Beyond the CpG: an integrative approach to decoding DNA methylation in immunometabolic health

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List of publications

1. **Sinke, L.**, van Dongen, J., Delerue, T., et al. "Epigenome-wide association study of circulating interleukin-6 connects DNA methylation to immunometabolic and inflammatory disease." ***Commun Bio.*** 9(1):242 (2026)

2. **Sinke, L.,** Delerue, T., Wilson, R., et al. "DNA methylation of genes involved in lipid metabolism as a driver of adiponectin levels and metabolic disease." ***Diabetologia.*** 69(1):127-145 (2026)

3. Liu, Y., Vukic, M., Hannon, E., Hailing, M., Walker, E., **Sinke, L.,** et al. "Identification of SENP7 and UTF1/VENTX as new loci influencing clustered protocadherin methylation across blood and brain using a genome-wide association study." ***Mol Psych.*** 31(3):1556-1568 (2026)

4. **Sinke, L.,** van Iterson, M., Cats, D., et al. "DNAmArray: streamlined workflow for the quality control, normalization, and analysis of Illumina methylation array data (v3.0)." ***Zenodo.*** (2025)

5. **Sinke, L.,** Beekman, M., Raz, Y., et al. "Tissue-specific methylomic responses to a lifestyle intervention in older adults associate with metabolic and physiological health improvements." ***Aging Cell.*** 24(4): e14431 (2025)

6. Reilly, N. A., Sonnet, F., Dekkers, K. F., Kwekkeboom, J. C., **Sinke, L.,** et al. "Oleic acid triggers metabolic rewiring of T cells poising them for T helper 9 differentiation." ***iScience.*** 27(4): 109496 (2024)

7. Costeira, R., Daimiel Ruiz, L., Gehrmann, T., Bogaards, F., Villicaña S., **Sinke, L.,** et al. "DNA methylation and gene expression trajectories of human postprandial metabolism." ***bioRxiv***. (2024)

8. Lange de Luna, J., Nounu, A., Neumeyer, S., **Sinke, L.,** et al. "Epigenome-wide association study of dietary fatty acid intake." ***Clin Epigenetics.*** 16(1): 29 (2024)

9. Costeira, R., Evangelista, L., Wilson, R., Yan, X., Hellbach, F., **Sinke, L.,** et al. "Metabolomic biomarkers of habitual B vitamin intakes unveil novel differentially methylated positions in the human epigenome." ***Clin Epigenetics.*** 15(1): 166 (2023)

10. Liu, Y., **Sinke, L.,** Jonkman, T. H., et al. "The inactive X chromosome accumulates widespread epigenetic variability with age." ***Clin Epigenetics.*** 15(1): 135 (2023)

11. Hellbach, F., **Sinke, L.,** Costeira, R., et al. "Pooled analysis of epigenome-wide association studies of food consumption in KORA, TwinsUK, and LLS." ***Eur J Nutr.*** 62(3): 1357-1375 (2023)

12. **Sinke, L.,** Cats, D., and Heijmans, B. T. "Omixer: multivariate and reproducible sample randomization to proactively counter batch effects in omics studies." ***Bioinformatics.*** 37(18): 3051-3052 (2021)

13. Mndeme, F. G., Mmbaga, B. T., Kim, M. J., **Sinke, L.,** et al. "Red reflex examination in reproductive and child health clinics for early detection of paediatric cataract and ocular media disorders: cross-sectional diagnostic accuracy and feasibility studies from Kilimanjaro, Tanzania." ***Eye (Lond).*** 35(5): 1347-1353 (2021)

14. Mangtani, P., Nguipdop-Djomo, P., Keogh, R., **Trinder, L.,** et al. "Observational study to estimate the changes in the effectiveness of bacillus Calmette-Guérin (BCG) vaccination with time since vaccination for preventing tuberculosis in the UK." ***Health Technol Assess.*** 21(39): 1-54 (2017)

Curriculum Vitae

Lucy Sinke was born in London on the 17th of March, 1990. She completed her secondary school education at James Allen's Girls' School in London, England. In 2008, she began her academic journey, enrolling in a Neuroscience B.Sc. at King's College London. It was here, during an internship simulating visual cortical neurons in MATLAB, that she discovered her passion for computational biology. To build on this interest, she pursued additional statistical qualifications and went on to complete an M.Sc. in Medical Statistics at the London School of Hygiene and Tropical Medicine (LSHTM) in 2014. During this period, she became proficient in statistical programming, including with R, STATA, and SAS, applying these tools to uncover how Huntington's disease progression affects cognition and mood. Lucy then continued her work as a Research Fellow at the International Centre for Eye Health (ICEH), where she supported clinical Ph.D. candidates by designing and statistically analysing studies.

In 2019, following emigration to The Netherlands, Lucy embarked on her Ph.D. journey in the Molecular Epidemiology group at Leiden University Medical Centre (LUMC). Here, under the guidance of Prof. dr. Bas Heijmans and Prof. dr. P. Eline Slagboom, she focused on developing and refining genomic study designs, data processing pipelines, and integrative analytical methodology. Lucy used these approaches to examine how DNA methylation impacts immunometabolic health across the life course, with the results of this research outlined in this thesis. Her work was part of the DIMENSION consortium and supported by the Joint Programming Initiative on a Healthy Diet for a Healthy Life (JPI-HDHL). During her Ph.D., Lucy collaborated with research groups both within the Netherlands and abroad, and presented her findings at national and international scientific conferences.

In 2024, Lucy began a new chapter as a postdoctoral researcher at the Leiden Academic Centre for Drug Research (LACDR). Here, in the group of Prof. dr. Bob van de Water and Dr. Giulia Callegaro, she is advancing the field of toxicogenomics and risk assessment by exploring how co-regulatory gene networks respond to chemical stressors across a diverse spectrum of *in vitro* test systems.

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We actually did it! After half a decade of curiosity, spirit, and perserverance, the credits of my Ph.D. journey are officially rolling. Looking back, at all the triumphant victories and trying setbacks, I'm immensely grateful to have been granted the opportunity to develop into the scientist I am today. I would love nothing more than to continue immersing myself into the fascinating world of molecular biology for all of the years to come.

Naturally, I did not reach this milestone alone. It would have been singularly impossible without the support of my family, friends, and colleagues. Your belief in me made all the difference.

First and foremost, to my supervisors. I will always remember how you entrusted me with this project and gave me space to thrive. Bas, your endless enthusiasm for science has been invaluable since our very first meeting. Throughout all of our wild, wonderful, and wacky ideas, you have always made time for me and I will truly miss our discussions. Eline, your incredible work ethic coupled with such a genuine sense of fun is admirable and I am deeply proud to have been a part of your research group.

To my fellow epigenomics enthusiasts: Jazmin, Yunfeng, Manhoor, Laura, Thomas, Tom, and Koen. Thank you for making our work life warm and continuing to make me feel welcome whenever our paths cross. Pia and Nathalie, from the very beginning you both shared this journey with me and reminded me that I was not alone.

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Giulia and Bob, thank you for so warmly welcoming me into your research group. It has been a genuine pleasure to share in your passion for toxicogenomics, and to see science and research from a fresh and new perspective. And to my (not so) new colleagues: Imke, Steven, Sibel, Mick, Tamara, Kirsten, Xuesong, Martijn, Tessa, Sylvia, Mazène, Natasha, Vera, Lukas, Hugo, Hanneke, Gerhard, and Dario. I'm excited to find out what we can accomplish together!

Mummy and daddy, I miss you both more than words can say. Your instilled a love in me for science, teaching, and mathematics from such a young age. From practicing times tables on the bus to helping you grade homework on photosynthesis (although I don't know how much help I was!). Without you, I quite literally would not be here. Some days are easier than others, but not being able to share this book with you breaks my heart. I take comfort in the knowledge that you would both be so proud of me, and I will cherish the time we had and the love you gave me for the rest of my life.

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"Everything's got to end sometime. Otherwise nothing would ever get started." -- The Doctor.