004
Completion date:	27/05/2008
Supervisor:	Prof. Cisca Wijmenga
Title of thesis:	"*Genome-wide approaches towards identification of susceptibility genes in complex diseases*"

Master's degree

University:	**Utrecht University**
Date:	28/10/2002
Studies:	Biomedical Sciences
Main subject:	Genetics and genomics

One year of philosophy

University:	**Radboud University, Nijmegen**
Date:	2002 - 2003
Studies:	Philosophy (with a stipend from the Radboud Foundation

Current and past employment

2016 – onwards	**Head of Research and Education section**	Permanent	Department of Genetics, University Medical Centre Groningen.
2014 – onwards	**Associate Professor**	Permanent	University Medical Centre Groningen, University of Groningen, the Netherlands.
2009 – 2014	**Assistant Professor**	Permanent	University Medical Centre Groningen, University of Groningen, the Netherlands.
2008 – 2011	**Postdoctoral Fellow**	Fixed-term	Queen Mary University of London, Institute of Cell and Molecular Science, London (UK).
2008 – 2009	**Postdoctoral Fellow** (0.7 fte)	Fixed-term	University Medical Centre Groningen, University of Groningen, the Netherlands.
2008 – 2009	**Postdoctoral Fellow** (0.3 fte)	Fixed-term	Queen Mary University of London, London(UK). Group leader: Prof. David van Heel. Funded by an NGI fellowship.
2006	**Research Fellow**	Fixed-term	Wellcome Trust Centre for Human Genetics, Oxford (UK). Group leader: Prof. Lon Cardon.

International activities

International visits

June – August 2014 **Visiting Scientist,** Broad Institute, Boston (USA) in the lab of Dr. Aviv Regev.

International collaborations

(1) International blood-eQTL consortium

I am the initiator and leader of a large blood eQTL consortium (eQTLGen, 2010 – present), in which over 20 international research groups are collaborating. Through this consortium I am currently leading a large-scale eQTL meta-analysis, aiming to identify the downstream effects of disease-associated genetic variants: http://www.genenetwork.nl/eqtlgen.

(2) Tune Pers (Broad Institute, MIT, Harvard Medical School, Boston, USA)

This is a collaboration to develop novel statistical methods for finding disease genes.

(3) Tonu Esko & Andres Metspalu (Estonian Genome Center of the University of Tartu, Estonia)

This is a long-standing international collaboration. Several PhD students from Tartu have visited my lab, where we collaborate on various methylation and expression related projects.

(4) Peter Visscher (University of Queensland, Australia)

Collaboration on eQTL analysis.

Grants

Grants (Principal Investigator)	**Amount**	**Year of award**
Proof-of-concept grant: towards a clinical genetics decision support system, BBMRI	€140,000	2016
ERC Starting Grant, European Research Council: Identification of environmental risk factors by exploiting eQTLs	€1,500,000	2014
VIDI Grant, NWO/ZonMW (Netherlands Organisation for Scientific Research): Identification of downstream effects through *trans*-eQTL analysis	€800,000	2014
VENI Grant, NWO/ZonMW (Netherlands Organisation for Scientific Research): Role of copy number variation in disease and eQTLs	€250,000	2010
Horizon Breakthrough Grant, Netherlands Genomics Initiative: Copy number variation	€100,000	2009
Grants (Co-Applicant)		
BBMRI Rainbow Project Grant: Functional genomics (Co-PI), €2m in total	€2,000,000	2011
EU FP7 Grant: European multidisciplinary ALS network identification to cure motor neuron degeneration, Euro-MOTOR, €9m in total (Work package leader)	€450,000	2010
RaakPro Grant, Stichting Innovatie Alliantie: Development of high-performance bioinformatics tools, €600,000 in total (Co-applicant)	€10,000	2009

Scholarships

	Amount	**Year of award**
Netherlands Genomics Initiative (NGI) Fellowship Grant for visiting the Wellcome Trust Centre for Human Genetics, Oxford, UK, as a principal investigator	€5,000	2006
Radboud Foundation, Nijmegen, Stipend to study Philosophy for 1 year	€5,000	2002

Awards and prizes

	Amount	**Year of award**
Winner Researcher of the Year University Medical Centre Groningen, the Netherlands	€100,000	2015
Winner Gold European Design Award for "The Living Cell" exhibit in the ERIBA Research Institute, Groningen	–	2013
Lindau Nobel Laureate meeting, invited participant, Lindau, Germany	–	2011
Winner Young Scientist of the Year award in Bioinformatics NBIC Conference, Lunteren, the Netherlands	€1,250	2010
Winner Red Dot Design award for corporate identity of Hubrecht Institute (Utrecht), Essen, Germany	–	2010
Winner Young Scientist Award for best PhD thesis in Genetics Dutch Society of Human Genetics, Veldhoven	€1,250	2009

Winner Red Dot Design award for corporate identity of International Celiac Disease Symposium, Essen, Germany	–	2008
Winner Young Scientist Award, European Mathematical Genetics Meeting 2008	€50	2008
Winner Application Showcase, Netherlands Bioinformatics Conference	€300	2007
Winner Talma Eyckman Prize for M.Sc. thesis, University Medical Center Utrecht	€1,250	2002

Invited Lectures to International Meetings in last five years

1. *Identifying scRNA-seq eQTLs*, Satellite symposium 10XGenomics, European Society of Human Genetics, Copenhagen, Denmark (2017).
2. *Identification of downstream molecular effects using trans-eQTLs*, EPFL seminar session, Lausanne, Switzerland (2017)
3. *Understanding downstream consequences of disease-associated genetic variants through eQTL and meQTL analysis.* Global human medicine meeting, Barcelona, Spain (2016)
4. *Machine Learning for Personalized Medicine*, ESHG ancillary meeting, Barcelona, Spain (2016)
5. *Integration of multi-omics data*, Fifth course in Next-Generation Sequencing, Bertinoro, Italy (2016)
6. *Identification of downstream molecular effects for thousands of genetic risk factors*, Wellcome Trust Sanger Centre, Hinxton, Cambridge, UK (2015)
7. *Identification of downstream molecular effects for thousands of genetic risk factors*, Lausanne, Switzerland (2015)
8. *Transcriptome of the Netherlands*, Illumina User Meeting, Cannes, France (2015)
9. *Identification of downstream molecular effects for thousands of genetic risk factors*, Nantes, France (2015)
10. *Downstream expression effects of (rare) genetic variants.* Annual Meeting of the Arbeitsgemeinschaft für Gen-Diagnostik, Potsdam, Germany (2014)
11. *Identification of key genes that drive disease through trans-eQTL analysis.* EuroBATS meeting, London, UK (2014)
12. *Extending pathways by using gene expression data of 80,000 arrays, with an application to GWAS.* CHARGE consortium conference, Los Angeles, USA (2014)
13. *Gaining insight in the functional consequences of disease associated genetic variants.* Research retreat Turku University, Turku, Finland (2013)
14. *Trans-eQTL mapping in over 8,000 samples reveals genetic variants that define hallmarks of disease.* Basel Computational Biology Conference (BC2), Basel, Switzerland (2013)
15. *Let there be light: dark matters in autoimmunity*. Genomics Day Conference, Lausanne, Switzerland (2013)
16. *eQTLs: cell type specificity in cis and trans.* European Society of Human Genetics, Neurenberg, Germany (2012)
17. *Identification of the downstream consequences of genetic variants through genetical genomics and gene network reconstruction.* Gene Forum 2012, Tartu, Estonia (2012)
18. *The genetic background of hypertension and nephropathy: genome-wide association studies.* National Internal Medicine conference, Maastricht, the Netherlands (2012)

Scientific committees and other positions

2017 – present	Chair of "Off-road" grant from Dutch Medical Research Council (NWO-ZonMw)
2016 – present	Appointed a member of De Jonge Akademie (The Young Academy), Royal Society of Arts and Sciences (KNAW)
2016 – present	Appointed a member of Young Academy Groningen
2016	Chair of "Off-road" grant from Dutch Medical Research Council (NWO-ZonMw)
2015 – present	Scientific Program Committee member, European Society of Human Genetics
2014 – present	Grant review committee member, Fonds de la Recherche Scientifique, Belgium
2013 – present	Co-organizer 2-day departmental retreat
2012 – present	Initiator and leader international expression and methylation quantitative trait locus consortium (eQTLGen)
2012 – 2017	Chair of department's weekly scientific research meeting

2009 – present	Regular reviewer for PNAS, PloS Genetics, Nature, Nature Genetics, Nucleic Acids Research, Genome Biology and EJHG
2011 – present	Member of CHARGE consortium (Cohorts for Heart and Aging Research in Genomic Epidemiology)
2011 – present	Co-PI of Biobanking and Biomolecular Resources Research Infrastructure project "Functional Genomics", providing data and infrastructure for nation-wide functional genomic research
2011 – present	Member of PhD thesis assessment committees (>10)
2009 – 2012	LifeLines Scientific Board Member

Academic staff supervised

Completed PhD theses (4):

1. Marc Jan Bonder (2017), graduated *cum laude* on 22 March 2017 with his thesis: "The interplay between genetics, the microbiome, DNA-methylation & gene-expression."
2. Daria Zhernakova (2016), graduated on 12 Sept 2016 with her thesis on: " Multi-omics approaches for better understanding of the downstream effects of genetic risk factors.".
3. Serena Sanna (2016), graduated on 9 May 2016 with her thesis: "Enhancing genetic discoveries with population-specific reference panels." She is now a postdoc in the Dept. of Genetics, UMCG.
4. Harm-Jan Westra (2014), graduated *cum laude* on 17 Sept 2014 with his thesis: "Interpreting disease genetics using functional genomics." So far Westra has published some 70 peer-reviewed papers (6 as first or second author). He is first author on a paper in Nature Genetics and was awarded an NWO Rubicon grant to visit Harvard Medical School for two years.

Currently *promotor* and supervisor of 4 PhD students:

- Juha Karjalainen, started in 2011: reconstruction of gene networks in cancer
- Niek de Klein, started in 2015: allele-specific expression
- Annique Claringbould, started in 2015: *trans*-eQTL analysis
- Marion Dam, started in 2015: single-cell RNA-seq

Supervisor of 2 post-docs

Supervisor of over 15 graduate, masters and undergraduate students from 2003 – present.

Teaching Activities

2017	MSc courses in "New Biology/Big Data analyses", University of Groningen
2017	Workshop organizer at ESHG 2017, Copenhagen, "How to develop your career in science"
2016	Visit Siemens Groningen, presentation on the use of big data to better diagnose patients, Groningen, the Netherlands, 30 June
2016	Landelijk overleg Genetici, Utrecht, the Netherlands, 16 June
2016	NIOO, Wageningen UR, the Netherlands, 6 June
2016	Building the future of health, UMCG, Groningen, the Netherlands, 2 June
2016	Cell Biology, UMCG, Groningen, the Netherlands, 26 May
2016	Global human biomedicine project meeting in Barcelona, Spain, 11 April
2016	Workshop organizer at ESHG 2016, Barcelona, "How to develop your career in science"
2013	Organizing and teaching a graduate school PhD course,: "High- throughput next-generation biology", University Medical Centre Groningen (UMCG), Groningen, the Netherlands
2008 – present	Teaching a B.Sc. student course "Molecular Genetics and Genomics", University of Groningen, the Netherlands
2008 – present	Teaching a GUIDE PhD student course "Design and data analysis of microarray expression studies", UMCG, Groningen, the Netherlands
2006 – present	Teaching a Ph.D. student course "SNPs and human disease", Erasmus MC, Rotterdam, the Netherlands
2008, 2010	Teaching a PhD student course "Advances in population-based studies of complex genetic disorders", Erasmus MC, Rotterdam, the Netherlands
2006 – 2008	Teaching an M.Sc. student course "Bioinformatics", Utrecht University, Utrecht, the Netherlands

2004 – 2007 Teaching fundamentals of genetics to undergraduate medicine students, Utrecht University, Utrecht, the Netherlands

Outreach/Media

2017 Developing your career in science. Challenges when starting your own group (UG seminar)
2016 Interview on Radio Noord on the value of genetic data for improving health
2016 Interview on the ability to predict grey hair based on DNA, published in Volkskrant (Dutch national newspaper)
2014 Two-page interview on my research in NRC Handelsblad (Dutch national newspaper), 11 Jan. 2014 "*Draaien aan de knoppen van de genexpressie*" by Wim Köhler. http://www.nrc.nl/handelsblad/van/2014/januari/11/draaien-aan-de-knoppen-van-de-genexpressie-1336685
2013 Two radio interviews on national Dutch radio stations (Radio 1 and Radio 5)
2012 Initiator of "The Living Cell": a permanent exhibition of an interactive cell in the ERIBA research building, which won a Gold European Design Award (June 2013). www.bright.nl/de-leukste-biologieles-ooit-living-cell www.cleverfranke.com/cf/en/project/umcg---living-cell/project.php?id=156
2012 Interview and near full-page visualization on data analysis and visualization in NRC Handelsblad, 17 April 2012. Social media visualization: Is it possible to predict the weather based on Twitter messages? http://www.nrc.nl/handelsblad/van/2012/april/17/zon-wind-neerslag-en-veel-grijze-stippen-1093462
2009 – 2012 Involved in science exhibits for the general public (Qu3 pavilion) at the annual Noorderzon Performing Arts Festival, Groningen.
2010 Second prize in the *Academische Jaarprijs* competition on communicating science to a wide audience", team member for Dept. of Genetics, UMCG.
2009 Involved in explaining the topic of Healthy Aging to the King and Queen of Sweden and Queen Beatrix during their official visit to Groningen (April 23, 2009).

Extra Curricular Activities

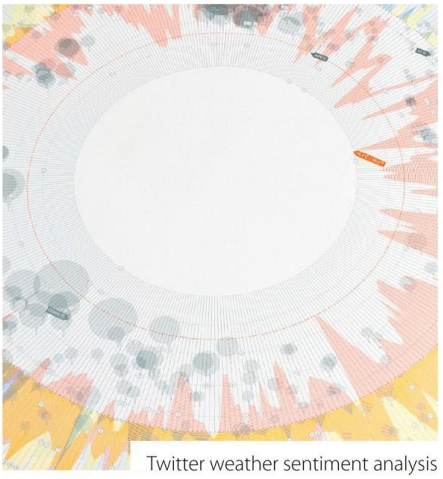
Graphic design and data visualisation

Co-founder of the graphics design company CleverFranke (with Thomas Clever and Gert Franke, http://www.cleverfranke.com) specializing in data visualization. Clients include Google, Elsevier, KLM, Philips, KPMG, Wired, Vodafone, and The New York Times.

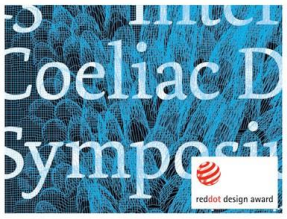
Responsible for various scientific art exhibitions and experiments, including:

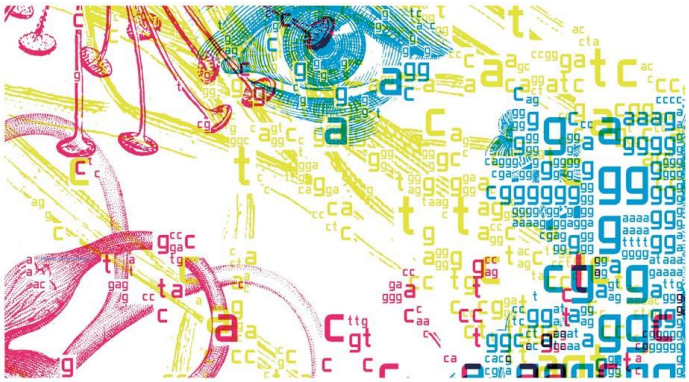
2013 The living cell: permanent exhibition of an interactive single cell in the ERIBA research institute (European Design Gold award)
2012 Social media visualization: Is it possible to predict the weather based on Twitter messages?
2010 Corporate identity Hubrecht Institute (Red Dot Design award)
2009 Corporate identity VIRGO consortium
2008 Life of a PhD student: Set of data visualizations on the life of being a PhD student
2008 Corporate identity International Celiac Disease Symposium (Red Dot Design award)
2007 Corporate identity Netherlands Proteomics Center
2007 Corporate identity Netherlands Bioinformatics Center (Dutch Design selection)

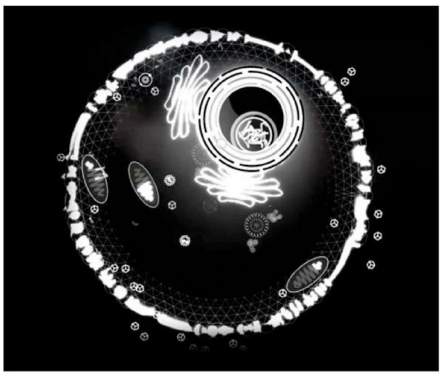
Scientific corporate identities and data visualisations:



Twitter weather sentiment analysis







Living Cell Exhibition

Research achievements

The research line that I have been developing over the last six years targets the development and application of computational algorithms to functional genomics datasets. The foundation for this work was laid during my PhD (2008, *cum laude*) when I developed new, cutting-edge computational and statistical methods for conducting genome-wide association studies (GWAS) and reconstructing gene networks using gene expression data.

After my graduation, I took up concurrent post-doc positions in London (Institute of Cell and Molecular Science, Queen Mary University), and Groningen (University Medical Centre Groningen). In London, I worked on the genetics of immune-mediated diseases (i.e. celiac disease) and in Groningen, on the development of methods to identify the effects of GWAS risk-SNPs on gene expression levels (Franke and Jansen, *Methods Mol Bio* 2009). My post-doc work resulted in a landmark paper (Dubois et al. *Nature Genetics* 2010, cited >620 times) that combined my work in London and Groningen. In this paper we demonstrated that there were many independent genetic risk-variants in celiac disease and that they mostly increase disease-risk by altering gene expression levels.

As senior author, I subsequently developed various computational methods and software to increase statistical power to identify such effects on gene expression (Westra et al. *Bioinformatics* 2010). By using these methods, I was able to demonstrate that the genetic risk-variants for many other diseases also have an effect on gene-expression levels (Fehrmann et al. *PLoS Genetics* 2011), and that these genetic variants often affect gene expression levels only in specific cell types (Fu et al. *PLoS Genetics* 2012, Westra et al. *PLoS Genetics* 2015). We showed that SNPs also affect the expression levels of many long non-coding genes (lncRNAs, Kumar et al. *PLoS Genetics* 2013) and that they can affect poly-adenylation of genes (Zhernakova et al. *PLoS Genetics* 2013).

Through a large-scale, blood eQTL meta-analysis consortium that I initiated in 2010 and that I am currently leading, we then identified downstream (*trans*-eQTL) effects for over 100 risk-SNPs (Westra et al. *Nature Genetics*, 2013). Our work has shown that, by using functional genomics approaches, we can identify previously unknown pathways for many different diseases.

Another considerable focus point is the development of novel methods to reuse publicly available data. We recently integrated gene expression data from 80,000 microarrays to accurately predict gene functions and to gain better insight into cancer (Fehrmann et al. *Nature Genetics* 2015), developed DEPICT (Pers et al. *Nature Communications* 2015) to use these predicted gene functions to better interpret GWAS findings, and developed strategies to integrate genetic variation, gene expression and methylation data. (my recent last-author papers include Zhernakova et al. *Nature Genetics* 2017 and Bonder et al. *Nature Genetics* 2017).

Currently, my group is concentrating on integrating multi-omics datasets, such as conducting large-scale *trans*-QTL meta-analyses in >30,000 samples, in conjunction with single-cell RNA-seq data (a paper reporting results of our single-cell RNA-seq eQTL work is currently under review by *Nature Genetics*), to identify likely causal genes for diseases that might be targetable by drugs, and to help develop computational strategies to increase the diagnostic yield in clinical genetics, by integrating RNA-seq, whole-genome sequencing data, and gene function prediction.

6 Sept. 2017

- - - - - - - - - -

Peer-reviewed publications/Impact

From Google Scholar, per 12 September 2017

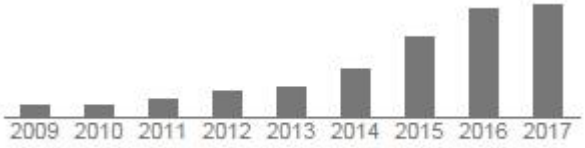
Number of peer-reviewed publications	173
Number of book chapters	2

Papers in high-impact journals: *Nature* (10x, IF 42); *Science* (2x, IF 31); *New Engl. J. Med.* (1, IF 59), *Nature Genetics* (36x, IF 31), *PLoS* Genetics (16x, IF 7)

Publication statistics Google Scholar

H-Index:	63
i10-index:	152
Total number of citations:	19016

Citations per year:



Franke's most highly cited, last-author paper has 644 citations to date: *Systematic identification of trans eQTLs as putative drivers of known disease associations*, Westra HJ et al. *Nature Genetics* 2013.

Full list of publications (in reverse chronological order)

Papers in high-impact journals (top 10%) are indicated:
* Impact factor > 8
** Impact factor > 20
*** Impact factor > 30

1. Matzaraki V, Gresnigt MS, Jaeger M, Ricaño-Ponce I, Johnson MD, Oosting M, **Franke L.**, Withoff S, Perfect JR, Joosten LAB, Kullberg BJ, van de Veerdonk FL, Jonkers I, Li Y, Wijmenga C, Netea MG, Kumar V. **An integrative genomics approach identifies novel pathways that influence candidaemia susceptibility**. *PLoS One. 2017;12(7):e0180824.*

2. Nolte IM, van der Most PJ, Alizadeh BZ, de Bakker PI, Boezen HM, Bruinenberg M, **Franke L.**, van der Harst P, Navis G, Postma DS, Rots MG, Stolk RP, Swertz MA, Wolffenbuttel BH, Wijmenga C, Snieder H. **Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study.** *Eur J Hum Genet. 2017;25(7):877-885.*

3. *** Tang AT, Choi JP, Kotzin JJ, Yang Y, Hong CC, Hobson N, Girard R, Zeineddine HA, Lightle R, Moore T, Cao Y, Shenkar R, Chen M, Mericko P, Yang J, Li L, Tanes C, Kobuley D, Võsa U, Whitehead KJ, Li DY, **Franke L**, Hart B, Schwaninger M, Henao-Mejia J, Morrison L, Kim H, Awad IA, Zheng X, Kahn ML. **Endothelial TLR4 and the microbiome drive cerebral cavernous malformations.** *Nature. 2017;545(7654):305-310.*

4. *** Day FR, Thompson DJ, Helgason H, Chasman DI, Finucane H, Sulem P, Ruth KS, Whalen S, Sarkar AK, Albrecht E, Altmaier E, Amini M, Barbieri CM, Boutin T, Campbell A, Demerath E, Giri A, He C, Hottenga JJ, Karlsson R, Kolcic I, Loh PR, Lunetta KL, Mangino M, Marco B, McMahon G, Medland SE, Nolte IM, Noordam R, Nutile T, Paternoster L, Perjakova N, Porcu E, Rose LM, Schraut KE, Segrè AV, Smith AV, Stolk L, Teumer A, Andrulis IL, Bandinelli S, Beckmann MW, Benitez J, Bergmann S, Bochud M, Boerwinkle E, Bojesen SE, Bolla MK, Brand JS, Brauch H, Brenner H, Broer L, Brüning T, Buring JE, Campbell H, Catamo E, Chanock S, Chenevix-Trench G, Corre T, Couch FJ, Cousminer DL, Cox A, Crisponi L, Czene K, Davey Smith G, de Geus EJCN, de Mutsert R, De Vivo I, Dennis J, Devilee P, Dos-Santos-Silva I, Dunning AM, Eriksson JG, Fasching PA, Fernández-Rhodes L, Ferrucci L, Flesch-Janys D, **Franke L**, Gabrielson M, Gandin I, Giles GG, Grallert H, Gudbjartsson DF, Guénel P, Hall P, Hallberg E, Hamann U, Harris TB, Hartman CA, Heiss G, Hooning MJ, Hopper JL, Hu F, Hunter DJ, Ikram MA, Im HK, Järvelin MR, Joshi PK, Karasik D, Kellis M, Kutalik Z, LaChance G, Lambrechts D, Langenberg C, Launer LJ, Laven JSE, Lenarduzzi S, Li J, Lind PA, Lindstrom S, Liu Y, Luan J, Mägi R, Mannermaa A, Mbarek H, McCarthy MI, Meisinger C, Meitinger T, Menni C, Metspalu A, Michailidou K, Milani L, Milne RL, Montgomery GW, Mulligan AM, Nalls MA, Navarro P, Nevanlinna H, Nyholt DR, Oldehinkel AJ, O'Mara TA, Padmanabhan S, Palotie A, Pedersen N, Peters A, Peto J, Pharoah PDP, Pouta A, Radice P, Rahman I, Ring SM, Robino A, Rosendaal FR, Rudan I, Rueedi R, Ruggiero D, Sala CF, Schmidt MK, Scott RA, Shah M, Sorice R, Southey MC, Sovio U, Stampfer M, Steri M, Strauch K, Tanaka T, Tikkanen E, Timpson NJ, Traglia M, Truong T, Tyrer JP, Uitterlinden AG, Edwards DRV, Vitart V, Völker U, Vollenweider P, Wang Q, Widen E, van Dijk KW, Willemsen G, Winqvist R, Wolffenbuttel BHR, Zhao JH, Zoledziewska M, Zygmunt M, Alizadeh BZ, Boomsma DI, Ciullo M, Cucca F, Esko T, Franceschini N, Gieger C, Gudnason V, Hayward C, Kraft P, Lawlor DA, Magnusson PKE, Martin NG, Mook-Kanamori DO, Nohr EA, Polasek O, Porteous D, Price AL, Ridker PM, Snieder H, Spector TD, Stöckl D, Toniolo D, Ulivi S, Visser JA, Völzke H, Wareham NJ, Wilson JF; LifeLines Cohort Study; InterAct Consortium; kConFab/AOCS Investigators; Endometrial Cancer Association Consortium; Ovarian Cancer Association Consortium; PRACTICAL consortium, Spurdle AB, Thorsteindottir U, Pollard KS, Easton DF, Tung JY, Chang-Claude J, Hinds D, Murray A, Murabito JM, Stefansson K, Ong KK, Perry JRB. **Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk.** *Nat Genet. 2017. doi: 10.1038/ng.3841.*

5. Nolte IM, van der Most PJ, Alizadeh BZ, de Bakker PI, Boezen HM, Bruinenberg M, **Franke L**, van der Harst P, Navis G, Postma DS, Rots MG, Stolk RP, Swertz MA, Wolffenbuttel BH, Wijmenga C, Snieder H. Missing heritability: is the gap closing? **An analysis of 32 complex traits in the Lifelines Cohort Study.** *Eur J Hum Genet. 2017. doi: 10.1038/ejhg.2017.50.*

6. * Wild PS, Felix JF, Schillert A, Teumer A, Chen MH, Leening MJG, Völker U, Großmann V, Brody JA, Irvin MR, Shah SJ, Pramana S, Lieb W, Schmidt R, Stanton AV, Malzahn D, Smith AV, Sundström J, Minelli C, Ruggiero D, Lyytikäinen LP, Tiller D, Smith JG, Monnereau C, Di Tullio MR, Musani SK, Morrison AC, Pers TH, Morley M, Kleber ME, Aragam J, Benjamin EJ, Bis JC, Bisping E, Broeckel U, Cheng S, Deckers JW, Del Greco M F, Edelmann F, Fornage M, **Franke L**, Friedrich N, Harris TB, Hofer E, Hofman A, Huang J, Hughes AD, Kähönen M, Investigators K, Kruppa J, Lackner KJ, Lannfelt L, Laskowski R, Launer LJ, Leosdottir M, Lin H, Lindgren CM, Loley C, MacRae CA, Mascalzoni D, Mayet J, Medenwald D, Morris AP, Müller C, Müller-Nurasyid M, Nappo S, Nilsson PM, Nuding S, Nutile T, Peters A, Pfeufer A, Pietzner D, Pramstaller PP, Raitakari OT, Rice KM, Rivadeneira F, Rotter JI, Ruohonen ST, Sacco RL, Samdarshi TE, Schmidt H, Sharp ASP, Shields DC, Sorice R, Sotoodehnia N, Stricker BH, Surendran P, Thom S, Töglhofer AM, Uitterlinden AG, Wachter R, Völzke H, Ziegler A, Münzel T, März W, Cappola TP, Hirschhorn JN, Mitchell GF, Smith NL, Fox ER, Dueker ND, Jaddoe VWV, Melander O, Russ M, Lehtimäki T, Ciullo M, Hicks AA, Lind L, Gudnason V, Pieske B, Barron AJ, Zweiker R, Schunkert H, Ingelsson E, Liu K, Arnett DK, Psaty BM, Blankenberg S, Larson MG, Felix SB, Franco OH, Zeller T, Vasan RS, Dörr M. **Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function.** *J Clin Invest. 2017;127(5):1798-1812.*

7. Acuna-Hidalgo R, Deriziotis P, Steehouwer M, Gilissen C, Graham SA, van Dam S, Hoover-Fong J, Telegrafi AB, Destree A, Smigiel R, Lambie LA, Kayserili H, Altunoglu U, Lapi E, Uzielli ML, Aracena M, Nur BG, Mihci E, Moreira LM, Borges Ferreira V, Horovitz DD, da Rocha KM, Jezela-Stanek A, Brooks AS, Reutter H, Cohen JS, Fatemi A, Smitka M, Grebe TA, Di Donato N, Deshpande C, Vandersteen A, Marques Lourenço C, Dufke A, Rossier E, Andre G, Baumer A, Spencer C, McGaughran J, **Franke L**, Veltman JA, De Vries BB, Schinzel A, Fisher SE, Hoischen A, van Bon BW. **Overlapping SETBP1 gain-of-function mutations in Schinzel-Giedion syndrome and hematologic malignancies.** *PLoS Genet. 2017;13(3):e1006683.*

8. * McLaughlin RL, Schijven D, van Rheenen W, van Eijk KR, O'Brien M, Kahn RS, Ophoff RA, Goris A, Bradley DG, Al-Chalabi A, van den Berg LH, Luykx JJ, Hardiman O, Veldink JH; Project MinE GWAS Consortium; **Schizophrenia Working Group of the Psychiatric Genomics Consortium**. **Genetic correlation between amyotrophic lateral sclerosis and schizophrenia.** *Nat Commun. 2017;8:14774.*

9. Kasela S, Kisand K, Tserel L, Kaleviste E, Remm A, Fischer K, Esko T, Westra HJ, Fairfax BP, Makino S, Knight JC, **Franke L**, Metspalu A, Peterson P, Milani L. **Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells.** *PLoS Genet. 2017;13(3):e1006643.*

10. Kreiner E, Waage J, Standl M, Brix S, Pers TH, Couto Alves A, Warrington NM, Tiesler CM, Fuertes E, **Franke L**, Hirschhorn JN, James A, Simpson A, Tung JY, Koppelman GH, Postma DS, Pennell CE, Jarvelin MR, Custovic A, Timpson N, Ferreira MA, Strachan DP, Henderson J, Hinds D, Bisgaard H, Bønnelykke K. **Shared genetic variants suggest common pathways in allergy and autoimmune diseases.** *J Allergy Clin Immunol. 2017. pii: S0091-6749(17)30207-5.*

11. Soderquest K, Hertweck A, Giambartolomei C, Henderson S, Mohamed R, Goldberg R, Perucha E, **Franke L**, Herrero J, Plagnol V, Jenner RG, Lord GM. **Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease.** *PLoS Genet. 2017;13(2):e1006587.*

12. Van der Velde KJ, de Boer EN, van Diemen CC, Sikkema-Raddatz B, Abbott KM, Knopperts A, **Franke L**, Sijmons RH, de Koning TJ, Wijmenga C, Sinke RJ, Swertz MA. **GAVIN: Gene-Aware Variant INterpretation for medical sequencing.** *Genome Biol. 2017;18(1):6.*

13. Van Dam S, Võsa U, van der Graaf A, **Franke L**, de Magalhães JP. **Gene co-expression analysis for functional classification and gene-disease predictions.** *Brief Bioinform. 2017. pii: bbw139.*

14. *** Wahl S, Drong A, Lehne B, Loh M, Scott WR, Kunze S, Tsai PC, Ried JS, Zhang W, Yang Y, Tan S, Fiorito G, **Franke L**, Guarrera S, Kasela S, Kriebel J, Richmond RC, Adamo M, Afzal U, Ala-Korpela M, Albetti B, Ammerpohl O, Apperley JF, Beekman M, Bertazzi PA, Black SL, Blancher C, Bonder MJ, Brosch M, Carstensen-Kirberg M, de Craen AJ, de Lusignan S, Dehghan A, Elkalaawy M, Fischer K, Franco OH, Gaunt TR, Hampe J, Hashemi M, Isaacs A, Jenkinson A, Jha S, Kato N, Krogh V, Laffan M, Meisinger C, Meitinger T, Mok ZY, Motta V, Ng HK, Nikolakopoulou Z, Nteliopoulos G, Panico S, Pervjakova N, Prokisch H, Rathmann W, Roden M, Rota F, Rozario MA, Sandling JK, Schafmayer C, Schramm K, Siebert R, Slagboom PE, Soininen P, Stolk L, Strauch K, Tai ES, Tarantini L, Thorand B, Tigchelaar EF, Tumino R, Uitterlinden AG, van Duijn C, van Meurs JB, Vineis P, Wickremasinghe AR, Wijmenga C, Yang TP, Yuan W, Zhernakova A, Batterham RL, Smith GD, Deloukas P, Heijmans BT, Herder C, Hofman A, Lindgren CM, Milani L, van der Harst P, Peters A, Illig T, Relton CL, Waldenberger M, Järvelin MR, Bollati V, Soong R, Spector TD, Scott J, McCarthy MI, Elliott P, Bell JT, Matullo G, Gieger C, Kooner JS, Grallert H, Chambers JC. **Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity.** *Nature. 2017;541(7635):81-86.*

15. Amini M, Bashirova D, Prins BP, Corpeleijn E; LifeLines Cohort Study, Bruinenberg M, **Franke L**, Harst PV, Navis G, Wolffenbuttel BH, Stolk RP, Wijmenga C, Postma DS, Koppelman GH, Boezen HM, Vonk J, Snieder H, Alizadeh BZ. **Eosinophil count is a common factor for complex metabolic and pulmonary traits and diseases: the LifeLines Cohort Study.** *PLoS One. 2016;11(12):e0168480.*

16. *** Bonder MJ, Luijk R, Zhernakova DV, Moed M, Deelen P, Vermaat M, van Iterson M, van Dijk F, van Galen M, Bot J, Slieker RC, Jhamai PM, Verbiest M, Suchiman HE, Verkerk M, van der Breggen R, van Rooij J, Lakenberg N, Arindrarto W, Kielbasa SM, Jonkers I, van 't Hof P, Nooren I, Beekman M, Deelen J, van Heemst D, Zhernakova A, Tigchelaar EF, Swertz MA, Hofman A, Uitterlinden AG, Pool R, van Dongen J, Hottenga JJ, Stehouwer CD, van der Kallen CJ, Schalkwijk CG, van den Berg LH, van Zwet EW, Mei H, Li Y, Lemire M, Hudson TJ; BIOS Consortium, Slagboom PE, Wijmenga C, Veldink JH, van Greevenbroek MM, van Duijn CM, Boomsma DI, Isaacs A, Jansen R, van Meurs JB, 't Hoen PA, **Franke L**, Heijmans BT. **Disease variants alter transcription factor levels and methylation of their binding sites.** *Nat Genet. 2017;49(1):131-138.*

17. *** Zhernakova DV, Deelen P, Vermaat M, van Iterson M, van Galen M, Arindrarto W, van 't Hof P, Mei H, van Dijk F, Westra HJ, Bonder MJ, van Rooij J, Verkerk M, Jhamai PM, Moed M, Kielbasa SM, Bot J, Nooren I, Pool R, van Dongen J, Hottenga JJ, Stehouwer CD, van der Kallen CJ, Schalkwijk CG, Zhernakova A, Li Y, Tigchelaar EF, de Klein N, Beekman M, Deelen J, van Heemst D, van den Berg LH, Hofman A, Uitterlinden AG, van Greevenbroek MM, Veldink JH, Boomsma DI, van Duijn CM, Wijmenga C, Slagboom PE, Swertz MA, Isaacs A, van Meurs JB, Jansen R, Heijmans BT, 't Hoen PA, **Franke L. Identification of context-dependent expression quantitative trait loci in whole blood.** *Nat Genet. 2017;49(1):139-145.*

18. Kogelman LJ, Fu J, **Franke L**, Greve JW, Hofker M, Rensen SS, Kadarmideen HN. **Inter-tissue gene co-expression networks between metabolically healthy and unhealthy obese individuals.** *PLoS One. 2016;11(12):e0167519.*

19. Aguirre-Gamboa R, Joosten I, Urbano PC, van der Molen RG, van Rijssen E, van Cranenbroek B, Oosting M, Smeekens S, Jaeger M, Zorro M, Withoff S, van Herwaarden AE, Sweep FC, Netea RT, Swertz MA, **Franke L**, Xavier RJ, Joosten LA, Netea MG, Wijmenga C, Kumar V, Li Y, Koenen HJ. **Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits.** *Cell Rep. 2016;17(9):2474-2487.*

20. * Imhann F, Vich Vila A, Bonder MJ, Fu J, Gevers D, Visschedijk MC, Spekhorst LM, Alberts R, **Franke L**, van Dullemen HM, Ter Steege RW, Huttenhower C, Dijkstra G, Xavier RJ, Festen EA, Wijmenga C, Zhernakova A, Weersma RK. **Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease.** *Gut. 2016. pii: gutjnl-2016-312135.*

21. ** Li Y, Oosting M, Smeekens SP, Jaeger M, Aguirre-Gamboa R, Le KT, Deelen P, Ricaño-Ponce I, Schoffelen T, Jansen AF, Swertz MA, Withoff S, van de Vosse E, van Deuren M, van de Veerdonk F, Zhernakova A, van der Meer JW, Xavier RJ, **Franke L**, Joosten LA, Wijmenga C, Kumar V, Netea MG. **A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans.** *Cell. 2016;167(4):1099-1110.e14.*

22. * Marioni RE, Ritchie SJ, Joshi PK, Hagenaars SP, Okbay A, Fischer K, Adams MJ, Hill WD, Davies G; **Social Science Genetic Association Consortium**, Nagy R, Amador C, Läll K, Metspalu A, Liewald DC, Campbell A, Wilson JF, Hayward C, Esko T, Porteous DJ, Gale CR, Deary IJ. **Genetic variants linked to education predict longevity.** *Proc Natl Acad Sci U S A. 2016;113(47):13366-13371.*

23. *** Barban N, Jansen R, de Vlaming R, Vaez A, Mandemakers JJ, Tropf FC, Shen X, Wilson JF, Chasman DI, Nolte IM, Tragante V, van der Laan SW, Perry JR, Kong A; BIOS Consortium, Ahluwalia TS, Albrecht E, Yerges-Armstrong L, Atzmon G, Auro K, Ayers K, Bakshi A, Ben-Avraham D, Berger K, Bergman A, Bertram L, Bielak LF, Bjornsdottir G, Bonder MJ, Broer L, Bui M, Barbieri C, Cavadino A, Chavarro JE, Turman C, Concas MP, Cordell HJ, Davies G, Eibich P, Eriksson N, Esko T, Eriksson J, Falahi F, Felix JF, Fontana MA, **Franke L**, Gandin I, Gaskins AJ, Gieger C, Gunderson EP, Guo X, Hayward C, He C, Hofer E, Huang H, Joshi PK, Kanoni S, Karlsson R, Kiechl S, Kifley A, Kluttig A, Kraft P, Lagou V, Lecoeur C, Lahti J, Li-Gao R, Lind PA, Liu T, Makalic E, Mamasoula C, Matteson L, Mbarek H, McArdle PF, McMahon G, Meddens SF, Mihailov E, Miller M, Missmer SA, Monnereau C, van der Most PJ, Myhre R, Nalls MA, Nutile T, Kalafati IP, Porcu E, Prokopenko I, Rajan KB, Rich-Edwards J, Rietveld CA, Robino A, Rose LM, Rueedi R, Ryan KA, Saba Y, Schmidt D, Smith JA, Stolk L, Streeten E, Tönjes A, Thorleifsson G, Ulivi S, Wedenoja J, Wellmann J, Willeit P, Yao J, Yengo L, Zhao JH, Zhao W, Zhernakova DV, Amin N, Andrews H, Balkau B, Barzilai N, Bergmann S, Biino G, Bisgaard H, Bønnelykke K, Boomsma DI, Buring JE, Campbell H, Cappellani S, Ciullo M, Cox SR, Cucca F, Toniolo D, Davey-Smith G, Deary IJ, Dedoussis G, Deloukas P, van Duijn CM, de Geus EJ, Eriksson JG, Evans DA, Faul JD, Sala CF, Froguel P, Gasparini P, Girotto G, Grabe HJ, Greiser KH, Groenen PJ, de Haan HG, Haerting J, Harris TB, Heath AC, Heikkilä K, Hofman A, Homuth G, Holliday EG, Hopper J, Hyppönen E, Jacobsson B, Jaddoe VW, Johannesson M, Jugessur A, Kähönen M, Kajantie E, Kardia SL, Keavney B, Kolcic I, Koponen P, Kovacs P, Kronenberg F, Kutalik Z, La Bianca M, Lachance G, Iacono WG, Lai S, Lehtimäki T, Liewald DC; LifeLines Cohort Study, Lindgren CM, Liu Y, Luben R, Lucht M, Luoto R, Magnus P, Magnusson PK, Martin NG, McGue M, McQuillan R, Medland SE, Meisinger C, Mellström D, Metspalu A, Traglia M, Milani L, Mitchell P, Montgomery GW, Mook-Kanamori D, de Mutsert R, Nohr EA, Ohlsson C, Olsen J, Ong KK, Paternoster L, Pattie A, Penninx BW, Perola M, Peyser PA, Pirastu M, Polasek O, Power C, Kaprio J, Raffel LJ, Räikkönen K, Raitakari O, Ridker PM, Ring SM, Roll K, Rudan I, Ruggiero D, Rujescu D, Salomaa V, Schlessinger D, Schmidt H, Schmidt R, Schupf N, Smit J, Sorice R, Spector TD, Starr JM, Stöckl D, Strauch K, Stumvoll M, Swertz MA, Thorsteinsdottir U, Thurik AR, Timpson NJ, Tung JY, Uitterlinden AG, Vaccargiu S, Viikari J, Vitart V, Völzke H, Vollenweider P, Vuckovic D, Waage J, Wagner GG, Wang JJ, Wareham NJ, Weir DR, Willemsen G, Willeit J, Wright AF, Zondervan KT, Stefansson K, Krueger RF, Lee JJ, Benjamin DJ, Cesarini D, Koellinger PD, den Hoed M, Snieder H, Mills MC. **Genome-wide analysis identifies 12 loci influencing human reproductive behavior.** *Nat Genet. 2016;48(12):1462-1472.*

24. Kassam I, Qi T, Lloyd-Jones L, Holloway A, Jan Bonder M, Henders AK, Martin NG, Powell JE, **Franke L**, Montgomery GW, Visscher PM, McRae AF. **Evidence for mitochondrial genetic control of autosomal gene expression.** *Hum Mol Genet. 2016;25(24):5332-5338.*

25. *** Bonder MJ, Kurilshikov A, Tigchelaar EF, Mujagic Z, Imhann F, Vila AV, Deelen P, Vatanen T, Schirmer M, Smeekens SP, Zhernakova DV, Jankipersadsing SA, Jaeger M, Oosting M, Cenit MC, Masclee AA, Swertz MA, Li Y, Kumar V, Joosten L, Harmsen H, Weersma RK, **Franke L**, Hofker MH, Xavier RJ, Jonkers D, Netea MG, Wijmenga C, Fu J, Zhernakova A. **The effect of host genetics on the gut microbiome.** *Nat Genet. 2016;48(11):1407-1412.*

26. *** Iotchkova V, Huang J, Morris JA, Jain D, Barbieri C, Walter K, Min JL, Chen L, Astle W, Cocca M, Deelen P, Elding H, Farmaki AE, Franklin CS, Franberg M, Gaunt TR, Hofman A, Jiang T, Kleber ME, Lachance G, Luan J, Malerba G, Matchan A, Mead D, Memari Y, Ntalla I, Panoutsopoulou K, Pazoki R, Perry JR, Rivadeneira F, Sabater-Lleal M, Sennblad B, Shin SY, Southam L, Traglia M, van Dijk F, van Leeuwen EM, Zaza G, Zhang W; UK10K Consortium, Amin N, Butterworth A, Chambers JC, Dedoussis G, Dehghan A, Franco OH, **Franke L**, Frontini M, Gambaro G, Gasparini P, Hamsten A, Issacs A, Kooner JS, Kooperberg C, Langenberg C, Marz W, Scott RA, Swertz MA, Toniolo D, Uitterlinden AG, van Duijn CM, Watkins H, Zeggini E, Maurano MT, Timpson NJ, Reiner AP, Auer PL, Soranzo N. **Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps.** *Nat Genet. 2016;48(11):1303-1312*.

27. Van der Harst P, van Setten J, Verweij N, Vogler G, **Franke L**, Maurano MT, Wang X, Mateo Leach I, Eijgelsheim M, Sotoodehnia N, Hayward C, Sorice R, Meirelles O, Lyytikäinen LP, Polašek O, Tanaka T, Arking DE, Ulivi S, Trompet S, Müller-Nurasyid M, Smith AV, Dörr M, Kerr KF, Magnani JW, Del Greco M F, Zhang W, Nolte IM, Silva CT, Padmanabhan S, Tragante V, Esko T, Abecasis GR, Adriaens ME, Andersen K, Barnett P, Bis JC, Bodmer R, Buckley BM, Campbell H, Cannon MV, Chakravarti A, Chen LY, Delitala A, Devereux RB, Doevendans PA, Dominiczak AF, Ferrucci L, Ford I, Gieger C, Harris TB, Haugen E, Heinig M, Hernandez DG, Hillege HL, Hirschhorn JN, Hofman A, Hubner N, Hwang SJ, Iorio A, Kähönen M, Kellis M, Kolcic I, Kooner IK, Kooner JS, Kors JA, Lakatta EG, Lage K, Launer LJ, Levy D, Lundby A, Macfarlane PW, May D, Meitinger T, Metspalu A, Nappo S, Naitza S, Neph S, Nord AS, Nutile T, Okin PM, Olsen JV, Oostra BA, Penninger JM, Pennacchio LA, Pers TH, Perz S, Peters A, Pinto YM, Pfeufer A, Pilia MG, Pramstaller PP, Prins BP, Raitakari OT, Raychaudhuri S, Rice KM, Rossin EJ, Rotter JI, Schafer S, Schlessinger D, Schmidt CO, Sehmi J, Silljé HH, Sinagra G, Sinner MF, Slowikowski K, Soliman EZ, Spector TD, Spiering W, Stamatoyannopoulos JA, Stolk RP, Strauch K, Tan ST, Tarasov KV, Trinh B, Uitterlinden AG, van den Boogaard M, van Duijn CM, van Gilst WH, Viikari JS, Visscher PM, Vitart V, Völker U, Waldenberger M, Weichenberger CX, Westra HJ, Wijmenga C, Wolffenbuttel BH, Yang J, Bezzina CR, Munroe PB, Snieder H, Wright AF, Rudan I, Boyer LA, Asselbergs FW, van Veldhuisen DJ, Stricker BH, Psaty BM, Ciullo M, Sanna S, Lehtimäki T, Wilson JF, Bandinelli S, Alonso A, Gasparini P, Jukema JW, Kääb S, Gudnason V, Felix SB, Heckbert SR, de Boer RA, Newton-Cheh C, Hicks AA, Chambers JC, Jamshidi Y, Visel A, Christoffels VM, Isaacs A, Samani NJ, de Bakker PI. **52 genetic loci influencing myocardial mass.** *J Am Coll Cardiol. 2016;68(13):1435-48.*

28. Slieker RC, van Iterson M, Luijk R, Beekman M, Zhernakova DV, Moed MH, Mei H, van Galen M, Deelen P, Bonder MJ, Zhernakova A, Uitterlinden AG, Tigchelaar EF, Stehouwer CD, Schalkwijk CG, van der Kallen CJ, Hofman A, van Heemst D, de Geus EJ, van Dongen J, Deelen J, van den Berg LH, van Meurs J, Jansen R, 't Hoen PA, **Franke L**, Wijmenga C, Veldink JH, Swertz MA, van Greevenbroek MM, van Duijn CM, Boomsma DI; **BIOS consortium**, Slagboom PE, Heijmans BT. **Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms.** *Genome Biol. 2016;17(1):191.*

29. *** Ehret GB, Ferreira T, Chasman DI, Jackson AU, Schmidt EM, Johnson T, Thorleifsson G, Luan J, Donnelly LA, Kanoni S, Petersen AK, Pihur V, Strawbridge RJ, Shungin D, Hughes MF, Meirelles O, Kaakinen M, Bouatia-Naji N, Kristiansson K, Shah S, Kleber ME, Guo X, Lyytikäinen LP, Fava C, Eriksson N, Nolte IM, Magnusson PK, Salfati EL, Rallidis LS, Theusch E, Smith AJ, Folkersen L, Witkowska K, Pers TH, Joehanes R, Kim SK, Lataniotis L, Jansen R, Johnson AD, Warren H, Kim YJ, Zhao W, Wu Y, Tayo BO, Bochud M; CHARGE-EchoGen Consortium; CHARGE-HF Consortium; Wellcome Trust Case Control Consortium, Absher D, Adair LS, Amin N, Arking DE, Axelsson T, Baldassarre D, Balkau B, Bandinelli S, Barnes MR, Barroso I, Bevan S, Bis JC, Bjornsdottir G, Boehnke M, Boerwinkle E,

Bonnycastle LL, Boomsma DI, Bornstein SR, Brown MJ, Burnier M, Cabrera CP, Chambers JC, Chang IS, Cheng CY, Chines PS, Chung RH, Collins FS, Connell JM, Döring A, Dallongeville J, Danesh J, de Faire U, Delgado G, Dominiczak AF, Doney AS, Drenos F, Edkins S, Eicher JD, Elosua R, Enroth S, Erdmann J, Eriksson P, Esko T, Evangelou E, Evans A, Fall T, Farrall M, Felix JF, Ferrières J, Ferrucci L, Fornage M, Forrester T, Franceschini N, Franco OH, Franco-Cereceda A, Fraser RM, Ganesh SK, Gao H, Gertow K, Gianfagna F, Gigante B, Giulianini F, Goel A, Goodall AH, Goodarzi MO, Gorski M, Gräßler J, Groves CJ, Gudnason V, Gyllensten U, Hallmans G, Hartikainen AL, Hassinen M, Havulinna AS, Hayward C, Hercberg S, Herzig KH, Hicks AA, Hingorani AD, Hirschhorn JN, Hofman A, Holmen J, Holmen OL, Hottenga JJ, Howard P, Hsiung CA, Hunt SC, Ikram MA, Illig T, Iribarren C, Jensen RA, Kähönen M, Kang HM, Kathiresan S, Keating BJ, Khaw KT, Kim YK, Kim E, Kivimaki M, Klopp N, Kolovou G, Komulainen P, Kooner JS, Kosova G, Krauss RM, Kuh D, Kutalik Z, Kuusisto J, Kvaløy K, Lakka TA, Lee NR, Lee IT, Lee WJ, Levy D, Li X, Liang KW, Lin H, Lin L, Lindström J, Lobbens S, Männistö S, Müller G, Müller-Nurasyid M, Mach F, Markus HS, Marouli E, McCarthy MI, McKenzie CA, Meneton P, Menni C, Metspalu A, Mijatovic V, Moilanen L, Montasser ME, Morris AD, Morrison AC, Mulas A, Nagaraja R, Narisu N, Nikus K, O'Donnell CJ, O'Reilly PF, Ong KK, Paccaud F, Palmer CD, Parsa A, Pedersen NL, Penninx BW, Perola M, Peters A, Poulter N, Pramstaller PP, Psaty BM, Quertermous T, Rao DC, Rasheed A, Rayner NW, Renström F, Rettig R, Rice KM, Roberts R, Rose LM, Rossouw J, Samani NJ, Sanna S, Saramies J, Schunkert H, Sebert S, Sheu WH, Shin YA, Sim X, Smit JH, Smith AV, Sosa MX, Spector TD, Stančáková A, Stanton AV, Stirrups KE, Stringham HM, Sundstrom J, Swift AJ, Syvänen AC, Tai ES, Tanaka T, Tarasov KV, Teumer A, Thorsteinsdottir U, Tobin MD, Tremoli E, Uitterlinden AG, Uusitupa M, Vaez A, Vaidya D, van Duijn CM, van Iperen EP, Vasan RS, Verwoert GC, Virtamo J, Vitart V, Voight BF, Vollenweider P, Wagner A, Wain LV, Wareham NJ, Watkins H, Weder AB, Westra HJ, Wilks R, Wilsgaard T, Wilson JF, Wong TY, Yang TP, Yao J, Yengo L, Zhang W, Zhao JH, Zhu X, Bovet P, Cooper RS, Mohlke KL, Saleheen D, Lee JY, Elliott P, Gierman HJ, Willer CJ, **Franke L**, Hovingh GK, Taylor KD, Dedoussis G, Sever P, Wong A, Lind L, Assimes TL, Njølstad I, Schwarz PE, Langenberg C, Snieder H, Caulfield MJ, Melander O, Laakso M, Saltevo J, Rauramaa R, Tuomilehto J, Ingelsson E, Lehtimäki T, Hveem K, Palmas W, März W, Kumari M, Salomaa V, Chen YD, Rotter JI, Froguel P, Jarvelin MR, Lakatta EG, Kuulasmaa K, Franks PW, Hamsten A, Wichmann HE, Palmer CN, Stefansson K, Ridker PM, Loos RJ, Chakravarti A, Deloukas P, Morris AP, Newton-Cheh C, Munroe PB. **The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals.** *Nat Genet. 2016;48(10):1171-84.*

30. *** Netea MG, Joosten LA, Li Y, Kumar V, Oosting M, Smeekens S, Jaeger M, Ter Horst R, Schirmer M, Vlamakis H, Notebaart R, Pavelka N, Aguirre-Gamboa RR, Swertz MA, Tunjungputri RN, van de Heijden W, Franzosa EA, Ng A, Graham D, Lassen K, Schraa K, Netea-Maier R, Smit J, de Mast Q, van de Veerdonk F, Kullberg BJ, Tack C, van de Munckhof I, Rutten J, van der Graaf J, **Franke L**, Hofker M, Jonkers I, Platteel M, Maatman A, Fu J, Zhernakova A, van der Meer JW, Dinarello CA, van der Ven A, Huttenhouwer C, Koenen H, Joosten I, Xavier RJ, Wijmenga C. **Understanding human immune function using the resources from the Human Functional Genomics Project.** *Nat Med. 2016;22(8):831-3.*

31. *** van Rheenen W, Shatunov A, Dekker AM, McLaughlin RL, Diekstra FP, Pulit SL, van der Spek RA, Võsa U, de Jong S, Robinson MR, Yang J, Fogh I, van Doormaal PT, Tazelaar GH, Koppers M, Blokhuis AM, Sproviero W, Jones AR, Kenna KP, van Eijk KR, Harschnitz O, Schellevis RD, Brands WJ, Medic J, Menelaou A, Vajda A, Ticozzi N, Lin K, Rogelj B, Vrabec K, Ravnik-Glavač M, Koritnik B, Zidar J, Leonardis L, Grošelj LD, Millecamps S, Salachas F, Meininger V, de Carvalho M, Pinto S, Mora JS, Rojas-García R, Polak M, Chandran S, Colville S, Swingler R, Morrison KE, Shaw PJ, Hardy J, Orrell RW, Pittman A, Sidle K, Fratta P, Malaspina A, Topp S, Petri S, Abdulla S, Drepper C, Sendtner M, Meyer T, Ophoff RA, Staats KA, Wiedau-Pazos M, Lomen-Hoerth C, Van Deerlin VM, Trojanowski JQ, Elman L, McCluskey L, Basak AN, Tunca C, Hamzeiy H, Parman Y, Meitinger T, Lichtner P, Radivojkov-Blagojevic M, Andres CR, Maurel C, Bensimon G, Landwehrmeyer B, Brice A, Payan CA, Saker-Delye S, Dürr A, Wood NW, Tittmann L, Lieb W, Franke A, Rietschel M, Cichon S, Nöthen MM, Amouyel P, Tzourio C, Dartigues JF, Uitterlinden AG, Rivadeneira F, Estrada K, Hofman A, Curtis C, Blauw HM, van der Kooi AJ, de Visser M, Goris A, Weber M, Shaw CE, Smith BN, Pansarasa O, Cereda C, Del Bo R, Comi GP, D'Alfonso S, Bertolin C, Sorarù G, Mazzini L, Pensato V, Gellera C, Tiloca C, Ratti A, Calvo A, Moglia C, Brunetti M, Arcuti S, Capozzo R, Zecca C, Lunetta C, Penco S, Riva N, Padovani A, Filosto M, Muller B, Stuit RJ; PARALS Registry; SLALOM Group; SLAP Registry; FALS Sequencing Consortium; SLAGEN Consortium; NNIPPS Study Group, Blair I, Zhang K, McCann EP, Fifita JA, Nicholson GA, Rowe DB, Pamphlett R, Kiernan MC, Grosskreutz J, Witte OW, Ringer T, Prell T, Stubendorff B, Kurth I, Hübner CA, Leigh PN, Casale F, Chio A, Beghi E, Pupillo E, Tortelli R, Logroscino G, Powell J, Ludolph AC, Weishaupt JH, Robberecht W, Van Damme P, **Franke L**, Pers TH, Brown RH, Glass JD, Landers JE, Hardiman O, Andersen PM, Corcia P, Vourc'h P, Silani V, Wray NR, Visscher PM, de Bakker PI, van Es MA, Pasterkamp RJ, Lewis CM, Breen G, Al-Chalabi A, van den Berg LH, Veldink JH. **Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis.** *Nat Genet. 2016;48(9):1043-8.*

32. *** Li Y, Oosting M, Deelen P, Ricaño-Ponce I, Smeekens S, Jaeger M, Matzaraki V, Swertz MA, Xavier RJ, **Franke L**, Wijmenga C, Joosten LA, Kumar V, Netea MG. **Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi.** *Nat Med. 2016;22(8):952-60.*

33. * Ben-David U, Ha G, Khadka P, Jin X, Wong B, **Franke L**, Golub TR. **The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis.** *Nat Commun. 2016;7:12160.*

34. Dekkers KF, van Iterson M, Slieker RC, Moed MH, Bonder MJ, van Galen M, Mei H, Zhernakova DV, van den Berg LH, Deelen J, van Dongen J, van Heemst D, Hofman A, Hottenga JJ, van der Kallen CJ, Schalkwijk CG, Stehouwer CD, Tigchelaar EF, Uitterlinden AG, Willemsen G, Zhernakova A, **Franke L**, 't Hoen PA, Jansen R, van Meurs J, Boomsma DI, van Duijn CM, van Greevenbroek MM, Veldink JH, Wijmenga C; BIOS Consortium, van Zwet EW, Slagboom PE, Jukema JW, Heijmans BT. **Blood lipids influence DNA methylation in circulating cells.** *Genome Biol. 2016;17(1):138.*

35. *** Gormley P, Anttila V, Winsvold BS, Palta P, Esko T, Pers TH, Farh KH, Cuenca-Leon E, Muona M, Furlotte NA, Kurth T, Ingason A, McMahon G, Ligthart L, Terwindt GM, Kallela M, Freilinger TM, Ran C, Gordon SG, Stam AH, Steinberg S, Borck G, Koiranen M, Quaye L, Adams HH, Lehtimäki T, Sarin AP, Wedenoja J, Hinds DA, Buring JE, Schürks M, Ridker PM, Hrafnsdottir MG, Stefansson H, Ring SM, Hottenga JJ, Penninx BW, Färkkilä M, Artto V, Kaunisto M, Vepsäläinen S, Malik R, Heath AC, Madden PA, Martin NG, Montgomery GW, Kurki MI, Kals M, Mägi R, Pärn K, Hämäläinen E, Huang H, Byrnes AE**, Franke L**, Huang J, Stergiakouli E, Lee PH, Sandor C, Webber C, Cader Z, Muller-Myhsok B, Schreiber S, Meitinger T, Eriksson JG, Salomaa V, Heikkilä K, Loehrer E, Uitterlinden AG, Hofman A, van Duijn CM, Cherkas L, Pedersen LM, Stubhaug A, Nielsen CS, Männikkö M, Mihailov E, Milani L, Göbel H, Esserlind AL, Christensen AF, Hansen TF, Werge T; International Headache Genetics Consortium, Kaprio J, Aromaa AJ, Raitakari O, Ikram MA, Spector T, Järvelin MR, Metspalu A, Kubisch C, Strachan DP, Ferrari MD, Belin AC, Dichgans M, Wessman M, van den Maagdenberg AM, Zwart JA, Boomsma DI, Smith GD, Stefansson K, Eriksson N, Daly MJ, Neale BM, Olesen J, Chasman DI, Nyholt DR, Palotie A. **Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine.** *Nat Genet. 2016;48(8):856-66.*

36. *** Okbay A, Beauchamp JP, Fontana MA, Lee JJ, Pers TH, Rietveld CA, Turley P, Chen GB, Emilsson V, Meddens SF, Oskarsson S, Pickrell JK, Thom K, Timshel P, de Vlaming R, Abdellaoui A, Ahluwalia TS, Bacelis J, Baumbach C, Bjornsdottir G, Brandsma JH, Pina Concas M, Derringer J, Furlotte NA, Galesloot TE, Girotto G, Gupta R, Hall LM, Harris SE, Hofer E, Horikoshi M, Huffman JE, Kaasik K, Kalafati IP, Karlsson R, Kong A, Lahti J, van der Lee SJ, deLeeuw C, Lind PA, Lindgren KO, Liu T, Mangino M, Marten J, Mihailov E, Miller MB, van der Most PJ, Oldmeadow C, Payton A, Pervjakova N, Peyrot WJ, Qian Y, Raitakari O, Rueedi R, Salvi E, Schmidt B, Schraut KE, Shi J, Smith AV, Poot RA, St Pourcain B, Teumer A, Thorleifsson G, Verweij N, Vuckovic D, Wellmann J, Westra HJ, Yang J, Zhao W, Zhu Z, Alizadeh BZ, Amin N, Bakshi A, Baumeister SE, Biino G, Bønnelykke K, Boyle PA, Campbell H, Cappuccio FP, Davies G, De Neve JE, Deloukas P, Demuth I, Ding J, Eibich P, Eisele L, Eklund N, Evans DM, Faul JD, Feitosa MF, Forstner AJ, Gandin I,

Gunnarsson B, Halldórsson BV, Harris TB, Heath AC, Hocking LJ, Holliday EG, Homuth G, Horan MA, Hottenga JJ, de Jager PL, Joshi PK, Jugessur A, Kaakinen MA, Kähönen M, Kanoni S, Keltigangas-Järvinen L, Kiemeney LA, Kolcic I, Koskinen S, Kraja AT, Kroh M, Kutalik Z, Latvala A, Launer LJ, Lebreton MP, Levinson DF, Lichtenstein P, Lichtner P, Liewald DC; LifeLines Cohort Study, Loukola A, Madden PA, Mägi R, Mäki-Opas T, Marioni RE, Marques-Vidal P, Meddens GA, McMahon G, Meisinger C, Meitinger T, Milaneschi Y, Milani L, Montgomery GW, Myhre R, Nelson CP, Nyholt DR, Ollier WE, Palotie A, Paternoster L, Pedersen NL, Petrovic KE, Porteous DJ, Räikkönen K, Ring SM, Robino A, Rostapshova O, Rudan I, Rustichini A, Salomaa V, Sanders AR, Sarin AP, Schmidt H, Scott RJ, Smith BH, Smith JA, Staessen JA, Steinhagen-Thiessen E, Strauch K, Terracciano A, Tobin MD, Ulivi S, Vaccargiu S, Quaye L, van Rooij FJ, Venturini C, Vinkhuyzen AA, Völker U, Völzke H, Vonk JM, Vozzi D, Waage J, Ware EB, Willemsen G, Attia JR, Bennett DA, Berger K, Bertram L, Bisgaard H, Boomsma DI, Borecki IB, Bültmann U, Chabris CF, Cucca F, Cusi D, Deary IJ, Dedoussis GV, van Duijn CM, Eriksson JG, Franke B, **Franke L**, Gasparini P, Gejman PV, Gieger C, Grabe HJ, Gratten J, Groenen PJ, Gudnason V, van der Harst P, Hayward C, Hinds DA, Hoffmann W, Hyppönen E, Iacono WG, Jacobsson B, Järvelin MR, Jöckel KH, Kaprio J, Kardia SL, Lehtimäki T, Lehrer SF, Magnusson PK, Martin NG, McGue M, Metspalu A, Pendleton N, Penninx BW, Perola M, Pirastu N, Pirastu M, Polasek O, Posthuma D, Power C, Province MA, Samani NJ, Schlessinger D, Schmidt R, Sørensen TI, Spector TD, Stefansson K, Thorsteinsdottir U, Thurik AR, Timpson NJ, Tiemeier H, Tung JY, Uitterlinden AG, Vitart V, Vollenweider P, Weir DR, Wilson JF, Wright AF, Conley DC, Krueger RF, Davey Smith G, Hofman A, Laibson DI, Medland SE, Meyer MN, Yang J, Johannesson M, Visscher PM, Esko T, Koellinger PD, Cesarini D, Benjamin DJ. **Genome-wide association study identifies 74 loci associated with educational attainment.** *Nature. 2016;533(7604):539-42.*

37. * van Dongen J, Nivard MG, Willemsen G, Hottenga JJ, Helmer Q, Dolan CV, Ehli EA, Davies GE, van Iterson M, Breeze CE, Beck S; **BIOS Consortium**, Suchiman HE, Jansen R, van Meurs JB, Heijmans BT, Slagboom PE, Boomsma DI. **Genetic and environmental influences interact with age and sex in shaping the human methylome.** *Nat Commun. 2016 Apr 7;7:11115.*

38. Franke B, Stein JL, Ripke S, Anttila V, Hibar DP, van Hulzen KJ, Arias-Vasquez A, Smoller JW, Nichols TE, Neale MC, McIntosh AM, Lee P, McMahon FJ, Meyer-Lindenberg A, Mattheisen M, Andreassen OA, Gruber O, Sachdev PS, Roiz-Santiañez R, Saykin AJ, Ehrlich S, Mather KA, Turner JA, Schwarz E, Thalamuthu A, Yao Y, Ho YY, Martin NG, Wright MJ; **Schizophrenia Working Group of the Psychiatric Genomics Consortium**; Psychosis Endophenotypes International Consortium; Wellcome Trust Case Control Consortium 2; Enigma Consortium, O'Donovan MC, Thompson PM, Neale BM, Medland SE, Sullivan PF. **Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept.** *Nat Neurosci. 2016;19(3):420-31.*

39. Ligthart S, Steenaard RV, Peters MJ, van Meurs JB, Sijbrands EJ, Uitterlinden AG, Bonder MJ; **BIOS consortium**, Hofman A, Franco OH, Dehghan A. **Tobacco smoking is associated with DNA methylation of diabetes susceptibility genes.** *Diabetologia. 2016;59(5):998-1006.*

40. *** Sekar A, Bialas AR, de Rivera H, Davis A, Hammond TR, Kamitaki N, Tooley K, Presumey J, Baum M, Van Doren V, Genovese G, Rose SA, Handsaker RE; **Schizophrenia Working Group of the Psychiatric Genomics Consortium**, Daly MJ, Carroll MC, Stevens B, McCarroll SA. **Schizophrenia risk from complex variation of complement component 4.** *Nature. 2016;530(7589):177-83*.

41. Bigdeli TB, Ripke S, Bacanu SA, Lee SH, Wray NR, Gejman PV, Rietschel M, Cichon S, St Clair D, Corvin A, Kirov G, McQuillin A, Gurling H, Rujescu D, Andreassen OA, Werge T, Blackwood DH, Pato CN, Pato MT, Malhotra AK, O'Donovan MC, Kendler KS, Fanous AH; **Schizophrenia Working Group of the Psychiatric Genomics Consortium**. **Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness**. *Am J Med Genet B Neuropsychiatr Genet. 2016;171B(2):276-89.*

42. * Vilhjálmsson BJ, Yang J, Finucane HK, Gusev A, Lindström S, Ripke S, Genovese G, Loh PR, Bhatia G, Do R, Hayeck T, Won HH; **Schizophrenia Working Group of the Psychiatric Genomics Consortium**, Discovery, Biology, and Risk of Inherited Variants in Breast Cancer (DRIVE) study, Kathiresan S, Pato M, Pato C, Tamimi R, Stahl E, Zaitlen N, Pasaniuc B, Belbin G, Kenny EE, Schierup MH, De Jager P, Patsopoulos NA, McCarroll S, Daly M, Purcell S, Chasman D, Neale B, Goddard M, Visscher PM, Kraft P, Patterson N, Price AL. **Modeling linkage disequilibrium increases accuracy of polygenic risk scores**. *Am J Hum Genet. 2015;97(4):576-92.*

43. Amin N, Allebrandt KV, van der Spek A, Müller-Myhsok B, Hek K, Teder-Laving M, Hayward C, Esko T, van Mill JG, Mbarek H, Watson NF, Melville SA, Del Greco FM, Byrne EM, Oole E, Kolcic I, Chen TH, Evans DS, Coresh J, Vogelzangs N, Karjalainen J, Willemsen G, Gharib SA, Zgaga L, Mihailov E, Stone KL, Campbell H, Brouwer RW, Demirkan A, Isaacs A, Dogas Z, Marciante KD, Campbell S, Borovecki F, Luik AI, Li M, Hottenga JJ, Huffman JE, van den Hout MC, Cummings SR, Aulchenko YS, Gehrman PR, Uitterlinden AG, Wichmann HE, Müller-Nurasyid M, Fehrmann RS, Montgomery GW, Hofman A, Kao WH, Oostra BA, Wright AF, Vink JM, Wilson JF, Pramstaller PP, Hicks AA, Polasek O, Punjabi NM, Redline S, Psaty BM, Heath AC, Merrow M, Tranah GJ, Gottlieb DJ, Boomsma DI, Martin NG, Rudan I, Tiemeier H, van IJcken WF, Penninx BW, Metspalu A, Meitinger T, **Franke L**, Roenneberg T, van Duijn CM. **Genetic variants in RBFOX3 are associated with sleep latency.** *Eur J Hum Genet. 2016;24:1488-1495.*

44. *** Zhernakova A, Kurilshikov A, Bonder MJ, Tigchelaar EF, Schirmer M, Vatanen T, Mujagic Z, Vila AV, Falony G, Vieira-Silva S, Wang J, Imhann F, Brandsma E, Jankipersadsing SA, Joossens M, Cenit MC, Deelen P, Swertz MA; LifeLines cohort study, Weersma RK, Feskens EJ, Netea MG, Gevers D, Jonkers D, **Franke L**, Aulchenko YS, Huttenhower C, Raes J, Hofker MH, Xavier RJ, Wijmenga C, Fu J. **Population- based metagenomics analysis reveals markers for gut microbiome composition and diversity**. Science. 2016;352(6285):565-9.

45. *** Okbay A, Baselmans BM, De Neve JE, Turley P, Nivard MG, Fontana MA, Meddens SF, Linnér RK, Rietveld CA, Derringer J, Gratten J, Lee JJ, Liu JZ, de Vlaming R, Ahluwalia TS, Buchwald J, Cavadino A, Frazier-Wood AC, Furlotte NA, Garfield V, Geisel MH, Gonzalez JR, Haitjema S, Karlsson R, van der Laan SW, Ladwig KH, Lahti J, van der Lee SJ, Lind PA, Liu T, Matteson L, Mihailov E, Miller MB, Minica CC, Nolte IM, Mook-Kanamori D, van der Most PJ, Oldmeadow C, Qian Y, Raitakari O, Rawal R, Realo A, Rueedi R, Schmidt B, Smith AV, Stergiakouli E, Tanaka T, Taylor K, Wedenoja J, Wellmann J, Westra HJ, Willems SM, Zhao W; LifeLines Cohort Study, Amin N, Bakshi A, Boyle PA, Cherney S, Cox SR, Davies G, Davis OS, Ding J, Direk N, Eibich P, Emeny RT, Fatemifar G, Faul JD, Ferrucci L, Forstner A, Gieger C, Gupta R, Harris TB, Harris JM, Holliday EG, Hottenga JJ, De Jager PL, Kaakinen MA, Kajantie E, Karhunen V, Kolcic I, Kumari M, Launer LJ, Franke L, Li-Gao R, Koini M, Loukola A, Marques-Vidal P, Montgomery GW, Mosing MA, Paternoster L, Pattie A, Petrovic KE, Pulkki- Råback L, Quaye L, Räikkönen K, Rudan I, Scott RJ, Smith JA, Sutin AR, Trzaskowski M, Vinkhuyzen AE, Yu L, Zabaneh D, Attia JR, Bennett DA, Berger K, Bertram L, Boomsma DI, Snieder H, Chang SC, Cucca F, Deary IJ, van Duijn CM, Eriksson JG, Bültmann U, de Geus EJ, Groenen PJ, Gudnason V, Hansen T, Hartman CA, Haworth CM, Hayward C, Heath AC, Hinds DA, Hyppönen E, Iacono WG, Järvelin MR, Jöckel KH, Kaprio J, Kardia SL, Keltikangas-Järvinen L, Kraft P, Kubzansky LD, Lehtimäki T, Magnusson PK, Martin NG, McGue M, Metspalu A, Mills M, de Mutsert R, Oldehinkel AJ, Pasterkamp G, Pedersen NL, Plomin R, Polasek O, Power C, Rich SS, Rosendaal FR, den Ruijter HM, Schlessinger D, Schmidt H, Svento R, Schmidt R, Alizadeh BZ, Sørensen TI, Spector TD, Steptoe A, Terracciano A, Thurik AR, Timpson NJ, Tiemeier H, Uitterlinden AG, Vollenweider P, Wagner GG, Weir DR, Yang J, Conley DC, Smith GD, Hofman A, Johannesson M, Laibson DI, Medland SE, Meyer MN, Pickrell JK, Esko T, Krueger RF, Beauchamp JP, Koellinger PD, Benjamin DJ, Bartels M, Cesarini D. **Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome- wide analyses.** *Nat Genet. 2016;48(6):624-33.*

46. *** Ellinghaus D, Jostins L, Spain SL, Cortes A, Bethune J, Han B, Park YR, Raychaudhuri S, Pouget JG, Hübenthal M, Folseraas T, Wang Y, Esko T, Metspalu A, Westra HJ, **Franke L**, Pers TH, Weersma RK, Collij V, D'Amato M, Halfvarson J, Jensen AB, Lieb W, Degenhardt F, Forstner AJ, Hofmann A; International IBD Genetics Consortium (IIBDGC); International Genetics of Ankylosing Spondylitis Consortium (IGAS); International PSC Study Group (IPSCSG); Genetic Analysis of Psoriasis Consortium (GAPC); Psoriasis Association Genetics Extension (PAGE), Schreiber S, Mrowietz U, Juran BD, Lazaridis KN, Brunak S, Dale AM, Trembath RC, Weidinger S, Weichenthal M, Ellinghaus E, Elder JT, Barker JN, Andreassen OA, McGovern DP, Karlsen TH, Barrett JC, Parkes M, Brown MA, Franke A. **Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci.** *Nat Genet. 2016 May;48(5):510-8.*

47. Verweij N, Mateo Leach I, Isaacs A, Arking DE, Bis JC, Pers TH, van den Berg ME, Lyytikäinen LP, Barnett P, Wang X; LifeLines Cohort Study, Soliman EZ, van Duijn CM, Kähönen M, van Veldhuisen DJ, Kors JA, Raitakari OT, Silva CT, Lehtimäki T, Hillege HL, Hirschhorn JN, Boyer LA, van Gilst WH, Alonso A, Sotoodehnia N, Eijgelsheim M, de Boer RA, de Bakker PI**, Franke L**, van der Harst P**. Twenty-eight genetic loci associated with ST-T wave amplitudes of the electrocardiogram.** *Hum Mol Genet. 2016;25(10):2093-2103*

48. Ricaño-Ponce I, Zhernakova DV, Deelen P, Luo O, Li X, Isaacs A, Karjalainen J, Di Tommaso J, Borek ZA, Zorro MM, Gutierrez-Achury J, Uitterlinden AG, Hofman A, van Meurs J; BIOS consortium; Lifelines Cohort Study, Netea MG, Jonkers IH, Withoff S, van Duijn CM, Li Y, Ruan Y, **Franke L**, Wijmenga C, Kumar V**. Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs.** *J Autoimmun. 2016 Apr;68:62-74.*

49. * Lu Y, Day FR, Gustafsson S, Buchkovich ML, Na J, Bataille V, Cousminer DL, Dastani Z, Drong AW, Esko T, Evans DM, Falchi M, Feitosa MF, Ferreira T, …, **Franke** L, Han J, Hunter DJ, Karjalainen J, Karpe F, Kaplan RC, Kooner JS, McCarthy MI, Murabito JM, Morris AP, Bishop JA, North KE, Ohlsson C, Ong KK, Prokopenko I, Richards JB, Schadt EE, Spector TD, Widén E, Willer CJ, Yang J, Ingelsson E, Mohlke KL, Hirschhorn JN, Pospisilik JA, Zillikens MC, Lindgren C, Kilpeläinen TO, Loos RJ. **New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk.** *Nat Commun. 2016 Feb 1;7:10495*

50. * 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, …, **Franke L**, …, O'Connell JR, Susztak K, Hamet P, Tremblay J, de Boer IH, Böger CA, Goessling W, Chasman DI, Köttgen A, Kao WH, Fox CS. **Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function.** *Nat Commun. 2016 Jan21;7:10023.*

51. Pers TH, Timshel P, Ripke S, Lent S, Sullivan PF, O'Donovan MC, **Franke L**, Hirschhorn JN; Schizophrenia Working Group of the Psychiatric Genomics Consortium. **Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes.** *Hum Mol Genet. 2016 Mar 15;25(6):1247-54*

52. * Imhann F, Bonder MJ, Vich Vila A, Fu J, Mujagic Z, Vork L, Tigchelaar EF, Jankipersadsing SA, Cenit MC, Harmsen HJ, Dijkstra G, **Franke L**, Xavier RJ, Jonkers D, Wijmenga C, Weersma RK, Zhernakova A. **Proton pump inhibitors affect the gut microbiome.** *Gut. 2016;65(5):740-8.*

53. Felix JF, Bradfield JP, Monnereau C, van der Valk RJ, Stergiakouli E, Chesi A, Gaillard R, Feenstra B, Thiering E, Kreiner-Møller E, Mahajan A, Pitkänen N, Joro R, Cavadino A, Huikari V, Franks S, Groen-Blokhuis MM, Cousminer DL, Marsh JA, Lehtimäki T, Curtin JA, Vioque J, Ahluwalia TS, Myhre R, Price TS, Vilor-Tejedor N, Yengo L, Grarup N, Ntalla I, Ang W, Atalay M, Bisgaard H, Blakemore AI, Bonnefond A, Carstensen L; Bone Mineral Density in Childhood Study (BMDCS); Early Genetics and Lifecourse Epidemiology (EAGLE) consortium,Eriksson J, Flexeder C, Franke L, Geller F, Geserick M, Hartikainen AL, Haworth CM, Hirschhorn JN, Hofman A, Holm JC, Horikoshi M, Hottenga JJ, Huang J, Kadarmideen HN, Kähönen M, Kiess W, Lakka HM, Lakka TA, Lewin AM, Liang L, Lyytikäinen LP, Ma B, Magnus P, McCormack SE, McMahon G, Mentch FD, Middeldorp CM, Murray CS, Pahkala K, Pers TH, Pfäffle R, Postma DS, Power C, Simpson A, Sengpiel V, Tiesler CM, Torrent M, Uitterlinden AG, van Meurs JB, Vinding R, Waage J, Wardle J, Zeggini E, Zemel BS, Dedoussis GV, Pedersen O, Froguel P, Sunyer J, Plomin R, Jacobsson B, Hansen T, Gonzalez JR, Custovic A, Raitakari OT, Pennell CE, Widén E, Boomsma DI, Koppelman GH, Sebert S, Järvelin MR, Hyppönen E, McCarthy MI, Lindi V, Harri N, Körner A, Bønnelykke K, Heinrich J, Melbye M, Rivadeneira F, Hakonarson H, Ring SM, Smith GD, Sørensen TI, Timpson NJ, Grant SF, Jaddoe VW; Early Growth Genetics (EGG) Consortium; Bone Mineral Density in Childhood Study BMDCS. **Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index.** *Hum Mol Genet. 2016 Jan 15;25(2):389-403.*

54. Gutierrez-Achury J, Zorro MM, Ricaño-Ponce I, Zhernakova DV; Coeliac Disease Immunochip Consortium, RACI Consortium, Diogo D, Raychaudhuri S, Franke L, Trynka G, Wijmenga C, Zhernakova A. **Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis.** *Hum Mol Genet. 2016;25(1):180-90.*

55. * Peters MJ, Joehanes R, Pilling LC, Schurmann C, Conneely KN, Powell J, Reinmaa E, Sutphin GL, Zhernakova A, Schramm K, Wilson YA, Kobes S, Tukiainen T; NABEC/UKBEC Consortium, Ramos YF, Göring HH, Fornage M, Liu Y, Gharib SA, Stranger BE, De Jager PL, Aviv A, Levy D, Murabito JM, Munson PJ, Huan T, Hofman A, Uitterlinden AG, Rivadeneira F, van Rooij J, Stolk L, Broer L, Verbiest MM, Jhamai M, Arp P, Metspalu A, Tserel L, Milani L, Samani NJ, Peterson P, Kasela S, Codd V, Peters A, Ward-Caviness CK, Herder C, Waldenberger M, Roden M, Singmann P, Zeilinger S, Illig T, Homuth G, Grabe HJ, Völzke H, Steil L, Kocher T, Murray A, Melzer D, Yaghootkar H, Bandinelli S, Moses EK, Kent JW, Curran JE, Johnson MP, Williams-Blangero S, Westra HJ, McRae AF, Smith JA, Kardia SL, Hovatta I, Perola M, Ripatti S, Salomaa V, Henders AK, Martin NG, Smith AK, Mehta D, Binder EB, Nylocks KM, Kennedy EM, Klengel T, Ding J, Suchy-Dicey AM, Enquobahrie DA, Brody J, Rotter JI, Chen YD, Houwing-Duistermaat J, Kloppenburg M, Slagboom PE, Helmer Q, den Hollander W, Bean S, Raj T, Bakhshi N, Wang QP, Oyston LJ, Psaty BM, Tracy RP, Montgomery GW, Turner ST, Blangero J, Meulenbelt I, Ressler KJ, Yang J, Franke L, Kettunen J, Visscher PM, Neely GG, Korstanje R, Hanson RL, Prokisch H, Ferrucci L, Esko T, Teumer A, van Meurs JB, Johnson AD. **The transcriptional landscape of age in human peripheral blood.** *Nat Commun. 2015 Oct 22;6:8570.*

56. Kogelman LJ, Zhernakova DV, Westra HJ, Cirera S, Fredholm M, Franke L, Kadarmideen HN. **An integrative systems genetics approach reveals potential causal genes and pathways related to obesity.** *Genome Med. 2015 Oct 20;7(1):105.*

57. Winkler TW, Justice AE, Graff M, Barata L, Feitosa MF, Chu S, Czajkowski J, Esko T, Fall T, Kilpeläinen TO, Lu Y, Mägi R, Mihailov E, Pers TH, …, Franke L, …, North KE, Borecki IB, Kutalik Z, Loos RJ. **The influence of age and sex on genetic associations with adult body size and shape: a large-scale genome-wide interaction study.** *PLoS Genet. 2015 Oct 1;11(10):e1005378*

58. *** Day FR, Ruth KS, Thompson DJ, Lunetta KL, Pervjakova N, Chasman DI, Stolk L, Finucane HK, Sulem P, Bulik-Sullivan B, Esko T, Johnson AD, Elks CE, Franceschini N, He C, Altmaier E, Brody JA, Franke L, Huffman JE, …, Price AL, Stefansson K, Visser JA, Ong KK, Chang-Claude J, Murabito JM, Perry JR, Murray A**. Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair.** *Nat Genet. 2015;47(11):1294-303.*

59. *** Kato N, Loh M, Takeuchi F, Verweij N, …, Franke L, Heijman BT, Holbrook JD, Isaacs A, Kim BJ, Lin X, Liu J, März W, Metspalu A, Mohlke KL, Sanghera DK, Shu XO, van Meurs JB, Vithana E, Wickremasinghe AR, Wijmenga C, Wolffenbuttel BH, Yokota M, Zheng W, Zhu D, Vineis P, Kyrtopoulos SA, Kleinjans JC, McCarthy MI, Soong R, Gieger C, Scott J, Teo YY, He J, Elliott P, Tai ES, van

der Harst P, Kooner JS, Chambers JC. **Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation.** *Nat Genet. 2015 Nov;47(11):1282-93.*

60. Fu J, Bonder MJ, Cenit MC, Tigchelaar EF, Maatman A, Dekens JA, Brandsma E, Marczynska J, Imhann F, Weersma RK, Franke L, Poon TW, Xavier RJ, Gevers D, Hofker MH, Wijmenga C, Zhernakova A**. The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids.** *Circ Res. 2015 Oct 9;117(9):817-24.*

61. Tigchelaar EF, Zhernakova A, Dekens JA, Hermes G, Baranska A, Mujagic Z, Swertz MA, Muñoz AM, Deelen P, Cénit MC, Franke L, Scholtens S, Stolk RP, Wijmenga C, Feskens EJ. **Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics.** *BMJ Open. 2015;28;5(8):e006772.*

62. *** 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. **Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations.** *Nat Genet. 2015 Sep;47(9):979-986.*

63. * Shah S, Bonder MJ, Marioni RE, Zhu Z, McRae AF, Zhernakova A, Harris SE, Liewald D, Henders AK, Mendelson MM, Liu C, Joehanes R, Liang L; BIOS Consortium, Levy D, Martin NG, Starr JM, Wijmenga C, Wray NR, Yang J, Montgomery GW, **Franke L**, Deary IJ, Visscher PM. **Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations.** *Am J Hum Genet. 2015 Jul 2;97(1):75-85.*

64. * Draisma HH, Pool R, Kobl M, Jansen R, Petersen AK, Vaarhorst AA, Yet I, Haller T, Demirkan A, Esko T, Zhu G, Böhringer S, Beekman M, van Klinken JB, Römisch-Margl W, Prehn C, Adamski J, de Craen AJ, van Leeuwen EM, Amin N, Dharuri H, Westra HJ, **Franke L**, de Geus EJ, Hottenga JJ, Willemsen G, Henders AK, Montgomery GW, Nyholt DR, Whitfield JB, Penninx BW, Spector TD, Metspalu A, Eline Slagboom P, van Dijk KW, 't Hoen PA, Strauch K, Martin NG, van Ommen GJ, Illig T, Bell JT, Mangino M, Suhre K, McCarthy MI, Gieger C, Isaacs A, van Duijn CM, Boomsma DI. **Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels**. *Nat Commun. 2015 Jun 12;6:7208.*

65. **Franke L**, El Bannoudi H, Jansen DT, Kok K, Trynka G, Diogo D, Swertz M, Fransen K, Knevel R, Gutierrez-Achury J, Ärlestig L, Greenberg JD, Kremer J, Pappas DA, Kanterakis A, Weersma RK, van der Helm-van Mil AH, Guryev V, Rantapää-Dahlqvist S, Gregersen PK, Plenge RM, Wijmenga C, Huizinga TW, Ioan-Facsinay A, Toes RE, Zhernakova A. **Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes.** *Eur J Hum Genet. 2016; 24(2):263-270.*

66. *** Surakka I, Horikoshi M, Mägi R, Sarin AP, Mahajan A, Lagou V, Marullo L, Ferreira T, Miraglio B, Timonen S, Kettunen J, Pirinen M, Karjalainen J, Thorleifsson G, Hägg S, Hottenga JJ, Isaacs A, Ladenvall C, Beekman M, Esko T, Ried JS, Nelson CP, Willenborg C, Gustafsson S, Westra HJ, Blades M, de Craen AJ, de Geus EJ, Deelen J, Grallert H, Hamsten A, Havulinna AS, Hengstenberg C, Houwing- Duistermaat JJ, Hyppönen E, Karssen LC, Lehtimäki T, Lyssenko V, Magnusson PK, Mihailov E, Müller-Nurasyid M, Mpindi JP, Pedersen NL, Penninx BW, Perola M, Pers TH, Peters A, Rung J, Smit JH, Steinthorsdottir V, Tobin MD, Tsernikova N, van Leeuwen EM, Viikari JS, Willems SM, Willemsen G, Schunkert H, Erdmann J, Samani NJ, Kaprio J, Lind L, Gieger C, Metspalu A, Slagboom PE, Groop L, van Duijn CM, Eriksson JG, Jula A, Salomaa V, Boomsma DI, Power C, Raitakari OT, Ingelsson E, Järvelin MR, Thorsteinsdottir U, Franke L, Ikonen E, Kallioniemi O, Pietiäinen V, Lindgren CM, Stefansson K, Palotie A, McCarthy MI, Morris AP, Prokopenko I, Ripatti S; ENGAGE Consortium. **The impact of low-frequency and rare variants on lipid levels.** *Nat Genet. 2015 Jun;47(6):589-97*

67. Westra HJ, Arends D, Esko T, Peters MJ, Schurmann C, Schramm K, Kettunen J, Yaghootkar H, Fairfax BP, Andiappan AK, Li Y, Fu J, Karjalainen J, Platteel M, Visschedijk M, Weersma RK, Kasela S, Milani L, Tserel L, Peterson P, Reinmaa E, Hofman A, Uitterlinden AG, Rivadeneira F, Homuth G, Petersmann A, Lorbeer R, Prokisch H, Meitinger T, Herder C, Roden M, Grallert H, Ripatti S, Perola M, Wood AR, Melzer D, Ferrucci L, Singleton AB, Hernandez DG, Knight JC, Melchiotti R, Lee B, Poidinger M, Zolezzi F, Larbi A, Wang de Y, van den Berg LH, Veldink JH, Rotzschke O, Makino S, Salomaa V, Strauch K, Völker U, van Meurs JB, Metspalu A, Wijmenga C, Jansen RC, **Franke L**. **Cell Specific eQTL Analysis without Sorting Cells.** *PLoS Genet. 2015 May 8;11(5):e1005223*

68. Deelen P, Zhernakova DV, de Haan M, van der Sijde M, Bonder MJ, Karjalainen J, van der Velde KJ, Abbott KM, Fu J, Wijmenga C, Sinke RJ, Swertz MA, **Franke L**. **Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels.** *Genome Med. 2015 Mar 27;7(1):30.*

69. Peyrot WJ, Lee SH, Milaneschi Y, Abdellaoui A, Byrne EM, Esko T, de Geus EJ, Hemani G, Hottenga JJ, Kloiber S, Levinson DF, Lucae S; Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium (Corporate Collaborator), Martin NG, Medland SE, Metspalu A, Milani L, Noethen MM, Potash JB, Rietschel M, Rietveld CA, Ripke S, Shi J; Social Science Genetic Association Consortium Corporate Collaborator, Willemsen G, Zhu Z, Boomsma DI, Wray NR, Penninx BW; Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium Corporate Collaborator; Social Science Genetic Association Consortium Corporate Collaborator. **The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects.** *Mol Psychiatry. 2015Jun;20(6):735-43*.

70. * Chan Y, Salem RM, Hsu YH, McMahon G, Pers TH, Vedantam S, Esko T, Guo MH, Lim ET; GIANT Consortium, **Franke L**, Smith GD, Strachan DP, Hirschhorn JN. **Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development.** *Am J Hum Genet. 2015 May 7;96(5):695-708.*

71. *** 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. **Genetic studies of body mass index yield new insights for obesity biology**. *Nature. 2015 Feb 12;518(7538):197-206.*

72. *** 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. **New genetic loci link adipose and insulin biology to body fat distribution.** *Nature. 2015 Feb 12;518(7538):187-96.*

73. Jin P, Andiappan AK, Quek JM, Lee B, Au B, Sio YY, Irwanto A, Schurmann C, Grabe HJ, Suri BK, Matta SA, Westra HJ, **Franke L**, Esko T, Sun L, Zhang X, Liu H, Zhang F, Larbi A, Xu X, Poidinger M, Liu J, Chew FT, Rotzschke O, Shi L, Wang de Y. **A functional**

brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. *J Allergy Clin Immunol. 2015 Jun;135(6):1486-93.e8.*

74. *** Bulik-Sullivan BK, Loh PR, Finucane HK, Ripke S, Yang J; Schizophrenia Working Group of the Psychiatric Genomics Consortium, Patterson N, Daly MJ, Price AL, Neale BM. **LD Score regression distinguishes confounding from polygenicity in genome-wide association studies.** *Nat Genet. 2015 Mar;47(3):291-5.*

75. * Pers TH, Karjalainen JM, Chan Y, Westra HJ, Wood AR, Yang J, Lui JC, Vedantam S, Gustafsson S, Esko T, Frayling T, Speliotes EK; Genetic Investigation of ANthropometric Traits (GIANT) Consortium, Boehnke M, Raychaudhuri S, Fehrmann RS, Hirschhorn JN, **Franke L**. **Biological interpretation of genome-wide association studies using predicted gene functions.** *Nat Commun. 2015 Jan 19;6:5890.*

76. *** Fehrmann RS, Karjalainen JM, Krajewska M, Westra HJ, Maloney D, Simeonov A, Pers TH, Hirschhorn JN, Jansen RC, Schultes EA, van Haagen HH, de Vries EG, te Meerman GJ, Wijmenga C, van Vugt MA, **Franke L**. **Gene expression analysis identifies global gene dosage sensitivity in cancer.** *Nat Genet. 2015 Feb;47(2):115-25.*

77. Deelen P, Bonder MJ, van der Velde KJ, Westra HJ, Winder E, Hendriksen D, **Franke L**, Swertz MA. **Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration**. *BMC Res Notes. 2014 Dec 11;7:901.*

78. Pierce BL, Tong L, Chen LS, Rahaman R, Argos M, Jasmine F, Roy S, Paul-Brutus R, Westra HJ, **Franke L**, Esko T, Zaman R, Islam T, Rahman M, Baron JA, Kibriya MG, Ahsan H. **Mediation analysis demonstrates that trans-eQTLs are often explained by cis- mediation: a genome-wide analysis among 1,800 South Asians.** *PLoS Genet. 2014;10(12):e1004818*

79. * Gusev A, Lee SH, Trynka G, Finucane H, Vilhjálmsson BJ, Xu H, Zang C, Ripke S, Bulik-Sullivan B, Stahl E; Schizophrenia Working Group of the Psychiatric Genomics Consortium; SWE-SCZ Consortium, Kähler AK, Hultman CM, Purcell SM, McCarroll SA, Daly M, Pasaniuc B, Sullivan PF, Neale BM, Wray NR, Raychaudhuri S, Price AL; Schizophrenia Working Group of the Psychiatric Genomics Consortium; SWE-SCZ Consortium. **Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases.** *Am J Hum Genet. 2014 Nov 6;95(5):535-52*.

80. Hrdlickova B, Kumar V, Kanduri K, Zhernakova DV, Tripathi S, Karjalainen J, Lund RJ, Li Y, Ullah U, Modderman R, Abdulahad W, Lähdesmäki H, **Franke L**, Lahesmaa R, Wijmenga C, Withoff S. **Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity.** *Genome Med. 2014 Oct 28;6(10):88.*

81. * Benyamin B, Esko T, Ried JS, Radhakrishnan A, Vermeulen SH, Traglia M, Gögele M, Anderson D, Broer L, Podmore C, Luan J, Kutalik Z, Sanna S, van der Meer P, Tanaka T, Wang F, Westra HJ, **Franke L**, Mihailov E, Milani L, Hälldin J, Winkelmann J, Meitinger T, Thiery J, Peters A, Waldenberger M, Rendon A, Jolley J, Sambrook J, Kiemeney LA, Sweep FC, Sala CF, Schwienbacher C, Pichler I, Hui J, Demirkan A, Isaacs A, Amin N, Steri M, Waeber G, Verweij N, Powell JE, Nyholt DR, Heath AC, Madden PA, Visscher PM, Wright MJ, Montgomery GW, Martin NG, Hernandez D, Bandinelli S, van der Harst P, Uda M, Vollenweider P, Scott RA, Langenberg C, Wareham NJ; InterAct Consortium, van Duijn C, Beilby J, Pramstaller PP, Hicks AA, Ouwehand WH, Oexle K, Gieger C, Metspalu A, Camaschella C, Toniolo D, Swinkels DW, Whitfield JB. **Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis.** *Nat Commun. 2014 Oct 29;5:4926*

82. Bonder MJ, Kasela S, Kals M, Tamm R, Lokk K, Barragan I, Buurman WA, Deelen P, Greve JW, Ivanov M, Rensen SS, van Vliet-Ostaptchouk JV, Wolfs MG, Fu J, Hofker MH, Wijmenga C, Zhernakova A, Ingelman-Sundberg M, **Franke L**, Milani L. **Genetic and epigenetic regulation of gene expression in fetal and adult human livers.** *BMC Genomics. 2014 Oct 4;15(1):860.*

83. Van der Valk RJ, Kreiner-Møller E, Kooijman MN, Guxens M, Stergiakouli E, Sääf A, Bradfield JP, Geller F, Hayes MG, Cousminer DL, Körner A, Thiering E, Curtin JA, Myhre R, Huikari V, Joro R, Kerkhof M, Warrington NM, Pitkänen N, Ntalla I, Horikoshi M, Veijola R, Freathy RM, Teo YY, Barton SJ, Evans DM, Kemp JP, St Pourcain B, Ring SM, Smith GD, Bergström A, Kull I, Hakonarson H, Mentch FD, Bisgaard H, Chawes B, Stokholm J, Waage J, Eriksen P, Sevelsted A, Melbye M; Early Genetics & Lifecourse Epidemiology (EAGLE) Consortium, van Duijn CM, Medina-Gomez C, Hofman A, de Jongste JC, Taal HR, Uitterlinden AG; Genetic Investigation of ANthropometric Traits (GIANT) Consortium, Armstrong LL, Eriksson J, Palotie A, Bustamante M, Estivill X, Gonzalez JR, Llop S, Kiess W, Mahajan A, Flexeder C, Tiesler CM, Murray CS, Simpson A, Magnus P, Sengpiel V, Hartikainen AL, Keinanen-Kiukaanniemi S, Lewin A, Da Silva Couto Alves A, Blakemore AI, Buxton JL, Kaakinen M, Rodriguez A, Sebert S, Vaarasmaki M, Lakka T, Lindi V, Gehring U, Postma DS, Ang W, Newnham JP, Lyytikäinen LP, Pahkala K, Raitakari OT, Panoutsopoulou K, Zeggini E, Boomsma DI, Groen-Blokhuis M, Ilonen J, **Franke L**, Hirschhorn JN, Pers TH, Liang L, Huang J, Hocher B, Knip M, Saw SM, Holloway JW, Melén E, Grant SF, Feenstra B, Lowe WL, Widén E, Sergeyev E, Grallert H, Custovic A, Jacobsson B, Jarvelin MR, Atalay M, Koppelman GH, Pennell CE, Niinikoski H, Dedoussis GV, McCarthy MI, Frayling TM, Sunyer J, Timpson NJ, Rivadeneira F, Bønnelykke K, Jaddoe VW; for the Early Growth Genetics (EGG) Consortium. **A novel common variant in DCST2 is associated with length in early life and height in adulthood.** *Hum Mol Genet. 2014; 24(4):1155-68.*

84. The Coffee and Caffeine Genetics Consortium, Cornelis MC, Byrne EM, Esko T, Nalls MA, Ganna A, Paynter N, Monda KL, Amin N, Fischer K, Renstrom F, Ngwa JS, Huikari V, Cavadino A, Nolte IM, Teumer A, Yu K, Marques-Vidal P, Rawal R, Manichaikul A, Wojczynski MK, Vink JM, Zhao JH, Burlutsky G, Lahti J, Mikkilä V, Lemaitre RN, Eriksson J, Musani SK, Tanaka T, Geller F, Luan J, Hui J, Mägi R, Dimitriou M, Garcia ME, Ho WK, Wright MJ, Rose LM, Magnusson PK, Pedersen NL, Couper D, Oostra BA, Hofman A, Ikram MA, Tiemeier HW, Uitterlinden AG, van Rooij FJ, Barroso I, Johansson I, Xue L, Kaakinen M, Milani L, Power C, Snieder H, Stolk RP, Baumeister SE, Biffar R, Gu F, Bastardot F, Kutalik Z, Jacobs DR Jr, Forouhi NG, Mihailov E, Lind L, Lindgren C, Michaëlsson K, Morris A, Jensen M, Khaw KT, Luben RN, Wang JJ, Männistö S, Perälä MM, Kähönen M, Lehtimäki T, Viikari J, Mozaffarian D, Mukamal K, Psaty BM, Döring A, Heath AC, Montgomery GW, Dahmen N, Carithers T, Tucker KL, Ferrucci L, Boyd HA, Melbye M, Treur JL, Mellström D, Hottenga JJ, Prokopenko I, Tönjes A, Deloukas P, Kanoni S, Lorentzon M, Houston DK, Liu Y, Danesh J, Rasheed A, Mason MA, Zonderman AB, **Franke L**, Kristal BS; International Parkinson's Disease Genomics Consortium (IPDGC); North American Brain Expression Consortium (NABEC); UK Brain Expression Consortium (UKBEC), Karjalainen J, Reed DR, Westra HJ, Evans MK, Saleheen D, Harris TB, Dedoussis G, Curhan G, Stumvoll M, Beilby J, Pasquale LR, Feenstra B, Bandinelli S, Ordovas JM, Chan AT, Peters U, Ohlsson C, Gieger C, Martin NG, Waldenberger M, Siscovick DS, Raitakari O, Eriksson JG, Mitchell P, Hunter DJ, Kraft P, Rimm EB, Boomsma DI, Borecki IB, Loos RJ, Wareham NJ, Vollenweider P, Caporaso N, Grabe HJ, Neuhouser ML, Wolffenbuttel BH, Hu FB, Hyppönen E, Järvelin MR, Cupples LA, Franks PW, Ridker PM, van Duijn CM, Heiss G, Metspalu A, North KE, Ingelsson E, Nettleton JA, van Dam RM, Chasman DI. **Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption.** *Mol Psychiatry. 2014 Oct 7.*

85. *** Perry JR, Day F, Elks CE, Sulem P, Thompson DJ, Ferreira T, He C, Chasman DI, Esko T, Thorleifsson G, Albrecht E, Ang WQ, Corre T, Cousminer DL, Feenstra B, Franceschini N, Ganna A, Johnson AD, Kjellqvist S, Lunetta KL, McMahon G, Nolte IM, Paternoster L, Porcu E, Smith AV, Stolk L, Teumer A, Tšernikova N, Tikkanen E, Ulivi S, Wagner EK, Amin N, Bierut LJ, Byrne EM, Hottenga JJ, Koller DL, Mangino M, Pers TH, Yerges-Armstrong LM, Hua Zhao J, Andrulis IL, Anton-Culver H, Atsma F, Bandinelli S, Beckmann MW, Benitez J, Blomqvist C, Bojesen SE, Bolla MK, Bonanni B, Brauch H, Brenner H, Buring JE, Chang-Claude J, Chanock S, Chen J, Chenevix-Trench G, Collée JM, Couch FJ, Couper D, Coviello AD, Cox A, Czene K, D'adamo AP, Davey Smith G, De Vivo I, Demerath EW, Dennis J, Devilee P, Dieffenbach AK, Dunning AM, Eiriksdottir G, Eriksson JG, Fasching PA,

Ferrucci L, Flesch-Janys D, Flyger H, Foroud T, **Franke L**, Garcia ME, García-Closas M, Geller F, de Geus EE, Giles GG, Gudbjartsson DF, Gudnason V, Guénel P, Guo S, Hall P, Hamann U, Haring R, Hartman CA, Heath AC, Hofman A, Hooning MJ, Hopper JL, Hu FB, Hunter DJ, Karasik D, Kiel DP, Knight JA, Kosma VM, Kutalik Z, Lai S, Lambrechts D, Lindblom A, Mägi R, Magnusson PK, Mannermaa A, Martin NG, Masson G, McArdle PF, McArdle WL, Melbye M, Michailidou K, Mihailov E, Milani L, Milne RL, Nevanlinna H, Neven P, Nohr EA, Oldehinkel AJ, Oostra BA, Palotie A, Peacock M, Pedersen NL, Peterlongo P, Peto J, Pharoah PD, Postma DS, Pouta A, Pylkäs K, Radice P, Ring S, Rivadeneira F, Robino A, Rose LM, Rudolph A, Salomaa V, Sanna S, Schlessinger D, Schmidt MK, Southey MC, Sovio U, Stampfer MJ, Stöckl D, Storniolo AM, Timpson NJ, Tyrer J, Visser JA, Vollenweider P, Völzke H, Waeber G, Waldenberger M, Wallaschofski H, Wang Q, Willemsen G, Winqvist R, Wolffenbuttel BH, Wright MJ; Australian Ovarian Cancer Study; GENICA Network; kConFab; LifeLines Cohort Study; InterAct Consortium; Early Growth Genetics (EGG) Consortium, Boomsma DI, Econs MJ, Khaw KT, Loos RJ, McCarthy MI, Montgomery GW, Rice JP, Streeten EA, Thorsteinsdottir U, van Duijn CM, Alizadeh BZ, Bergmann S, Boerwinkle E, Boyd HA, Crisponi L, Gasparini P, Gieger C, Harris TB, Ingelsson E, Järvelin MR, Kraft P, Lawlor D, Metspalu A, Pennell CE, Ridker PM, Snieder H, Sørensen TI, Spector TD, Strachan DP, Uitterlinden AG, Wareham NJ, Widen E, Zygmunt M, Murray A, Easton DF, Stefansson K, Murabito JM, Ong KK. **Parent-of-origin- specific allelic associations among 106 genomic loci for age at menarche.** *Nature. 2014 Oct 2;514(7520):92-7.*

86. *** Hemani G, Shakhbazov K, Westra HJ, Esko T, Henders AK, McRae AF, Yang J, Gibson G, Martin NG, Metspalu A, **Franke L**, Montgomery GW, Visscher PM, Powell JE. Hemani et al. **Reply**. *Nature. 2014 Oct 2;514(7520):E5-6*

87. Kogelman LJ, Cirera S, Zhernakova DV, Fredholm M, **Franke L**, Kadarmideen HN. **Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model.** *BMC Med Genomics. 2014 Sep 30;7(1):57.*

88. *** Wood AR, Esko T, Yang J, Vedantam S, Pers TH, Gustafsson S, Chu AY, Estrada K, Luan J, Kutalik Z, Amin N, Buchkovich ML, Croteau- Chonka DC, Day FR, Duan Y, Fall T, Fehrmann R, Ferreira T, Jackson AU, Karjalainen J, Lo KS, Locke AE, Mägi R, Mihailov E, Porcu E, Randall JC, Scherag A, Vinkhuyzen AA, Westra HJ, Winkler TW, Workalemahu T, Zhao JH, Absher D, Albrecht E, Anderson D, Baron J, Beekman M, Demirkan A, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Fraser RM, Goel A, Gong J, Justice AE, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Lui JC, Mangino M, Leach IM, Medina-Gomez C, Nalls MA, Nyholt DR, Palmer CD, Pasko D, Pechlivanis S, Prokopenko I, Ried JS, Ripke S, Shungin D, Stancáková A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Afzal U, Arnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Bolton JL, Böttcher Y, Boyd HA, Bruinenberg M, Buckley BM, Buyske S, Caspersen IH, Chines PS, Clarke R, Claudi- Boehm S, Cooper M, Daw EW, De Jong PA, Deelen J, Delgado G, Denny JC, Dhonukshe-Rutten R, Dimitriou M, Doney AS, Dörr M, Eklund N, Eury E, Folkersen L, Garcia ME, Geller F, Giedraitis V, Go AS, Grallert H, Grammer TB, Gräßler J, Grönberg H, de Groot LC, Groves CJ, Haessler J, Hall P, Haller T, Hallmans G, Hannemann A, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hemani G, Henders AK, Hillege HL, Hlatky MA, Hoffmann W, Hoffmann P, Holmen O, Houwing-Duistermaat JJ, Illig T, Isaacs A, James AL, Jeff J, Johansen B, Johansson A, Jolley J, Juliusdottir T, Junttila J, Kho AN, Kinnunen L, Klopp N, Kocher T, Kratzer W, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Lu Y, Lyssenko V, Magnusson PK, Mahajan A, Maillard M, McArdle WL, McKenzie CA, McLachlan S, McLaren PJ, Menni C, Merger S, Milani L, Moayyeri A, Monda KL, Morken MA, Müller G, Müller-Nurasyid M, Musk AW, Narisu N, Nauck M, Nolte IM, Nöthen MM, Oozageer L, Pilz S, Rayner NW, Renstrom F, Robertson NR, Rose LM, Roussel R, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Schunkert H, Scott RA, Sehmi J, Seufferlein T, Shi J, Silventoinen K, Smit JH, Smith AV, Smolonska J, Stanton AV, Stirrups K, Stott DJ, Stringham HM, Sundström J, Swertz MA, Syvänen AC, Tayo BO, Thorleifsson G, Tyrer JP, van Dijk S, van Schoor NM, van der Velde N, van Heemst D, van Oort FV, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Waldenberger M, Wennauer R, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Bergmann S, Biffar R, Blangero J, Boomsma DI, Bornstein SR, Bovet P, Brambilla P, Brown MJ, Campbell H, Caulfield MJ, Chakravarti A, Collins R, Collins FS, Crawford DC, Cupples LA, Danesh J, de Faire U, den Ruijter HM, Erbel R, Erdmann J, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Gansevoort RT, Gejman PV, Gieger C, Golay A, Gottesman O, Gudnason V, Gyllensten U, Haas DW, Hall AS, Harris TB, Hattersley AT, Heath AC, Hengstenberg C, Hicks AA, Hindorff LA, Hingorani AD, Hofman A, Hovingh GK, Humphries SE, Hunt SC, Hypponen E, Jacobs KB, Jarvelin MR, Jousilahti P, Jula AM, Kaprio J, Kastelein JJ, Kayser M, Kee F, Keinanen-Kiukaanniemi SM, Kiemeney LA, Kooner JS, Kooperberg C, Koskinen S, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lupoli S, Madden PA, Männistö S, Manunta P, Marette A, Matise TC, McKnight B, Meitinger T, Moll FL, Montgomery GW, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Ouwehand WH, Pasterkamp G, Peters A, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ritchie M, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Sebert S, Sever P, Shuldiner AR, Sinisalo J, Steinthorsdottir V, Stolk RP, Tardif JC, Tönjes A, Tremblay A, Tremoli E, Virtamo J, Vohl MC; The Electronic Medical Records and Genomics (eMERGE) Consortium; The MIGen Consortium; The PAGE Consortium; The LifeLines Cohort Study, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PI, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hayes MG, Hui J, Hunter DJ, Hveem K, Jukema JW, Kaplan RC, Kivimaki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Powell JE, Power C, Quertermous T, Rauramaa R, Reinmaa E, Ridker PM, Rivadeneira F, Rotter JI, Saaristo TE, Saleheen D, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Strauch K, Stumvoll M, Tuomilehto J, Uusitupa M, van der Harst P, Völzke H, Walker M, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Zanen P, Deloukas P, Heid IM, Lindgren CM, Mohlke KL, Speliotes EK, Thorsteinsdottir U, Barroso I, Fox CS, North KE, Strachan DP, Beckmann JS, Berndt SI, Boehnke M, Borecki IB, McCarthy MI, Metspalu A, Stefansson K, Uitterlinden AG, van Duijn CM, **Franke L**, Willer CJ, Price AL, Lettre G, Loos RJ, Weedon MN, Ingelsson E, O'Connell JR, Abecasis GR, Chasman DI, Goddard ME, Visscher PM, Hirschhorn JN, Frayling TM. **Defining the role of common variation in the genomic and biological architecture of adult human height.** *Nat Genet. 2014*;46(11):1173-86.

89. Smolonska J, Koppelman GH, Wijmenga C, Vonk JM, Zanen P, Bruinenberg M, CurjuricI, Imboden M, Thun G-A, **Franke L**, Probst-Hensch NM, Nürnberg P, Riemersma RA, van Schayck CP, Loth DW, Brusselle GG, Stricker BH, Hofman A, Uitterlinden AG, Lahousse L, London SJ, Loehr LR, Manichaikul A, Barr RG, Donohue KM, Rich SS, Pare P, Bossé Y, Hao K, van den Berge M, Groen HJM, Lammers J-W, Mali W, Boezen HM, Postma DS. **Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis.** *The European Respiratory J 2014 Oct:44(4):860-72.*

90. * Rietveld CA, Esko T, Davies G, Pers TH, Turley P, Benyamin B, Chabris CF, Emilsson V, Johnson AD, Lee JJ, Leeuw Cd, Marioni RE, Medland SE, Miller MB, Rostapshova O, van der Lee SJ, Vinkhuyzen AA, Amin N, Conley D, Derringer J, van Duijn CM, Fehrmann R, **Franke L**, Glaeser EL, Hansell NK, Hayward C, Iacono WG, Ibrahim-Verbaas C, Jaddoe V, Karjalainen J, Laibson D, Lichtenstein P, Liewald DC, Magnusson PK, Martin NG, McGue M, McMahon G, Pedersen NL, Pinker S, Porteous DJ, Posthuma D, Rivadeneira F, Smith BH, Starr JM, Tiemeier H, Timpson NJ, Trzaskowski M, Uitterlinden AG, Verhulst FC, Ward ME, Wright MJ, Davey Smith G, Deary IJ, Johannesson M, Plomin R, Visscher PM, Benjamin DJ, Cesarini D, Koellinger PD. **Common genetic variants associated with cognitive performance identified using the proxy-phenotype method.** *PNAS USA 2014 Sep 23; 111(38):13790-4*

91. * Kumar V, Cheng SC, Johnson MD, Smeekens SP, Wojtowicz A, Giamarellos-Bourboulis E, Karjalainen J, **Franke L**, Withoff S, Plantinga TS, van de Veerdonk FL, van der Meer JW, Joosten LA, Sokol H, Bauer H, Herrmann BG, Bochud PY, Marchetti O, Perfect JR, Xavier RJ, Kullberg BJ, Wijmenga C, Netea MG. **Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia.** *Nat Commun. 2014 Sep8;5:4675.*

92. Kumar V, Gutierrez-Achury J, Kanduri K, Almeida R, Hrdlickova B, Zhernakova DV, Westra HJ, Karjalainen J, Ricaño-Ponce I, Li Y, Stachurska A, Tigchelaar EF, Abdulahad WH, Lähdesmäki H, Hofker MH, Zhernakova A, **Franke L**, Lahesmaa R, Wijmenga C, Withoff S. **Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels.** *Hum Mol Genet. 2014 Sep 4. pii: ddu453.*

93. Andiappan AK, Narayanan S, Myers RA, Lee B, Nieuwenhuis MA, Nardin A, Park CS, Shin HD, Kim JH, Westra HJ, **Franke L**, Esko T, Metspalu A, Teo YY, Saw SM, Chuen KC, Jianjun L, Koppelman GH, Postma DS, Poidinger M, Connolly JE, Wang DY, Rotzschke O, Curotto de Lafaille MA, Chew FT**. Genetic variants of inducible costimulator are associated with allergic asthma susceptibility.** *J Allergy Clin Immunol. 2014 Aug 7*

94. *** Gockel I, Becker J, Wouters MM, Niebisch S, Gockel HR, Hess T, Ramonet D, Zimmermann J, Vigo AG, Trynka G, de León AR, de la Serna JP, Urcelay E, Kumar V, **Franke L**, Westra HJ, Drescher D, Kneist W, Marquardt JU, Galle PR, Mattheisen M, Annese V, Latiano A, Fumagalli U, Laghi L, Cuomo R, Sarnelli G, Müller M, Eckardt AJ, Tack J, Hoffmann P, Herms S, Mangold E, Heilmann S, Kiesslich R, von Rahden BH, Allescher HD, Schulz HG, Wijmenga C, Heneka MT, Lang H, Hopfner KP, Nöthen MM, Boeckxstaens GE, de Bakker PI, Knapp M, Schumacher J. **Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia.** *Nat Genet. 2014 Aug;46(8):901-4.*

95. Cozen W, Timofeeva MN, Li D, Diepstra A, Hazelett D, Delahaye-Sourdeix M, Edlund CK, **Franke L**, Rostgaard K, Van Den Berg DJ, Cortessis VK, Smedby KE, Glaser SL, Westra HJ, Robison LL, Mack TM, Ghesquieres H, Hwang AE, Nieters A, de Sanjose S, Lightfoot T, Becker N, Maynadie M, Foretova L, Roman E, Benavente Y, Rand KA, Nathwani BN, Glimelius B, Staines A, Boffetta P, Link BK, Kiemeney L, Ansell SM, Bhatia S, Strong LC, Galan P, Vatten L, Habermann TM, Duell EJ, Lake A, Veenstra RN, Visser L, Liu Y, Urayama KY, Montgomery D, Gaborieau V, Weiss LM, Byrnes G, Lathrop M, Cocco P, Best T, Skol AD, Adami HO, Melbye M, Cerhan JR, Gallagher A, Taylor GM, Slager SL, Brennan P, Coetzee GA, Conti DV, Onel K, Jarrett RF, Hjalgrim H, van den Berg A, McKay JD. **A meta-analysis of Hodgkin lymphoma reveals 19p13.3 TCF3 as a novel susceptibility locus.** *Nat Commun. 2014 Jun 12;5:3856.*

96. Deelen P, Menelaou A, van Leeuwen EM, Kanterakis A, van Dijk F, Medina-Gomez C, Francioli LC, Hottenga JJ, Karssen LC, Estrada K, Kreiner-Møller E, Rivadeneira F, van Setten J, Gutierrez-Achury J, Westra HJ, **Franke L**, van Enckevort D, Dijkstra M, Byelas H, van Duijn CM; Genome of the Netherlands Consortium, de Bakker PI, Wijmenga C, Swertz MA. **Improved imputation quality of low-frequency and rare variants in European samples using the 'Genome of The Netherlands'.** *Eur J Hum Genet. 2014 Jun 4.*

97. Giambartolomei C, Vukcevic D, Schadt EE, **Franke L**, Hingorani AD, Wallace C, Plagnol V. **Bayesian test for colocalisation between pairs of genetic association studies using summary statistics.** *PLoS Genet. 2014 May 15;10(5):e1004383.*

98. * De Boer YS, van Gerven NM, Zwiers A, Verwer BJ, van Hoek B, van Erpecum KJ, Beuers U, van Buuren HR, Drenth JP, den Ouden JW, Verdonk RC, Koek GH, Brouwer JT, Guichelaar MM, Vrolijk JM, Kraal G, Mulder CJ, van Nieuwkerk CM, Fischer J, Berg T, Stickel F, Sarrazin C, Schramm C, Lohse AW, Weiler-Normann C, Lerch MM, Nauck M, Völzke H, Homuth G, Bloemena E, Verspaget HW, Kumar V, Zhernakova A, Wijmenga C, **Franke L**, Bouma G; Dutch Autoimmune Hepatitis Study Group; LifeLines Cohort study; Study of Health in Pomerania (SHIP). **Genome-wide association study identifies variants associated with autoimmune hepatitis type-1.** *Gastroenterology. 2014 Apr 22. pii: S0016-5085(14)00548-4.*

99. ** Winkler TW, Day FR, Croteau-Chonka DC, Wood AR, Locke AE, Mägi R, Ferreira T, Fall T, Graff M, Justice AE, Luan J, Gustafsson S, Randall JC, Vedantam S, Workalemahu T, Kilpeläinen TO, Scherag A, Esko T, Kutalik Z, Heid IM, Loos RJ; Genetic Investigation of Anthropometric Traits (GIANT) Consortium. **Quality control and conduct of genome-wide association meta-analyses.** *Nat Protoc. 2014 May;9(5):1192-212.*

100. Van Sommeren S, Janse M, Karjalainen J, Fehrmann R, **Franke L**, Fu J, Weersma RK. **Extraintestinal manifestations and complications in inflammatory bowel disease: from shared genetics to shared biological pathways.** *Inflamm Bowel Dis. 2014 Jun;20(6):987-94.*

101. * Li H, Chan L, Bartuzi P, Melton SD, Weber A, Ben-Shlomo S, Varol C, Raetz M, Mao X, Starokadomskyy P, van Sommeren S, Mokadem M, Schneider H, Weisberg R, Westra HJ, Esko T, Metspalu A, Kumar V, Faubion WA, Yarovinsky F, Hofker M, Wijmenga C, Kracht M, **Franke L**, Aguirre V, Weersma RK, Gluck N, van de Sluis B, Burstein E. **Copper metabolism domain-containing 1 represses genes that promote inflammation and protects mice from colitis and colitis-associated cancer**. *Gastroenterology. 2014 Apr 13. pii: S0016- 5085(14)00461-2.*

102. Fransen K, van Sommeren S, Westra HJ, Veenstra M, Lamberts LE, Modderman R, Dijkstra G, Fu J, Wijmenga C, **Franke L**, Weersma RK, van Diemen CC. **Correlation of genetic risk and messenger RNA expression in a Th17/IL23 pathway analysis in inflammatory bowel disease.** *Inflamm Bowel Dis. 2014 May;20(5):777-82*

103. *** Hemani G, Shakhbazov K, Westra HJ, Esko T, Henders AK, McRae AF, Yang J, Gibson G, Martin NG, Metspalu A, **Franke L**, Montgomery GW, Visscher PM, Powell JE. **Detection and replication of epistasis influencing transcription in humans.** *Nature. 2014 Apr 10;508(7495):249-53.*

104. Geremek M, Ziętkiewicz E, Bruinenberg M, **Franke L**, Pogorzelski A, Wijmenga C, Witt M. **Ciliary genes are down-regulated in bronchial tissue of primary ciliary dyskinesia patients.** *PLoS One. 2014 Feb 6;9(2):e88216.*

105. *** Okada Y, Wu D, Trynka G, Raj T, Terao C, Ikari K, Kochi Y, Ohmura K, Suzuki A, Yoshida S, Graham RR, Manoharan A, Ortmann W, Bhangale T, Denny JC, Carroll RJ, Eyler AE, Greenberg JD, Kremer JM, Pappas DA, Jiang L, Yin J, Ye L, Su DF, Yang J, Xie G, Keystone E, Westra HJ, Esko T, Metspalu A, Zhou X, Gupta N, Mirel D, Stahl EA, Diogo D, Cui J, Liao K, Guo MH, Myouzen K, Kawaguchi T, Coenen MJ, van Riel PL, van de Laar MA, Guchelaar HJ, Huizinga TW, Dieudé P, Mariette X, Bridges SL Jr, Zhernakova A, Toes RE, Tak PP, Miceli- Richard C, Bang SY, Lee HS, Martin J, Gonzalez-Gay MA, Rodriguez-Rodriguez L, Rantapää-Dahlqvist S, Arlestig L, Choi HK, Kamatani Y, Galan P, Lathrop M; RACI consortium; GARNET consortium, Eyre S, Bowes J, Barton A, de Vries N, Moreland LW, Criswell LA, Karlson EW, Taniguchi A, Yamada R, Kubo M, Liu JS, Bae SC, Worthington J, Padyukov L, Klareskog L, Gregersen PK, Raychaudhuri S, Stranger BE, De Jager PL, **Franke L**, Visscher PM, Brown MA, Yamanaka H, Mimori T, Takahashi A, Xu H, Behrens TW, Siminovitch KA, Momohara S, Matsuda F, Yamamoto K, Plenge RM. **Genetics of rheumatoid arthritis contributes to biology and drug discovery.** *Nature. 2014 Feb 20;506(7488):376-81.*

106. Almeida R, Ricaño-Ponce I, Kumar V, Deelen P, Szperl A, Trynka G, Gutierrez-Achury J, Kanterakis A, Westra HJ, **Franke L**, Swertz MA, Platteel M, Bilbao JR, Barisani D, Greco L, Mearin L, Wolters VM, Mulder C, Mazzilli MC, Sood A, Cukrowska B,

Núñez C, Pratesi R, Withoff S, Wijmenga C. **Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant.** *Hum Mol Genet. 2014 May 1;23(9):2481-9.*

107. Dharuri H, Henneman P, Demirkan A, van Klinken JB, Mook-Kanamori DO, Wang-Sattler R, Gieger C, Adamski J, Hettne K, Roos M, Suhre K, Van Duijn CM; EUROSPAN Consortia, van Dijk KW, 't Hoen PA. **Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles.** *BMC Genomics. 2013 Dec 9;14:865.*

108. Scholtens S, Postma DS, Moffatt MF, Panasevich S, Granell R, Henderson AJ, Melén E, Nyberg F, Pershagen G, Jarvis D, Ramasamy A, Wjst M, Svanes C, Bouzigon E, Demenais F, Kauffmann F, Siroux V, von Mutius E, Ege MJ, Braun-Fahrländer C, Genuneit J; GABRIELA study group, Brunekreef B, Smit HA, Wijga AH, Kerkhof M, Curjuric I, Imboden M, Thun GA, Probst-Hensch N, Freidin MB, Bragina EIu, Deev IA, Puzyrev VP, Daley D, Park J, Becker A, Chan-Yeung M, Kozyrskyj AL, Pare P, Marenholz I, Lau S, Keil T, Lee YA, Kabesch M, Wijmenga C, **Franke L**, Nolte IM, Vonk J, Kumar A, Farrall M, Cookson WO, Strachan DP, Koppelman GH, Boezen HM. **Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure.** *J Allergy Clin Immunol. 2014 Mar;133(3):885-8.*

109. Horvatovich P, **Franke L**, Bischoff R. **Proteomic studies related to genetic determinants of variability in protein concentrations.** *J Proteome Res. 2014 Jan 3;13(1):5-14. doi: 10.1021/pr400765y. Epub 2013 Dec 4. Review.*

110. *** Westra HJ, Peters MJ, Esko T, Yaghootkar H, Schurmann C, Kettunen J, Christiansen MW, Fairfax BP, Heim K, Powell JE, Zhernakova A, Veldink JH, van den Berg LH, Karjalainen J, Withoff S, Uitterlinden AG, Hofman A, Rivadeneira F, Renimaa E, Fischer K, Nelis M, Milani L, MElzer D, Ferrucci L, Singleton AB, Hernandez DG, Nalls MA, Homuth G, Nauck M, Radke D, Völkers U, Perola M, Salomaa V, Brody J, Suchy-Dicey A, Gharib SA, Enquobahrie DA, Lumley T, Montgomery GW, Makino S, Prokisch H, Herder C, Roden M, Grallert H, Meitinger T, Strauch K, Li Y, Jansen RC, Visscher PM, Knight JC, Psaty BM, Ripatti S, Teumer A, Frayling TM, Metspalu A, van Meurs JBJ, **Franke L**. **Systematic identification of *trans*-eQTLs as putative drivers of known disease associations.** *Nat Genet. 2013 Oct;45(10):1238-43*

111. * Hu YJ, Berndt SI, Gustafsson S, Ganna A; Genetic Investigation of ANthropometric Traits (GIANT) Consortium, Hirschhorn J, North KE, Ingelsson E, Lin DY. **Meta-analysis of gene-level associations for rare variants based on single-variant statistics.** *Am J Hum Genet. 2013 Aug 8;93(2):236-48. doi: 10.1016/j.ajhg.2013.06.011.*

112. Zhernakova DV, de Klerk E, Westra HJ, Mastrokolias A, Amini S, Ariyurek Y, Jansen R, Penninx BW, Hottenga JJ, Willensen G, de Geus EJ, Boomsma DI, Veldink JH, van den Berg LH, Wijmenga C, den Dunnen JT, van ommen GJB, 't Hoen PAC, **Franke L**. **DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and noncoding transcripts.** *PLoS genetics 2013, Jun;9(6),e1003594*

113. *** Rietveld CA, Medland SE, Derringer J, Yang J, Esko T, Martin NW, Westra HJ, Shakhbazov K, Abdellaoui A, Agrawal A, Albrecht E, Alizadeh BZ, Amin N, Barnard J, Baumeister SE, Benke KS, Bielak LF, Boatman JA, Boyle PA, Davies G, de Leeuw C, Eklund N, Evans DS, Ferhmann R, Fischer K, Gieger C, Gjessing HK, Hägg S, Harris JR, Hayward C, Holzapfel C, Ibrahim-Verbaas CA, Ingelsson E, Jacobsson B, Joshi PK, Jugessur A, Kaakinen M, Kanoni S, Karjalainen J, Kolcic I, Kristiansson K, Kutalik Z, Lahti J, Lee SH, Lin P, Lind PA, Liu Y, Lohman K, Loitfelder M, McMahon G, Vidal PM, Meirelles O, Milani L, Myhre R, Nuotio ML, Oldmeadow CJ, Petrovic KE, Peyrot WJ, Polasek O, Quaye L, Reinmaa E, Rice JP, Rizzi TS, Schmidt H, Schmidt R, Smith AV, Smith JA, Tanaka T, Terracciano A, van der Loos MJ, Vitart V, Völzke H, Wellmann J, Yu L, Zhao W, Allik J, Attia JR, Bandinelli S, Bastardot F, Beauchamp J, Bennett DA, Berger K, Bierut LJ, Boomsma DI, Bültmann U, Campbell H, Chabris CF, Cherkas L, Chung MK, Cucca F, de Andrade M, De Jager PL, De Neve JE, Deary IJ, Dedoussis GV, Deloukas P, Dimitriou M, Eiriksdottir G, Elderson MF, Eriksson JG, Evans DM, Faul JD, Ferrucci L, Garcia ME, Grönberg H, Gudnason V, Hall P, Harris JM, Harris TB, Hastie ND, Heath AC, Hernandez DG, Hoffmann W, Hofman A, Holle R, Holliday EG, Hottenga JJ, Iacono WG, Illig T, Järvelin MR, Kähönen M, Kaprio J, Kirkpatrick RM, Kowgier M, Latvala A, Launer LJ, Lawlor DA, Lehtimäki T, Li J, Lichtenstein P, Lichtner P, Liewald DC, Madden PA, Magnusson PK, Mäkinen TE, Masala M, McGue M, Metspalu A, Mielck A, Miller MB, Montgomery GW, Mukherjee S, Nyholt DR, Oostra BA, Palmer LJ, Palotie A, Penninx B, Perola M, Peyser PA, Preisig M, Räikkönen K, Raitakari OT, Realo A, Ring SM, Ripatti S, Rivadeneira F, Rudan I, Rustichini A, Salomaa V, Sarin AP, Schlessinger D, Scott RJ, Snieder H, St Pourcain B, Starr JM, Sul JH, Surakka I, Svento R, Teumer A; The LifeLines Cohort Study, Tiemeier H, van Rooij FJ, Van Wagoner DR,Vartiainen E, Viikari J, Vollenweider P, Vonk JM, Waeber G, Weir DR, Wichmann HE, Widen E, Willemsen G, Wilson JF, Wright AF, Conley D, Davey-Smith G, **Franke** L, Groenen PJ, Hofman A, Johannesson M, Kardia SL, Krueger RF, Laibson D, Martin NG, Meyer MN, Posthuma D, Thurik AR, Timpson NJ, Uitterlinden AG, van Duijn CM, Visscher PM, Benjamin DJ, Cesarini D, Koellinger PD. **GWAS of 126,559 individuals identifies genetic variants associated with educational attainment.** *Science. 2013 2013 Jun 21;340(6139):1467-71.*

114. * Romanos J, Rosén A, Kumar V, Trynka G, **Franke L**, Szperl A, Gutierrez-Achury J, van Diemen CC, Kanninga R, Jankipersadsing SA, Steck A, Eisenbarth G, van Heel DA, Cukrowska B, Bruno V, Mazzilli MC, Núñez C, Bilbao JR, Mearin ML, Barisani D, Rewers M, Norris JM, Ivarsson A, Boezen HM, Liu E, Wijmenga C; PreventCD Group. **Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants.** *Gut. 2014 Mar;63(3):415-22.*

115. Li G, Diogo D, Wu D, Spoonamore J, Dancik V, **Franke L**, Kurreeman F, Rossin EJ, Duclos G, Hartland C, Zhou X, Li K, Liu J, De Jager PL, Siminovitch KA, Zhernakova A, Raychaudhuri S, Bowes J, Eyre S, Padyukov L, Gregersen PK, Worthington J; Rheumatoid Arthritis Consortium International (RACI), Gupta N, Clemons PA, Stahl E, Tolliday N, Plenge RM. **Human genetics in rheumatoid arthritis guides a high-throughput drug screen of the CD40 signaling pathway.** *PLoS Genet. 2013 May;9(5):e1003487.*

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

CM, Ekelund U, Forouhi NG, Froguel P, Hingorani A, Ingelsson E, Kivimaki M, Kronmal RA, Kuh D, Lind L, Martin NG, Oostra BA, Pedersen NL, Quertermous T, Rotter JI, van der Schouw YT, Verschuren WM, Walker M, Albanes D, Arnar DO, Assimes TL, Bandinelli S, Boehnke M, de Boer RA, Bouchard C, Caulfield WL, Chambers JC, Curhan G, Cusi D, Eriksson J, Ferrucci L, van Gilst WH, Glorioso N, de Graaf J, Groop L, Gyllensten U, Hsueh WC, Hu FB, Huikuri HV, Hunter DJ, Iribarren C, Isomaa B, Jarvelin MR, Jula A, Kähönen M, Kiemeney LA, van der Klauw MM, Kooner JS, Kraft P, Iacoviello L, Lehtimäki T, Lokki ML, Mitchell BD, Navis G, Nieminen MS, Ohlsson C, Poulter NR, Qi L, Raitakari OT, Rimm EB, Rioux JD, Rizzi F, Rudan I, Salomaa V, Sever PS, Shields DC, Shuldiner AR, Sinisalo J, Stanton AV, Stolk RP, Strachan DP, Tardif JC, Thorsteinsdottir U, Tuomilehto J, van Veldhuisen DJ, Virtamo J, Viikari J, Vollenweider P, Waeber G, Widen E, Cho YS, Olsen JV, Visscher PM, Willer C, **Franke L**; Global BPgen Consortium; CARDIoGRAM Consortium, Erdmann J, Thompson JR; PR GWAS Consortium, Pfeufer A; QRS GWAS Consortium, Sotoodehnia N; QT-IGC Consortium, Newton-Cheh C; CHARGE-AF Consortium, Ellinor PT, Stricker BH, Metspalu A, Perola M, Beckmann JS, Smith GD, Stefansson K, Wareham NJ, Munroe PB, Sibon OC, Milan DJ, Snieder H, Samani NJ, Loos RJ. **Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders**. *Nat Genet. 2013 Apr 14;45(6):621-631.*

117. *** Cvejic A, Haer-Wigman L, Stephens JC, Kostadima M, Smethurst PA, Frontini M, van den Akker E, Bertone P, Bielczyk-Maczyńska E, Farrow S, Fehrmann RS, Gray A, de Haas M, Haver VG, Jordan G, Karjalainen J, Kerstens HH, Kiddle G, Lloyd-Jones H, Needs M, Poole J, Soussan AA, Rendon A, Rieneck K, Sambrook JG, Schepers H, Silljé HH, Sipos B, Swinkels D, Tamuri AU, Verweij N, Watkins NA, Westra HJ, Stemple D, **Franke L**, Soranzo N, Stunnenberg HG, Goldman N, van der Harst P, van der Schoot CE, Ouwehand WH, Albers CA. **SMIM1 underlies the Vel blood group and influences red blood cell traits.** *Nat Genet. 2013 Apr 26;45(5):542-5.*

118. *** Berndt SI, Gustafsson S, Mägi R, Ganna A, Wheeler E, Feitosa MF, Justice AE, Monda KL, Croteau-Chonka DC, Day FR, Esko T, Fall T, Ferreira T, Gentilini D, Jackson AU, Luan J, Randall JC, Vedantam S, Willer CJ, Winkler TW, Wood AR, Workalemahu T, Hu YJ, Lee SH, Liang L, Lin DY, Min JL, Neale BM, Thorleifsson G, Yang J, Albrecht E, Amin N, Bragg-Gresham JL, Cadby G, den Heijer M, Eklund N, Fischer K, Goel A, Hottenga JJ, Huffman JE, Jarick I, Johansson A, Johnson T, Kanoni S, Kleber ME, König IR, Kristiansson K, Kutalik Z, Lamina C, Lecoeur C, Li G, Mangino M, McArdle WL, Medina-Gomez C, Müller-Nurasyid M, Ngwa JS, Nolte IM, Paternoster L, Pechlivanis S, Perola M, Peters MJ, Preuss M, Rose LM, Shi J, Shungin D, Smith AV, Strawbridge RJ, Surakka I, Teumer A, Trip MD, Tyrer J, Van Vliet- Ostaptchouk JV, Vandenput L, Waite LL, Zhao JH, Absher D, Asselbergs FW, Atalay M, Attwood AP, Balmforth AJ, Basart H, Beilby J, Bonnycastle LL, Brambilla P, Bruinenberg M, Campbell H, Chasman DI, Chines PS, Collins FS, Connell JM, Cookson WO, de Faire U, de Vegt F, Dei M, Dimitriou M, Edkins S, Estrada K, Evans DM, Farrall M, Ferrario MM, Ferrières J, **Franke L**, Frau F, Gejman PV, Grallert H, Grönberg H, Gudnason V, Hall AS, Hall P, Hartikainen AL, Hayward C, Heard-Costa NL, Heath AC, Hebebrand J, Homuth G, Hu FB, Hunt SE, Hyppönen E, Iribarren C, Jacobs KB, Jansson JO, Jula A, Kähönen M, Kathiresan S, Kee F, Khaw KT, Kivimäki M, Koenig W, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Laitinen JH, Lakka TA, Langenberg C, Launer LJ, Lind L, Lindström J, Liu J, Liuzzi A, Lokki ML, Lorentzon M, Madden PA, Magnusson PK, Manunta P, Marek D, März W, Mateo Leach I, McKnight B, Medland SE, Mihailov E, Milani L, Montgomery GW, Mooser V, Mühleisen TW, Munroe PB, Musk AW, Narisu N, Navis G, Nicholson G, Nohr EA, Ong KK, Oostra BA, Palmer CN, Palotie A, Peden JF, Pedersen N, Peters A, Polasek O, Pouta A, Pramstaller PP, Prokopenko I, Pütter C, Radhakrishnan A, Raitakari O, Rendon A, Rivadeneira F, Rudan I, Saaristo TE, Sambrook JG, Sanders AR, Sanna S, Saramies J, Schipf S, Schreiber S, Schunkert H, Shin SY, Signorini S, Sinisalo J, Skrobek B, Soranzo N, Stančáková A, Stark K, Stephens JC, Stirrups K, Stolk RP, Stumvoll M, Swift AJ, Theodoraki EV, Thorand B, Tregouet DA, Tremoli E, Van der Klauw MM, van Meurs JB, Vermeulen SH, Viikari J, Virtamo J, Vitart V, Waeber G, Wang Z, Widén E, Wild SH, Willemsen G, Winkelmann BR, Witteman JC, Wolffenbuttel BH, Wong A, Wright AF, Zillikens MC, Amouyel P, Boehm BO, Boerwinkle E, Boomsma DI, Caulfield MJ, Chanock SJ, Cupples LA, Cusi D, Dedoussis GV, Erdmann J, Eriksson JG, Franks PW, Froguel P, Gieger C, Gyllensten U, Hamsten A, Harris TB, Hengstenberg C, Hicks AA, Hingorani A, Hinney A, Hofman A, Hovingh KG, Hveem K, Illig T, Jarvelin MR, Jöckel KH, Keinanen-Kiukaanniemi SM, Kiemeney LA, Kuh D, Laakso M, Lehtimäki T, Levinson DF, Martin NG, Metspalu A, Morris AD, Nieminen MS, Njølstad I, Ohlsson C, Oldehinkel AJ, Ouwehand WH, Palmer LJ, Penninx B, Power C, Province MA, Psaty BM, Qi L, Rauramaa R, Ridker PM, Ripatti S, Salomaa V, Samani NJ, Snieder H, Sørensen TI, Spector TD, Stefansson K, Tönjes A, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Vollenweider P, Wallaschofski H, Wareham NJ, Watkins H, Wichmann HE, Wilson JF, Abecasis GR, Assimes TL, Barroso I, Boehnke M, Borecki IB, Deloukas P, Fox CS, Frayling T, Groop LC, Haritunian T, Heid IM, Hunter D, Kaplan RC, Karpe F, Moffatt MF, Mohlke KL, O'Connell JR, Pawitan Y, Schadt EE, Schlessinger D, Steinthorsdottir V, Strachan DP, Thorsteinsdottir U, van Duijn CM, Visscher PM, Di Blasio AM, Hirschhorn JN, Lindgren CM, Morris AP, Meyre D, Scherag A, McCarthy MI, Speliotes EK, North KE, Loos RJ, Ingelsson E. **Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture**. *Nat Genet. 2013 Apr 26;45(5):501-12.*

119. Kumar V, Westra HJ, Karjalainen J, Zhernakova DV, Esko T, Hrdlickova B, Almeida R, Zhernakova A, Reinmaa E, Võsa U, Hofker MH, Fehrmann RS, Fu J, Withoff S, Metspalu A, Wijmenga C**, Franke L**. **Human disease-associated genetic variation impacts large intergenic non-coding RNA expression.** *PLoS Genet. 2013 Jan;9(1):e1003201.*

120. *** van der Harst P, Zhang W, Mateo Leach I, Rendon A, Verweij N, Sehmi J, Paul DS, Elling U, Allayee H, Li X, Radhakrishnan A, Tan ST, Voss K, Weichenberger CX, Albers CA, Al-Hussani A, Asselbergs FW, Ciullo M, Danjou F, Dina C, Esko T, Evans DM, Franke L, Gögele M, Hartiala J, Hersch M, Holm H, Hottenga JJ, Kanoni S, Kleber ME, Lagou V, Langenberg C, Lopez LM, Lyytikäinen LP, Melander O, Murgia F, Nolte IM, O'Reilly PF, Padmanabhan S, Parsa A, Pirastu N, Porcu E, Portas L, Prokopenko I, Ried JS, Shin SY, Tang CS, Teumer A, Traglia M, Ulivi S, Westra HJ, Yang J, Zhao JH, Anni F, Abdellaoui A, Attwood A, Balkau B, Bandinelli S, Bastardot F, Benyamin B, Boehm BO, Cookson WO, Das D, de Bakker PI, de Boer RA, de Geus EJ, de Moor MH, Dimitriou M, Domingues FS, Döring A, Engström G, Eyjolfsson GI, Ferrucci L, Fischer K, Galanello R, Garner SF, Genser B, Gibson QD, Girotto G, Gudbjartsson DF, Harris SE, Hartikainen AL, Hastie CE, Hedblad B, Illig T, Jolley J, Kähönen M, Kema IP, Kemp JP, Liang L, Lloyd-Jones H, Loos RJ, Meacham S, Medland SE, Meisinger C, Memari Y, Mihailov E, Miller K, Moffatt MF, Nauck M, Novatchkova M, Nutile T, Olafsson I, Onundarson PT, Parracciani D, Penninx BW, Perseu L, Piga A, Pistis G, Pouta A, Puc U, Raitakari O, Ring SM, Robino A, Ruggiero D, Ruokonen A, Saint-Pierre A, Sala C, Salumets A, Sambrook J, Schepers H, Schmidt CO, Silljé HH, Sladek R, Smit JH, Starr JM, Stephens J, Sulem P, Tanaka T, Thorsteinsdottir U, Tragante V, van Gilst WH, van Pelt LJ, van Veldhuisen DJ, Völker U, Whitfield JB, Willemsen G, Winkelmann BR, Wirnsberger G, Algra A, Cucca F, d'Adamo AP, Danesh J, Deary IJ, Dominiczak AF, Elliott P, Fortina P, Froguel P, Gasparini P, Greinacher A, Hazen SL, Jarvelin MR, Khaw KT, Lehtimäki T, Maerz W, Martin NG, Metspalu A, Mitchell BD, Montgomery GW, Moore C, Navis G, Pirastu M, Pramstaller PP, Ramirez-Solis R, Schadt E, Scott J, Shuldiner AR, Smith GD, Smith JG, Snieder H, Sorice R, Spector TD, Stefansson K, Stumvoll M, Tang WH, Toniolo D, Tönjes A, Visscher PM, Vollenweider P, Wareham NJ, Wolffenbuttel BH, Boomsma DI, Beckmann JS, Dedoussis GV, Deloukas P, Ferreira MA, Sanna S, Uda M, Hicks AA, Penninger JM, Gieger C, Kooner JS, Ouwehand WH, Soranzo N, Chambers JC. **Seventy-five genetic loci influencing the human red blood cell.** *Nature. 2012 Dec 20;492(7429):369-75.*

121. *** Eyre S, Bowes J, Diogo D, Lee A, Barton A, Martin P, Zhernakova A, Stahl E, Viatte S, McAllister K, Amos CI, Padyukov L, Toes RE, Huizinga TW, Wijmenga C, Trynka G, **Franke L**, Westra HJ, Alfredsson L, Hu X, Sandor C, de Bakker PI, Davila S, Khor CC, Heng KK, Andrews R, Edkins S, Hunt SE, Langford C, Symmons D; Biologics in Rheumatoid Arthritis Genetics and

Genomics Study Syndicate; Wellcome Trust Case Control Consortium, Concannon P, Onengut-Gumuscu S, Rich SS, Deloukas P, Gonzalez-Gay MA, Rodriguez- Rodriguez L, Ärlsetig L, Martin J, Rantapää-Dahlqvist S, Plenge RM, Raychaudhuri S, Klareskog L, Gregersen PK, Worthington J. **High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis.** *Nat Genet. 2012 Dec;44(12):1336-40.*

122. * Asselbergs FW, Guo Y, van Iperen EP, Sivapalaratnam S, Tragante V, Lanktree MB, Lange LA, Almoguera B, Appelman YE, Barnard J, Baumert J, Beitelshees AL, Bhangale TR, Chen YD, Gaunt TR, Gong Y, Hopewell JC, Johnson T, Kleber ME, Langaee TY, Li M, Li YR, Liu K, McDonough CW, Meijs MF, Middelberg RP, Musunuru K, Nelson CP, O'Connell JR, Padmanabhan S, Pankow JS, Pankratz N, Rafelt S, Rajagopalan R, Romaine SP, Schork NJ, Shaffer J, Shen H, Smith EN, Tischfield SE, van der Most PJ, van Vliet-Ostaptchouk JV, Verweij N, Volcik KA, Zhang L, Bailey KR, Bailey KM, Bauer F, Boer JM, Braund PS, Burt A, Burton PR, Buxbaum SG, Chen W, Cooper-Dehoff RM, Cupples LA, deJong JS, Delles C, Duggan D, Fornage M, Furlong CE, Glazer N, Gums JG, Hastie C, Holmes MV, Illig T, Kirkland SA, Kivimaki M, Klein R, Klein BE, Kooperberg C, Kottke-Marchant K, Kumari M, LaCroix AZ, Mallela L, Murugesan G, Ordovas J, Ouwehand WH, Post WS, Saxena R, Scharnagl H, Schreiner PJ, Shah T, Shields DC, Shimbo D, Srinivasan SR, Stolk RP, Swerdlow DI, Taylor HA Jr, Topol EJ, Toskala E, van Pelt JL, van Setten J, Yusuf S, Whittaker JC, Zwinderman AH; LifeLines Cohort Study, Anand SS, Balmforth AJ, Berenson GS, Bezzina CR, Boehm BO, Boerwinkle E, Casas JP, Caulfield MJ, Clarke R, Connell JM, Cruickshanks KJ, Davidson KW, Day IN, de Bakker PI, Doevendans PA, Dominiczak AF, Hall AS, Hartman CA, Hengstenberg C, Hillege HL, Hofker MH, Humphries SE, Jarvik GP, Johnson JA, Kaess BM, Kathiresan S, Koenig W, Lawlor DA, März W, Melander O, Mitchell BD, Montgomery GW, Munroe PB, Murray SS, Newhouse SJ, Onland-Moret NC, Poulter N, Psaty B, Redline S, Rich SS, Rotter JI, Schunkert H, Sever P, Shuldiner AR, Silverstein RL, Stanton A, Thorand B, Trip MD, Tsai MY, van der Harst P, van der Schoot E, van der Schouw YT, Verschuren WM, Watkins H, Wilde AA, Wolffenbuttel BH, Whitfield JB, Hovingh GK, Ballantyne CM, Wijmenga C, Reilly MP, Martin NG, Wilson JG, Rader DJ, Samani NJ, Reiner AP, Hegele RA, Kastelein JJ, Hingorani AD, Talmud PJ, Hakonarson H, Elbers CC, Keating BJ, Drenos F. **Large-scale gene-centric meta- analysis across 32 studies identifies multiple lipid loci.** *Am J Hum Genet. 2012 Nov 2;91(5):823-38.*

123. De Boer RA, Verweij N, van Veldhuisen DJ, Westra HJ, Bakker SJ, Gansevoort RT, Muller Kobold AC, van Gilst WH, **Franke L**, Mateo Leach I, van der Harst P. **A genome-wide association study of circulating galectin-3.** *PLoS One. 2012;7(10):e47385.*

124. * Franceschini N, van Rooij FJ, Prins BP, Feitosa MF, Karakas M, Eckfeldt JH, Folsom AR, Kopp J, Vaez A, Andrews JS, Baumert J, Boraska V, Broer L, Hayward C, Ngwa JS, Okada Y, Polasek O, Westra HJ, Wang YA, Del Greco M F, Glazer NL, Kapur K, Kema IP, Lopez LM, Schillert A, Smith AV, Winkler CA, Zgaga L; LifeLines Cohort Study, Bandinelli S, Bergmann S, Boban M, Bochud M, Chen YD, Davies G, Dehghan A, Ding J, Doering A, Durda JP, Ferrucci L, Franco OH, **Franke L**, Gunjaca G, Hofman A, Hsu FC, Kolcic I, Kraja A, Kubo M, Lackner KJ, Launer L, Loehr LR, Li G, Meisinger C, Nakamura Y, Schwienbacher C, Starr JM, Takahashi A, Torlak V, Uitterlinden AG, Vitart V, Waldenberger M, Wild PS, Kirin M, Zeller T, Zemunik T, Zhang Q, Ziegler A, Blankenberg S, Boerwinkle E, Borecki IB, Campbell H, Deary IJ, Frayling TM, Gieger C, Harris TB, Hicks AA, Koenig W, O' Donnell CJ, Fox CS, Pramstaller PP, Psaty BM, Reiner AP, Rotter JI, Rudan I, Snieder H, Tanaka T, van Duijn CM, Vollenweider P, Waeber G, Wilson JF, Witteman JC, Wolffenbuttel BH, Wright AF, Wu Q, Liu Y, Jenny NS, North KE, Felix JF, Alizadeh BZ, Cupples LA, Perry JR, Morris AP. **Discovery and fine mapping of serum protein loci through transethnic meta-analysis.** *Am J Hum Genet. 2012 Oct 5;91(4):744-53.*

125. Diekstra FP, Saris CG, van Rheenen W, **Franke L**, Jansen RC, van Es MA, van Vught PW, Blauw HM, Groen EJ, Horvath S, Estrada K, Rivadeneira F, Hofman A, Uitterlinden AG, Robberecht W, Andersen PM, Melki J, Meininger V, Hardiman O, Landers JE, Brown RH Jr, Shatunov A, Shaw CE, Leigh PN, Al-Chalabi A, Ophoff RA, van den Berg LH, Veldink JH. **Mapping of gene expression reveals CYP27A1 as a susceptibility gene for sporadic ALS.** *PLoS One. 2012;7(4):e35333.*

126. Demirkan A, van Duijn CM, Ugocsai P, Isaacs A, Pramstaller PP, Liebisch G, Wilson JF, Johansson Å, Rudan I, Aulchenko YS, Kirichenko AV, Janssens AC, Jansen RC, Gnewuch C, Domingues FS, Pattaro C, Wild SH, Jonasson I, Polasek O, Zorkoltseva IV, Hofman A, Karssen LC, Struchalin M, Floyd J, Igl W, Biloglav Z, Broer L, Pfeufer A, Pichler I, Campbell S, Zaboli G, Kolcic I, Rivadeneira F, Huffman J, Hastie ND, Uitterlinden A, **Franke L**, Franklin CS, Vitart V; DIAGRAM Consortium, Nelson CP, Preuss M; CARDIoGRAM Consortium, Bis JC, O'Donnell CJ, Franceschini N; CHARGE Consortium, Witteman JC, Axenovich T, Oostra BA, Meitinger T, Hicks AA, Hayward C, Wright AF, Gyllensten U, Campbell H, Schmitz G; EUROSPAN consortium. **Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations.** *PLoS Genet. 2012 Feb;8(2):e1002490.*

127. Fu J, Wolfs MG, Deelen P, Westra HJ, Fehrmann RS, Te Meerman GJ, Buurman WA, Rensen SS, Groen HJ, Weersma RK, van den Berg LH, Veldink J, Ophoff RA, Snieder H, van Heel D, Jansen RC, Hofker MH, Wijmenga C, **Franke L**. **Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression.** *PLoS Genet. 2012 Jan;8(1):e1002431.*

128. Johnson T, Gaunt TR, Newhouse SJ, Padmanabhan S, Tomaszewski M, Kumari M, Morris RW, Tzoulaki I, O'Brien ET, Poulter NR, Sever P, Shields DC, Thom S, Wannamethee SG, Whincup PH, Brown MJ, Connell JM, Dobson RJ, Howard PJ, Mein CA, Onipinla A, Shaw- Hawkins S, Zhang Y, Davey Smith G, Day IN, Lawlor DA, Goodall AH; Cardiogenics Consortium, Fowkes FG, Abecasis GR, Elliott P, GatevaV; Global BPgen Consortium, Braund PS, Burton PR, Nelson CP, Tobin MD, van der Harst P, Glorioso N, Neuvrith H, Salvi E, Staessen JA, Stucchi A, Devos N, Jeunemaitre X, Plouin PF, Tichet J, Juhanson P, Org E, Putku M, Sõber S, Veldre G, Viigimaa M, Levinsson A, Rosengren A, Thelle DS, Hastie CE, Hedner T, Lee WK, Melander O, Wahlstrand B, Hardy R, Wong A, Cooper JA, Palmen J, Chen L, Stewart AF, Wells GA, Westra HJ, Wolfs MG, Clarke R, Franzosi MG, Goel A, Hamsten A, Lathrop M, Peden JF, Seedorf U, Watkins H, Ouwehand WH, Sambrook J, Stephens J, Casas JP, Drenos F, Holmes MV, Kivimaki M, Shah S, Shah T, Talmud PJ, Whittaker J, Wallace C, Delles C, Laan M, Kuh D, Humphries SE, Nyberg F, Cusi D, Roberts R, Newton-Cheh C, **Franke L**, Stanton AV, Dominiczak AF, Farrall M, Hingorani AD, Samani NJ, Caulfield MJ, Munroe PB. **Blood pressure loci identified with a gene-centric array.** *Am J Hum Genet. 2011 Dec 9;89(6):688-700.*

129. *** Trynka G, Hunt KA, Bockett NA, Romanos J, Mistry V, Szperl A, Bakker SF, Bardella MT, Bhaw-Rosun L, Castillejo G, de la Concha EG, de Almeida RC, Dias KR, van Diemen CC, Dubois PC, Duerr RH, Edkins S, **Franke L**, Fransen K, Gutierrez J, Heap GA, Hrdlickova B, Hunt S, Izurieta LP, Izzo V, Joosten LA, Langford C, Mazzilli MC, Mein CA, Midah V, Mitrovic M, Mora B, Morelli M, Nutland S, Núñez C, Onengut-Gumuscu S, Pearce K, Platteel M, Polanco I, Potter S, Ribes-Koninckx C, Ricaño-Ponce I, Rich SS, Rybak A, Santiago JL, Senapati S, Sood A, Szajewska H, Troncone R, Varadé J, Wallace C, Wolters VM, Zhernakova A; Spanish Consortium on the Genetics of Coeliac Disease (CEGEC); PreventCD Study Group; Wellcome Trust Case Control Consortium (WTCCC), Thelma BK, Cukrowska B, Urcelay E, Bilbao JR, Mearin ML, Barisani D, Barrett JC, Plagnol V, Deloukas P, Wijmenga C, van Heel DA. **Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease.** *Nat Genet. 2011 Nov 6;43(12):1193-201.*

130. Sampietro ML, Trompet S, Verschuren JJ, Talens RP, Deelen J, Heijmans BT, de Winter RJ, Tio RA, Doevendans PA, Ganesh SK, Nabel EG, Westra HJ, **Franke** L, van den Akker EB, Westendorp RG, Zwinderman AH, Kastrati A, Koch W, Slagboom PE, de Knijff P, Jukema JW. **A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention.** *Hum Mol Genet. 2011 Dec 1;20(23):4748-57.*

131. Fehrmann RS, Jansen RC, Veldink JH, Westra HJ, Arends D, Bonder MJ, Fu J, Deelen P, Groen HJ, Smolonska A, Weersma RK, Hofstra RM, Buurman WA, Rensen S, Wolfs MG, Platteel M, Zhernakova A, Elbers CC, Festen EM, Trynka G, Hofker MH, Saris CG, Ophoff RA, van den Berg LH, van Heel DA, Wijmenga C, Te Meerman GJ, **Franke L**. **Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA.** *PLoS Genet. 2011 Aug;7(8):e1002197.*

132. *** Dolmans GH, Werker PM, Hennies HC, Furniss D, Festen EA, **Franke L**, Becker K, van der Vlies P, Wolffenbuttel BH, Tinschert S, Toliat MR, Nothnagel M, Franke A, Klopp N, Wichmann HE, Nürnberg P, Giele H, Ophoff RA, Wijmenga C; Dutch Dupuytren Study Group; German Dupuytren Study Group; LifeLines Cohort Study; BSSH-GODD Consortium. **Wnt signaling and Dupuytren's disease.** *N Engl J Med. 2011 Jul 28;365(4):307-17.*

133. Westra HJ, Jansen RC, Fehrmann RSN, te Meerman GJ, van Heel D, Wijmenga C, **Franke L. MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects.** *Bioinformatics. 2011 Aug 1;27(15):2104-11*

134. Hrdlickova B, Westra HJ, **Franke L**, Wijmenga C. **Celiac disease: moving from genetic associations to causal variants.** *Clin Genet. 2011 Sep;80(3):203-313. doi: 10.1111/j.1399-0004.2011.01707.x.*

135. Janse M, Lamberts LE, **Franke L**, Raychaudhuri S, Ellinghaus E, Boberg KM, Melum E, Folseraas T, Schrumpf E, Bergquist A, Björnsson E, Fu J, Westra HJ, Groen HJ, Fehrmann RS, Smolonska J, van den Berg LH, Ophoff RA, Porte RJ, Weismüller TJ, Wedemeyer J, Schramm C, Sterneck M, Günther R, Braun F, Vermeire S, Henckaerts L, Wijmenga C, Ponsioen CY, Schreiber S, Karlsen TH, Franke A, Weersma RK. **Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL and CARD9.** *Hepatology. 2011 Jun;53(6):1977-85.*

136. *** 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. **Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47.** *Nat Genet. 2011 Mar;43(3):246-52.*

137. *** Sotoodehnia N, Isaacs A, de Bakker PI, Dörr M, Newton-Cheh C, Nolte IM, van der Harst P, Müller M, Eijgelsheim M, Alonso A, Hicks AA, Padmanabhan S, Hayward C, Smith AV, Polasek O, Giovannone S, Fu J, Magnani JW, Marciante KD, Pfeufer A, Gharib SA, Teumer A, Li M, Bis JC, Rivadeneira F, Aspelund T, Köttgen A, Johnson T, Rice K, Sie MP, Wang YA, Klopp N, Fuchsberger C, Wild SH, Mateo Leach I, Estrada K, Völker U, Wright AF, Asselbergs FW, Qu J, Chakravarti A, Sinner MF, Kors JA, Petersmann A, Harris TB, Soliman EZ, Munroe PB, Psaty BM, Oostra BA, Cupples LA, Perz S, de Boer RA, Uitterlinden AG, Völzke H, Spector TD, Liu FY, Boerwinkle E, Dominiczak AF, Rotter JI, van Herpen G, Levy D, Wichmann HE, van Gilst WH, Witteman JC, Kroemer HK, Kao WH, Heckbert SR, Meitinger T, Hofman A, Campbell H, Folsom AR, van Veldhuisen DJ, Schwienbacher C, O'Donnell CJ, Volpato CB, Caulfield MJ, Connell JM, Launer L, Lu X, **Franke L**, Fehrmann RS, te Meerman G, Groen HJ, Weersma RK, van den Berg LH, Wijmenga C, Ophoff RA, Navis G, Rudan I, Snieder H, Wilson JF, Pramstaller PP, Siscovick DS, Wang TJ, Gudnason V, van Duijn CM, Felix SB, Fishman GI, Jamshidi Y, Stricker BH, Samani NJ, Kääb S, Arking DE. **Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction.** *Nat Genet. 2010 Dec;42(12):1068-76*

138. Martín JE, Alizadeh BZ, González-Gay MA, Balsa A, Pascual-Salcedo D, Fernández-Gutiérrez B, Raya E, **Franke L**, van't Slot R, Coenen MJ, van Riel P, Radstake TR, Koeleman BP, Martín J. **Identification of the oxidative stress-related gene MSRA as a rheumatoid arthritis susceptibility locus by genome-wide pathway analysis.** *Arthritis Rheum. 2010 Nov;62(11):3183-90.*

139. Fransen K, Visschedijk MC, van Sommeren S, Fu JY, **Franke L**, Festen EA, Stokkers PC, van Bodegraven AA, Crusius JB, Hommes DW, Zanen P, de Jong DJ, Wijmenga C, van Diemen CC, Weersma RK. **Analysis of SNPs with an effect on gene expression identifies UBE2L3 and BCL3 as potential new risk genes for Crohn's disease.** *Hum Mol Genet. 2010 Sep 1;19(17):3482-8.*

140. Knauff EA, Blauw HM, Pearson PL, Kok K, Wijmenga C, Veldink JH, van den Berg LH, Bouchard P, Fauser BC, **Franke L**; for the Dutch Primary Ovarian Insufficiency Consortium. **Copy number variants on the X chromosome in women with primary ovarian insufficiency.** *Fertil Steril. 2011 Apr;95(5):1584-1588.e1.*

141. Zhernakova A, Elbers CC, Fewerederb B, Romanos J, Trynka G, Dubois PC, de Kovel CGF, **Franke L**, Oosting M, Barisani D, Bardella MT, Finnish Celiac Disease Study Group, Joosten LA, Saavalainen P, van Heel DA, Catassi C, Netea MG, Wijmenga C. **Evolutionary and functional analysis of celiac risk loci reveals SH2B3 as a protective factor against bacterial infection.** *Am J Hum Genet. 2010 Jun 11;86(6):970-7.*

142. Wolfs MGM, Rensen SS, Verdam FJ, Greve JW, Sanjabi B, Bruinenberg M, Wijmenga C, van Haeften TW, Buurman WA, Hofker MH, **Franke L**. **Co-expressed immune and metabolic genes in visceral and subcutaneous adipose tissue from severely obese individuals are associated with plasma HDL and glucose levels: a microarray study.** *BMC Med Genomics. 2010 Aug 5;3:34.*

143. van Disseldorp J, **Franke L**, Eijkemans R, Broekmans F, Macklona N, Wijmenga C, Fauser B. **Genome-wide analysis shows no genomic predictors of ovarian response to stimulation by exogenous FSH for IVF.** *Reprod Biomed Online. 2011 Apr;22(4):382-8.*

144. *** Dubois PCA, Trynka G, **Franke L**, Hunt KA, Romanos J, Curtotti A, Zhernakova A, Heap GAR, Aêdány R, Aromaa A, Bardella MT, van den Berg, LH, Bockett NA, de la Concha EG, Dema B, Fehrmann RSN, Fernández-Arquero M, Fiatal S, Grandone E, Green PM, Groen HJM, Gwilliam R, Houwen RHJ, Hunt SE, Kaukinen K, Kelleher D, Korponay-Szabo I, Kurppa K, MacMathuna P, Mäki M, Mazzilli MC, McCann OT, Mearin ML, Mein CA, Mirza MM, Mistry V, Mora B, Morley KI, Mulder CJ, Murray JA, Núñez C, Oosterom E, Ophoff RA, Polanco I, Peltonen L, Platteel M, Rybak A, Salomaa V, Schweizer JJ, Sperandeo MP, Tack GJ, Turner G, Veldink JH, Verbeek WHM, Weersma RK, Wolters VM, Urcelay E, Cukrowska B, Greco L, Neuhausen SL, McManus R, Barisani D, Deloukas P, Barrett JC, Saavalainen P, Wijmenga C, van Heel DA. **Multiple common variants for celiac disease influencing immune gene expression.** *Nature Genetics, 2010 42, 295- 302.*

145. Heap GA, Yang JH, Downes K, Healy BC, Hunt KA, Bockett N, **Franke L**, Dubois PC, Mein CA, Dobson RJ, Albert TJ, Rodesch

MJ, Clayton DG, Todd JA, van Heel DA, Plagnol V. **Genome-wide analysis of allelic expression imbalance in human primary cells by high- throughput transcriptome resequencing.** *Hum Mol Genet. 2010 Jan 1;19(1):122-34.*

146. **Franke L**, Knauff EAH, van Es L, van der Schouw YT, Laven JSE, Lambalk CB, Goverde AJ, Christin-Maitre S, Wijmenga C, Fauser BCJM. **Genome-wide association study in premature ovarian failure patients reveals ADAMTS19 as a possible candidate gene.** *Hum Reprod. 2009 Sep;24(9):2372-8.*

147. **Franke L**, Buizer-Voskamp JE, Staal WG, van Daalen E, Kemner C, Ophoff RA, Vorstman JAS, van Engeland H, Wijmenga C. **Systematic genotype-phenotype analysis of autism susceptibility loci implicates additional symptoms to co-occur with autism.** *Eur J Hum Genet. 2010 May;18(5):588-95. doi: 10.1038/ejhg.2009.206. Epub 2009 Nov 25.*

148. Van der Zwaag B, **Franke L**, Poot M, Hochstenbach R, Spierenburg HA, Vorstman JAS, van Daalen E, de Jonge MV, Verbeek NE, Brilstra EH, van 't Slot R, Ophoff RA, van Es MA, Blauw HM, Veldink JH, Buizer-Voskamp JE, Beemer FA, van den Berg LH, Wijmenga C, Ploos van Amstel HK, van Engeland H, Burbach JPH, Staal WG. **Gene-network analysis identifies susceptibility genes related to glycobiology in autism.** *PLoS One. 2009 May28;4(5):e5324.*

149. Trynka G, Zhernakova A, Romanos J, **Franke L**, Hunt KA, Turner G, Bruinenberg M, Heap GA, Platteel M, Ryan AW, de Kovel C, Holmes GK, Howdle PD, Walters JR, Sanders DS, Mulder CJ, Mearin ML, Verbeek WH, Trimble V, Stevens FM, Kelleher D, Barisani D, Bardella MT, McManus R, van Heel DA, Wijmenga C. **Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF- kappaB signalling.** *Gut. 2009Aug;58(8):1078-83.*

150. Elbers CC, van Eijk KR, **Franke L**, Mulder F, van der Schouw YT, Wijmenga C, Onland-Moret NC. **Using genome-wide pathway analysis to unravel the etiology of complex diseases.** *Genet Epidemiol. 2009 Jul;33(5):419-31.*

151. Heap GA, Trynka G, Jansen RC, Bruinenberg M, Schwertz MA, Dinesen LC, Hunt KA, van Heel DA, **Franke L**. **Complex nature of SNP genotype effects on gene expression in primary human leucocytes.** *BMC Medical Genomics 2009, 2:1.*

152. **Franke L**, de Kovel CG, Aulchenko YS, Trynka G, Zhernakova A, Hunt KA, Blauw HM, van den Berg LH, Ophoff R, Deloukas P, van Heel DA, Wijmenga C. **Detection, imputation, and association analysis of small deletions and null alleles on oligonucleotide arrays.** *Am J Hum Genet. 2008Jun;82(6):1316-33.*

153. Zhernakova A, Festen EM, **Franke L**, Trynka G, van Diemen CC, Monsuur AJ, Bevova M, Nijmeijer RM, van 't Slot R, Heijmans R, Boezen HM, van Heel DA, van Bodegraven AA, Stokkers PC, Wijmenga C, Crusius JB, Weersma RK. **Genetic analysis of innate immunity in Crohn's disease and ulcerative colitis identifies two susceptibility loci harboring CARD9 and IL18RAP.** *Am J Hum Genet. 2008 May;82(5):1202-10.*

154. Hunt KA, **Franke L**, Deloukas P, Wijmenga C, van Heel DA. **No evidence in a large UK collection for celiac disease risk variants reported by a Spanish study.** *Gastroenterology. 2008 May;134(5):1629-30.*

155. *** Hunt KA, Zhernakova A, Turner G, Heap GA, **Franke L**, Bruinenberg M, Romanos J, Dinesen LC, Ryan AW, Panesar D, Gwilliam R, Takeuchi F, McLaren WM, Holmes GK, Howdle PD, Walters JR, Sanders DS, Playford RJ, Trynka G, Mulder CJ, Mearin ML, Verbeek WH, Trimble V, Stevens FM, O'Morain C, Kennedy NP, Kelleher D, Pennington DJ, Strachan DP, McArdle WL, Mein CA, Wapenaar MC, Deloukas P, McGinnis R, McManus R, Wijmenga C, van Heel DA. **Newly identified genetic risk variants for celiac disease related to the immune response.** *Nat Genet. 2008 Apr;40(4):395-402.*

156. ** Blauw HM, Veldink JH, van Es MA, van Vught PW, Saris CG, van der Zwaag B, **Franke L**, Burbach JP, Wokke JH, Ophoff RA, van den Berg LH. **Copy-number variation in sporadic amyotrophic lateral sclerosis: a genome-wide screen.** *Lancet Neurol. 2008 Apr;7(4):319-26.*

157. Van Vliet-Ostaptchouk JV, Onland-Moret NC, van Haeften TW, **Franke L**, Elbers CC, Shiri-Sverdlov R, van der Schouw YT, Hofker MH, Wijmenga C. **HHEX gene polymorphisms are associated with type 2 diabetes in the Dutch Breda cohort.** *Eur J Hum Genet. 2008 May;16(5):652-6.*

158. *** **Franke L**, van Es MA, van Vught PW, Blauw HM, Saris CG, Van den Bosch L, de Jong SW, de Jong V, Baas F, van't Slot R, Lemmens R, Schelhaas HJ, Birve A, Sleegers K, Van Broeckhoven C, Schymick JC, Traynor BJ, Wokke JH, Wijmenga C, Robberecht W, Andersen PM, Veldink JH, Ophoff RA, van den Berg LH. **Genetic variation in DPP6 is associated with susceptibility to amyotrophic lateral sclerosis.** *Nat Genet. 2008Jan;40(1):29-31.*

159. Zhernakova A, Alizadeh BZ, Bevova M, van Leeuwen MA, Coenen MJ, Franke B, **Franke L**, Posthumus MD, van Heel DA, van der Steege G, Radstake TR, Barrera P, Roep BO, Koeleman BP, Wijmenga C. **Novel association in chromosome 4q27 region with rheumatoid arthritis and confirmation of type 1 diabetes point to a general risk locus for autoimmune diseases.** *Am J Hum Genet. 2007 Dec;81(6):1284-8.*

160. ** **Franke L**, van Es MA, Van Vught PW, Blauw HM, Saris CG, Andersen PM, Van Den Bosch L, de Jong SW, van 't Slot R, Birve A, Lemmens R, de Jong V, Baas F, Schelhaas HJ, Sleegers K, Van Broeckhoven C, Wokke JH, Wijmenga C, Robberecht W, Veldink JH, Ophoff RA, van den Berg LH. **ITPR2 as a susceptibility gene in sporadic amyotrophic lateral sclerosis: a genome-wide association study.** *Lancet Neurol. 2007Oct;6(10):869-77.*

161. De Jong E, **Franke L**, Siebes A. **On the measurement of genetic interactions.** *AIP Conf. Proc. 2007 Sep 17;940:16-25.*

162. *** Van Heel DA, **Franke L**, Hunt KA, Gwilliam R, Zhernakova A, Inouye M, Wapenaar MC, Barnardo MC, Bethel G, Holmes GK, Feighery C, Jewell D, Kelleher D, Kumar P, Travis S, Walters JR, Sanders DS, Howdle P, Swift J, Playford RJ, McLaren WM, Mearin ML, Mulder CJ, McManus R, McGinnis R, Cardon LR, Deloukas P, Wijmenga C. **A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21.** *Nat Genet. 2007 Jul;39(7):827-9.*

163. Diosdado B, van Bakel H, Strengman E, **Franke L**, van Oort E, Mulder CJ, Wijmenga C, Wapenaar MC. **Neutrophil recruitment and barrier impairment in celiac disease: a genomic study.** *Clin Gastroenterol Hepatol. 2007 May;5(5):574-81.*

164. Elbers CC, Onland-Moret NC, **Franke L**, Niehoff AG, van der Schouw YT, Wijmenga C. **A strategy to search for common obesity and type 2 diabetes genes.** *Trends Endocrinol Metab. 2007 Jan-Feb;18(1):19-26.*

165. Malik R, **Franke L**, Siebes A. **Combination of text-mining algorithms increases the performance.** *Bioinformatics. 2006 Sep 1;22(17):2151-7.*

166. **Franke L**, van Bakel H, Fokkens L, de Jong ED, Egmont-Petersen M, Wijmenga C. **Reconstruction of a functional human gene network, with an application for prioritizing positional candidate genes.** *Am J Hum Genet 2006; 78(6):1011-1025.*

167. Vorstman JA, Staal WG, van Daalen E, van Engeland H, Hochstenbach PF, **Franke L**. **Identification of novel autism candidate regions through analysis of reported cytogenetic abnormalities associated with autism.** *Mol Psychiatry. 2006 Jan;11(1):1, 18-28.*

168. *** Monsuur AJ, de Bakker PI, Alizadeh BZ, Zhernakova A, Bevova MR, Strengman E, **Franke L**, van't Slot R, van Belzen MJ, Lavrijsen IC, Diosdado B, Daly MJ, Mulder CJ, Mearin ML, Meijer JW, Meijer GA, van Oort E, Wapenaar MC, Koeleman BP, Wijmenga C.

169. ***Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect.*** *Nat Genet. 2005 Dec;37(12):1341-4.*

170. Diosdado B, Stepniak DT, Monsuur AJ, **Franke L**, Wapenaar MC, Mearin ML, Koning F, Wijmenga C. **No genetic association of the human prolyl endopeptidase gene in the Dutch celiac disease population.** *Am J Physiol Gastrointest Liver Physiol. 2005 Sep;289(3):G495-500.*

171. Diosdado B, Wapenaar MC, **Franke L**, Duran KJ, Goerres MJ, Hadithi M, Crusius JB, Meijer JW, Duggan DJ, Mulder CJ, Holstege FC, Wijmenga C. **A microarray screen for novel candidate genes in coeliac disease pathogenesis.** *Gut. 2004 Jul;53(7):944-51.*

172. **Franke L**, van Bakel H, Diosdado B, van Belzen M, Wapenaar M, Wijmenga C. **TEAM: a tool for the integration of expression, and linkage and association maps.** *Eur J Hum Genet. 2004 Aug;12(8):633-8.*

173. Van Tilburg JH, Sandkuijl LA, **Franke L**, Strengman E, Pearson PL, van Haeften TW, Wijmenga C. **Genome-wide screen in obese pedigrees with type 2 diabetes mellitus from a defined Dutch population.** *Eur J Clin Invest. 2003 Dec;33(12):1070-4.*

Book chapters

1. Westra HJ, **Franke L**. From genome to function by studying eQTLs. Biochim Biophys Acta. 2014 May 4. pii: S0925-4439(14)00111-2.
2. **Franke L**, Jansen RC. eQTL analysis in humans. Methods Mol Biol. 2009;573:311-28. doi: 10.1007/978-1-60761-247-6_17.