Lukas Forer

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Institute of Genetic Epidemiology
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Date of birth:	27.06.1985
Place of birth:	Bruneck, Italy
Citizenship:	Italian
Academic titles:	Ph.D.
Languages:	German, English, Italian

Education:

1999-2004	Matura at Gewerbeoberschule Bruneck, Italy
2004-2010	Study of Computer Science at the University of Innsbruck (MSc) Title: *Genome-Wide Association Studies based on Copy Number Variations* Supervisors: Günther Specht and Sebastian Schönherr
2010-2014	Study of Computer Science at the University of Innsbruck (PhD) Title: *A MapReduce Workflow System for High-Throughput Detection and Analysis of Genetic Variations* Supervisors: Günther Specht und Anita Kloss-Brandstätter

Professional experience:

2006-2008	Scientific Software Developer European Academy of Bozen/Bolzano (EURAC), Italy
2008-2009	Scientific Software Developer Research Laboratory of the Department of Urology Medical University of Innsbruck
2009-2014	Scientific Assistant Institute of Genetic Epidemiology, Medical University of Innsbruck
2014-2023	Senior Scientist Institute of Genetic Epidemiology, Medical University of Innsbruck
2023-present	Assistant Professor of Genome Informatics Institute of Genetic Epidemiology, Medical University of Innsbruck

Awards:

2010	Scientific price of the Austrian Society for Human Genetics
2015	Best Paper Award, 38th International Convention on Information and Communication Technology, Electronics and Microelectronics (MIPRO)

Grants:

2010	Amazon AWS in Education Research Grant
2011	Aktion D. Swarovski & Co 2011(Co-PI) (**3,000 EUR)**
2013	Amazon AWS in Education Research Grant
2019	Subgrant University of Michigan, NIH (PI) (**124,700 USD**)
Since 2018	Project Askimed (Co-PI) (**560,000 EUR**)

Publications:	111 articles in journals and proceedings (13 as first or corresponding author, 29 as collaborator)	
Hirsch-Index:	37	[based on Google Scholar, 15.03.2025]
Citations:	> 16,000 citations	[based on Google Scholar, 15.03.2025]
Presentations:	> 30 oral presentations at national and international meetings	

Teaching:

2015	University of Applied Sciences Kufstein CRM and Information Mining I
2018	Medicine curriculum. Medical University of Innsbruck. Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.
2019	Medicine curriculum. Medical University of Innsbruck. Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.
2019	UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik. 31N008 Biostatistik I.
2019	Medicine curriculum. Medical University of Innsbruck. Modul1.06: Bausteine des Lebens II; Biologie
2020	Medicine curriculum. Medical University of Innsbruck. Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.
2020	UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik. 31N008 Biostatistik I.
2020	Medicine curriculum. Medical University of Innsbruck. Modul1.06: Bausteine des Lebens II; Biologie
2021	Medicine curriculum. Medical University of Innsbruck.

Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.

2021 UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik.
31N008 Biostatistik I.

2021 Medicine curriculum. Medical University of Innsbruck.
Modul1.06: Bausteine des Lebens II; Biologie

2022 Medicine curriculum. Medical University of Innsbruck.
Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.

2022 Medicine curriculum. Medical University of Innsbruck.
Praktikum der Gentischen Labordiagostik (LAB).

2022 UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik.
31N008 Biostatistik I.

2022 Molecular Medicine curriculum. Medical University of Innsbruck.
Modul MM 1.3: Statistik

2023 Medicine curriculum. Medical University of Innsbruck.
Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.

2023 PhD - Medical science. Medical University of Innsbruck.
Genetic Risk assessment for complex diseases (KF)

2023 UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik.
31N008 Biostatistik I.

2024 Molecular Medicine curriculum. Medical University of Innsbruck.
Modul MM 1.3: Statistik

2024 Medicine curriculum. Medical University of Innsbruck.
Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.

2024 PhD - Medical science. Medical University of Innsbruck.
Genetic Risk assessment for complex diseases (KF)

2024 Genetic Counselling. Medical University of Innsbruck.
Medizinische Genetik

2024 Medicine curriculum. Medical University of Innsbruck.
Modul 2.52 - Bausteine des Lebens 4 - Life Sciences 3

2024 UMIT - Private Universität für Gesundheitswissenschaften, Medizinische Informatik und Technik.
31N008 Biostatistik I.

2024 PhD - Medical science. Medical University of Innsbruck.
Brückenkurs Statistik für Clinical PhD

2025 Medicine curriculum. Medical University of Innsbruck.
Modul 2.52 - Bausteine des Lebens 4 - Life Sciences 3

2025 Medicine curriculum. Medical University of Innsbruck.
Mandatory course: Modul 3.30: Statistik für Diplomandinnen und Diplomanden.

2025 PhD - Medical science. Medical University of Innsbruck.

Genetic Risk assessment for complex diseases (KF)

2025 PhD - Medical science. Medical University of Innsbruck.
Scientific Computing and Reproducible Data Analysis in Biomedicine

Thesis advisory responsibilities:

2013	Michael Kopfensteiner, Baccalaureat thesis, University of Innsbruck
2013	Clemens Banas, Baccalaureat thesis, University of Innsbruck
2016	Clemens Banas, Master thesis, University of Innsbruck
2022	Martin Eberle, Master thesis, University of Innsbruck
2023	Jonas Jäger, Baccalaureat thesis, Medical University of Innsbruck
2024	Laurenz Greber, Diploma thesis, Medical University of Innsbruck
2024	Sophie Stückler, Diploma thesis, Medical University of Innsbruck
2024	Jakob Kröll, Diploma thesis, Medical University of Innsbruck
2024	Klara Welzig, Diploma thesis, Medical University of Innsbruck
2025	Florian Schnitzer, PhD thesis, Medical University of Innsbruck

Past and current collaborations (excludes consortia work):

Eurac Research Bozen/Bolzano (Dr. Christian Fuchsberger)

Johns Hopkins University (Dr. Enis Afgan)

University of Innsbruck (Prof. Günther Specht)

University of Michigan (Prof. Michael Boehnke, Prof. Goncalo Abecasis)

University of Zagreb (Dr. Davor Davidovic)

Medical University of Innsbruck (Prof. Johannes Zschocke, Prof. Heinz Zoller)

Consortia activities:

German Chronic Kidney Diseases Study (GCKD), Non-coding RNAs for personalised pain medicine (ncRNAPain), nonHFE-Registry Consortium, ApoA-IV-GWAS Consortium, Lp(a)-GWAS-Consortium, The Haplotype Reference Consortium (HRC), NHLBI Trans-Omics for Precision Medicine (TOPMed), The Genome Asia 100K project, HEVACC Study-Group

Software

All software is free to use and open source:

pgs-calc	Applying polygenic scores (PGS) on imputed genotypes. https://github.com/lukfor/pgs-calc
nf-gwas	Pipeline to perform state-of-the-art genome-wide association studies. https://genepi.github.io/nf-gwas
nf-test	Testing framework for Nextflow Pipelines.

	https://www.nf-test.com
Imputation Server	Free genotype phasing and imputation service. https://imputationserver.sph.umich.edu
mtDNA Server	Free service for the analysis of human mitochondrial DNA data. https://mtdna-server.uibk.ac.at
Haplogrep	Free service for mtDNA haplogroup classification using PhyloTree. http://haplogrep.i-med.ac.at/
Cloudgene	Open source framework to improve the usability of MapReduce programs and the reproducibility of workflows. http://www.cloudgene.io
Cloudflow	A MapReduce pipeline framework to simplify the pipeline creation in biomedical research, especially in the field of Genetics. https://github.com/genepi/cloudflow
CONAN	A software solution for categorizing, analyzing and associating CNVs with phenotypes. http://genepi-conan.i-med.ac.at
PedVizApi	Java API for the visual analysis of large and complex pedigrees. http://www.fuchsberger.it/pedvizapi

Publications

Original articles

(Publications with Impact-Factor > 10)

1. Fuchsberger C, Falchi M, **Forer L**, Pramstaller PP. PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. **Bioinformatics**. 2008; 24:279-81. PMID: 18033791

2. **Forer L**, Schönherr S, Weissensteiner H, Haider F, Kluckner T, Gieger C, Wichmann HE, Specht G, Kronenberg F, Kloss-Brandstätter A. CONAN: copy number variation analysis software for genome-wide association studies. **BMC Bioinformatics**. 2010;11:318. PMID: 20546565

3. Jacquemont S, Reymond A, Zufferey F, Harewood L, Walters RG, Kutalik Z, Martinet D, Shen Y, Valsesia A, Beckmann ND, Thorleifsson G, Belfiore M, Bouquillon S, Campion D, de Leeuw N, de Vries BB, Esko T, Fernandez BA, Fernández-Aranda F, Fernández-Real JM, Gratacòs M, Guilmatre A, Hoyer J, Jarvelin MR, Frank Kooy R, Kurg A, Le Caignec C, Männik K, Platt OS, Sanlaville D, Van Haelst MM, Villatoro Gomez S, Walha F, Wu BL, Yu Y, Aboura A, Addor MC, Alembik Y, Antonarakis SE, Arveiler B, Barth M, Bednarek N, Béna F, Bergmann S, Beri M, Bernardini L, Blaumeiser B, Bonneau D, Bottani A, Boute O, Brunner HG, Cailley D, Callier P, Chiesa J, Chrast J, Coin L, Coutton C, Cuisset JM, Cuvellier JC, David A, de Freminville B, Delobel B, Delrue MA, Demeer B, Descamps D, Didelot G, Dieterich K, Disciglio V, Doco-Fenzy M, Drunat S, Duban-Bedu B, Dubourg C, El-Sayed Moustafa JS, Elliott P, Faas BH, Faivre L, Faudet A, Fellmann F, Ferrarini A, Fisher R, Flori E, **Forer L**, Gaillard D, Gerard M, Gieger C, Gimelli S, Gimelli G, Grabe HJ, Guichet A, Guillin O, Hartikainen AL, Heron D, Hippolyte L, Holder M, Homuth G, Isidor B, Jaillard S, Jaros Z, Jiménez-Murcia S, Joly Helas G, Jonveaux P, Kaksonen S, Keren B, Kloss-Brandstätter A, Knoers NV, Koolen DA, Kroisel PM, Kronenberg F, Labalme A, Landais E, Lapi E, Layet V, Legallic S, Leheup B, Leube B, Lewis S, Lucas J, Macdermot KD, Magnusson P, Marshall C, Mathieu-Dramard M, McCarthy MI, Meitinger T, Antonietta Mencarelli M, Merla G, Moerman A, Mooser V, Morice-Picard F, Mucciolo M, Nauck M, Coumba Ndiaye N, Nordgren A, Pasquier L, Petit

F, Pfundt R, Plessis G, Rajcan-Separovic E, Paolo Ramelli G, Rauch A, Ravazzolo R, Reis A, Renieri A, Richart C, Ried JS, Rieubland C, Roberts W, Roetzer KM, Rooryck C, Rossi M, Saemundsen E, Satre V, Schurmann C, Sigurdsson E, Stavropoulos DJ, Stefansson H, Tengström C, Thorsteinsdóttir U, Tinahones FJ, Touraine R, Vallée L, van Binsbergen E, Van der Aa N, Vincent-Delorme C, Visvikis-Siest S, Vollenweider P, Völzke H, Vulto-van Silfhout AT, Waeber G, Wallgren-Pettersson C, Witwicki RM, Zwolinksi S, Andrieux J, Estivill X, Gusella JF, Gustafsson O, Metspalu A, Scherer SW, Stefansson K, Blakemore AI, Beckmann JS, Froguel P. Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. **Nature**. 2011; 478(7367):97-10. PMID: 21881559

4. Schönherr S*, **Forer L***, Weißensteiner H, Kronenberg F, Specht G, and Kloss-Brandstätter. A: Cloudgene: a graphical execution platform for MapReduce programs on private and public clouds. **BMC Bioinformatics**. 2012;13:200. PMID: 22888776. * authors contributed equally

5. Lamina C, **Forer L**, Schönherr S, Kollerits B, Ried JS, Gieger C, Peters A, Wichmann HE, Kronenberg F.Evaluation of gene-obesity interaction effects on cholesterol levels: a genetic predisposition score on HDL-cholesterol is modified by obesity. **Atherosclerosis**. 2012;225(2). PMID: 23058813

6. Weissensteiner H, Haun M, Schönherr S, Neuner M, **Forer L**, Specht G, Kloss-Brandstätter A, Kronenberg F, and Coassin. S: SNPflow: A Lightweight Application for the Processing, Storing and Automatic Quality Checking of Genotyping Assays. **PloS one**. 2013; 8(3). PMID: 23527209

7. Summerer M, Horst J, Erhart G, Weißensteiner H, Schönherr S, Pacher D, **Forer L**, Horst D, Manhart A, Horst B, Sanguansermsri T, Kloss-Brandstätter A. Large-scale mitochondrial DNA analysis in Southeast Asia reveals evolutionary effects of cultural isolation in the multi-ethnic population of Myanmar. **BMC Evolutionary Biology**. 2014; 14:17. PMID: 24467713

8. Raschenberger J, Kollerits B, Titze S, Köttgen A, Bärthlein B, Ekici AB, **Forer L**, Schönherr S, Weissensteiner H, Haun M, Wanner C, Eckardt KU, Kronenberg F; GCKD study Investigator. Association of relative telomere length with cardiovascular disease in a large chronic kidney disease cohort: The GCKD study. **Atherosclerosis**. 2015; 242(2):529-34. PMID: 26302167

9. Kloss-Brandstätter A, Weissensteiner H, Erhart G, Schäfer G, **Forer L**, Schönherr S, Pacher D, Seifarth C, Stöckl A, Fendt L, Sottsas I, Klocker H, Huck CW, Rasse M, Kronenberg F, Kloss FR. Validation of Next-Generation Sequencing of Entire Mitochondrial Genomes and the Diversity of Mitochondrial DNA Mutations in Oral Squamous Cell Carcinoma. **PLoS One**. 2015; 10(8):e0135643. PMID: 26262956

10. Spjuth O, Bongcam-Rudloff E, Hernández GC, **Forer L**, Giovacchini M, Guimera RV, Kallio A, Korpelainen E, Kańduła MM, Krachunov M, Kreil DP, Kulev O, Łabaj PP, Lampa S, Pireddu L, Schönherr S, Siretskiy A, Vassilev D. Experiences with workflows for automating data-intensive bioinformatics. **Biol Direct**. 2015; 10:43. PMID: 26282399

11. Raschenberger J, Kollerits B, Titze S, Köttgen A, Bärthlein B, Ekici AB, **Forer L**, Schönherr S, Weissensteiner H, Haun M, Wanner C, Eckardt KU, Kronenberg F; GCKD study Investigators. Do telomeres have a higher plasticity than thought? Results from the German Chronic Kidney Disease (GCKD) study as a high-risk. **Exp Gerontol**. 2015; 72:162-6. PMID: 26423240

12. Weissensteiner H, Pacher D, Kloss-Brandstätter A, **Forer L**, Specht G, Bandelt H.-J, Kronenberg F, Salas A, Schönherr S. HaploGrep 2: mitochondrial haplogroup

classification in the era of high-throughput sequencing. **Nucleic Acids Res**. 2016; 44(W1):W58-63. PMID: 27084951

13. Weissensteiner H*, **Forer L***, Fuchsberger C, Schöpf B, Kloss-Brandstätter A, Specht G, Kronenberg F, Schönherr S. mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. **Nucleic Acids Res**. 2016; 44(W1):W64-9. PMID: 27084948. * authors contributed equally

14. **Forer L**, Afgan E, Weißensteiner H, Davidovic D, Specht G, Kronenberg F, Schonherr S. Cloudflow - enabling faster biomedical pipelines with MapReduce and Spark. **Scalable Comput. Pract. Exp**. 2016. 17(2):103–114. DOI: 10.12694/scpe.v17i2.1159

15. Lamina C, Friedel S, Coassin S, Rueedi R, Yousri NA, Seppälä I, Gieger C, Schönherr S, **Forer L**, Erhart G, Kollerits B, Marques-Vidal P, Ried J, Waeber G, Bergmann S, Dähnhardt D, Stöckl A, Kiechl S, Raitakari OT, Kähönen M, Willeit J, Kedenko L, Paulweber B, Peters A, Meitinger T, Strauch K, Study Group K, Lehtimäki T, Hunt SC, Vollenweider P, Kronenberg F. A Genome-wide Association Meta-analysis on Apolipoprotein A-IV Concentrations. **Hum Mol Genet**. 2016; 25(16):3635-3646. PMID: 27412012

16. McCarthy S, Das S, Kretzschmar W, Delaneau O, Wood AR, Teumer A, Kang HM, Fuchsberger C, Danecek P, Sharp K, Luo Y, Sidore C, Kwong A, Timpson N, Koskinen S, Vrieze S, Scott LJ, Zhang H, Mahajan A, Veldink J, Peters U, Pato C, van Duijn CM, Gillies CE, Gandin I, Mezzavilla M, Gilly A, Cocca M, Traglia M, Angius A, Barrett JC, Boomsma D, Branham K, Breen G, Brummett CM, Busonero F, Campbell H, Chan A, Chen S, Chew E, Collins FS, Corbin LJ, Smith GD, Dedoussis G, Dorr M, Farmaki AE, Ferrucci L, **Forer L**, Fraser RM, Gabriel S, Levy S, Groop L, Harrison T, Hattersley A, Holmen OL, Hveem K, Kretzler M, Lee JC, McGue M, Meitinger T, Melzer D, Min JL, Mohlke KL, Vincent JB, Nauck M, Nickerson D, Palotie A, Pato M, Pirastu N, McInnis M, Richards JB, Sala C, Salomaa V, Schlessinger D, Schoenherr S, Slagboom PE, Small K, Spector T, Stambolian D, Tuke M, Tuomilehto J, Van den Berg LH, Van Rheenen W, Volker U, Wijmenga C, Toniolo D, Zeggini E, Gasparini P, Sampson MG, Wilson JF, Frayling T, de Bakker PI, Swertz MA, McCarroll S, Kooperberg C, Dekker A, Altshuler D, Willer C, Iacono W, Ripatti S, Soranzo N, Walter K, Swaroop A, Cucca F, Anderson CA, Myers RM, Boehnke M, McCarthy MI, Durbin R, Abecasis G, Marchini J. A reference panel of 64,976 haplotypes for genotype imputation. **Nat Genet**. 2016; 48(10):1279-83. PMID: 27548312

17. Das S*, **Forer L***, Schönherr S*, Sidore C, Locke AE, Kwong A, Vrieze SI, Chew EY, Levy S, McGue M, Schlessinger D, Stambolian D, Loh PR, Iacono WG, Swaroop A, Scott LJ, Cucca F, Kronenberg F, Boehnke M, Abecasis GR, Fuchsberger C. Next-generation genotype imputation service and methods. **Nat Genet**. 2016; 48(10):1284-7. PMID: 27571263.* authors contributed equally

18. Loh PR, Danecek P, Palamara PF, Fuchsberger C, A Reshef Y, K Finucane H, Schoenherr S, **Forer L**, McCarthy S, Abecasis GR, Durbin R, L Price A. Reference-based phasing using the Haplotype Reference Consortium panel. **Nat Genet**. 2016; 48(11):1443-1448. PMID: 27694958

19. Taliun D, Chothani SP, Schönherr S, **Forer L**, Boehnke M, Abecasis GR, Wang C. LASER server: ancestry tracing with genotypes or sequence reads. **Bioinformatics**. 2017; 33(13):2056-2058. PMID: 28200055

20. Coassin S, Erhart G, Weissensteiner H, Eca Guimarães de Araújo M, Lamina C, Schönherr S, **Forer L**, Haun M, Losso JL, Köttgen A, Schmidt K, Utermann G, Peters A, Gieger C, Strauch K, Finkenstedt A, Bale R, Zoller H, Paulweber B, Eckardt KU, Hüttenhofer A, Huber LA, Kronenberg F. A novel but frequent variant in LPA KIV-2 is

associated with a pronounced Lp(a) and cardiovascular risk reduction. **Eur Heart J.**. 2017; 38(23):1823-1831. PMID: 28444229

21. Mack S, Coassin S, Rueedi R, Yousri NA, Seppälä I, Gieger C, Schönherr S, **Forer L**, Erhart G, Marques-Vidal P, Ried J, Waeber G, Bergmann S, Dähnhardt D, Stöckl A, Raitakari OT, Kähönen M, Peters A, Meitinger T, Strauch K, KORA-Study Group, Kedenko L, Paulweber B, Lehtimäki T, Hunt SC, Vollenweider P, Lamina C, Kronenberg F. A genome-wide association meta-analysis on lipoprotein(a) concentrations adjusted for apolipoprotein(a) isoforms. **J Lipid Res**. 2017; 58(9):1834-1844. PMID: 28512139

22. Raputova J, Srotova I, Vlckova E, Sommer C, Üçeyler N, Birklein F, Rittner HL, Rebhorn C, Adamova B, Kovalova I, Kralickova Nekvapilova E, **Forer L**, Belobradkova J, Olsovsky J, Weber P, Dusek L, Jarkovsky J, Bednarik J. Sensory phenotype and risk factors for painful diabetic neuropathy: a cross-sectional observational study. **Pain**. 2017; 158(12):2340-2353. PMID: 28858986

23. Coassin S, Schönherr S, Weissensteiner H, Erhart G, **Forer L**, Losso JL, Lamina C, Haun M, Utermann G, Paulweber B, Specht G, Kronenberg F. A comprehensive map of single-base polymorphisms in the hype rvariable LPA kringle IV type 2 copy number variation region. **J Lipid Res**. 2019 Jan;60(1):186-199. PMID: 30413653

24. Lamina C, Kronenberg F, Stenvinkel P, Froissart M, **Forer L**, Schönherr S, Wheeler DC, Eckardt KU, Floege J. Association of changes in bone mineral parameters with mortality in haemodialysis patients: insights from the ARO cohort. **Nephrol Dial Transplant**. 2019 Apr 21. pii: gfz060. PMID: 31006013

25. Fazzini F, Lamina C, Fendt L, Schultheiss UT, Kotsis F, Hicks AA, Meiselbach H, Weissensteiner H, **Forer L**, Krane V, Eckardt KU, Köttgen A, Kronenberg F, GCKD Investigators. Mitochondrial DNA copy number is associated with mortality and infections in a large cohort of patients with chronic kidney disease. **Kidney International**. 2019 Aug. 2019 Aug; 96(2):480-488. PMID: 31248648

26. Dietz C, Müller M, Reinhold AK, Karch L, Schwab B, **Forer L**, Vlckova E, Brede EM, Jakubietz R, Üçeyler N, Meffert R, Bednarik J, Kress M, Sommer C, Dimova V, Birklein F, Rittner HL. What is normal trauma healing, what is Complex Regional Pain Syndrome I? An analysis of clinical and experimental biomarkers. **Pain**. 2019 Oct; 160(10):2278-2289. PMID: 31095096

27. Wall JD, Stawiski EW, Ratan A, Kim HL, Kim C, Gupta R, Suryamohan K, Gusareva ES, Purbojati RW, Bhangale T, Stepanov V, Kharkov V, Schröder MS, Ramprasad V, Tom J, Durinck S, Bei Q, Li J, Guillory J, Phalke S, Basu A, Stinson J, Nair S, Malaichamy S, Biswas NK, Chambers JC, Cheng KC, George JT, Khor SS, Kim JI, Cho B, Menon R, Sattibabu T, Bassi A, Deshmukh M, Verma A, Gopalan V, Shin JY, Pratapneni M, Santhosh S, Tokunaga K, Md-Zain BM, Chan KG, Parani M, Natarajan P, Hauser M, Allingham RR, Santiago-Turla C, Ghosh A, Gadde SGK, Fuchsberger C, **Forer L**, Schoenherr S, Sudoyo H, Lansing JS, Friedlaender J, Koki G, Cox MP, Hammer M, Karafet T, Ang KC, Mehdi SQ, Radha V, Mohan V, Majumder PP, Seshagiri S, Seo JS, Schuster SC, Peterson AS. The GenomeAsia 100K Project enables genetic discoveries across Asia. **Nature** 576 (7785), 106-111. 2019 Dec 4. PMID: 31802016

28. Schlosser P, Li Y, Sekula P, Raffler J, Grundner-Culemann F, Pietzner M, Cheng Y, Wuttke M, Steinbrenner I, Schultheiss UT, Kotsis F, Kacprowski T, **Forer L**, Hausknecht B, Ekici AB, Nauck M, Völker U; GCKD Investigators, Walz G, Oefner PJ, Kronenberg F, Mohney RP, Köttgen M, Suhre K, Eckardt KU, Kastenmüller G, Köttgen A. Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. **Nature Genetics** 52 (2), 167-176. 2020 Jan 20. PMID: 31959995

29. Fazzini F, Lamina C, Raschenberger J, Schultheiss UT, Kotsis F, Schönherr S, Weissensteiner H, **Forer L**, Steinbrenner I, Meiselbach H, Bärthlein B, Wanner C, Eckardt KU, Köttgen A, Kronenberg F, GCKD Investigators. Results from the German Chronic Kidney Disease (GCKD) study support association of relative telomere length with mortality in a large cohort of patients with moderate chronic kidney disease. **Kidney International 98** (2), 488-497. 2020 Apr 4. PMID: 32641227

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