

Niek de Klein

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🐙 github.com/npklein

🔗 scholar.google.com/citations?user=QNwjBnwAAAAAJ&hl

Education

- May 2015 – Sep 2021 **PhD Functional Genomics**
Genetics Department of University Medical Center Groningen, Groningen, the Netherlands.
Supervisor Prof. Lude Franke
Thesis title Genetic regulation of gene expression in brain and blood
DOI 10.33612/diss.178049845
- Sep 2012 – Aug 2014 **M. Sc. Bioinformatics**
Vrije Universiteit, Amsterdam, Netherlands
grade 8.6/10 (Cum laude)
- Sep 2008 – Aug 2012 **B. Sc. Bioinformatics**
HAN University of Applied Sciences, Nijmegen, Netherlands
grade 8.2/10

Employment

- Sep 2020 – Aug 2023 **Postdoctoral researcher**
Company Wellcome Sanger, Cambridge, United Kingdom
Lab Joint post-doc in labs of Dr. Emma Davenport and Dr. Gosia Trynka
Project For my postdoctoral research I use genotypes, single cell RNA-seq, CITE-seq, and vdj-seq data from individuals with Systemic Lupus Erythematosus to study clinical heterogeneity and the role of GWAS variants in regulating the immune system.

Skills

- 📌 ● refer to publications, see Research Publications section.

Genomics/Genetics

- Single cell **Experience** with computational analysis of single cell RNA-seq, CITE-seq, and vdj-seq.
- QTLs **Experience** with downstream analysis of eQTLs (2, 9, 12) as well as developing new software for calculating interaction eQTLs (8 and github.com/npklein/systemsgenetics/tree/master/Decon2)
- Differential expression (G/E)WAS **Experience** running differential expression analysis (10).
 Experience running EWAS as part of large consortium (4, 5).
- Method development **Experience** developing new methods for gene identification (17 and 18), gene ID mapping between species (16), improving protein identification from mass spectrometry (See B.Sc. and M.sc. internships), and identifying cell type specific eQTL effects in bulk data (8).

Coding

- Coding **Most experienced** in R Bash, Python. Experience in Java. Code on github.com/npklein. Code written during current employment is in a private repository, can share recent examples on request.

Skills (continued)

Databases	■ Experience with MySQL and SQLite
General	
Writing	■ Experience writing scientific articles (See Research Publications below).
Teaching and supervision	■ Experience giving workshops and lectures (See Teaching below). Experience supervising students (See Teaching below for details.)
Presenting work	■ Regular presentations at group and departmental level. Presenting monthly for stakeholders from industry on project progress as part of OpenTargets private-public collaboration.
Languages	■ Strong reading, writing and speaking competencies for English and Dutch (native).

Internships

During M.Sc.

Jan – Jun 2014	■ Connecting multiple gene expression signatures with candidate drugs for boosting heart regeneration potential. Supervisor Dr. Francisco Azuaje Institute CRD-Sant��, Luxembourg, Luxembourg Grade 9/10 https://github.com/npklein/drugFinder
Aug – Dec 2013	■ Clustering of MS/MS spectra to improve peptide and protein identification. Supervisor Dr. Tham Pham Institute Cancer Center Amsterdam, Amsterdam, Netherlands Grade 9/10

During B.Sc.





Feb – Jun 2012	■ Methods to assess the reproducibility and coverage of tandem mass spectrometry data in phosphoproteomics experiments. Supervisor Dr. David Martin Institute Wellcome Trust, Dundee, Scotland Grade 9/10 https://github.com/npklein/pyMSA
Sep – Dec 2010	■ How widespread are microProteins and how did they evolve? Supervisor Dr. Sue Rhee Institute Carnegie Institute for Life Sciences, Stanford, USA Grade 8/10 https://github.com/npklein/miP3

Teaching







Courses and seminars

16 Jun 2022	■ Lecture basics of eQTL analysis and colocalisations Wellcome Sanger departmental retreat
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Teaching (continued)

- Sep 2019  **Lecture + workshop gene expression**
Lecture on gene expression + workshop differential gene expression and pathway analysis
Data Science for Life Sciences Master students of the Hanze University of Applied Sciences Groningen
Course material at npklein.github.io/Teaching-modules/.
- Sep – Oct 2017  **Introduction to Biomolecular Sciences**
Co-coordinated, created, and supervised various genetics workshops.
Biomolecular Science Master students of the Rijksuniversiteit Groningen
Course material at npklein.github.io/iBMS.
- 26 Aug 2016  **Invited Talk + Workshop Genotyping from RNAseq**
Lecture + workshop on how to call genotypes from RNAseq data at the Estonian Genome Center.
- 22 Jun 2016  **Enriching biobanks using genotype data**
BIKE Summer School seminar

Student (co)-supervision

- Mar 2021 –  Ziyang Ke
PhD student
Metabolic pathway perturbation in single cells
- May 2022 – Jul 2022  Haerin Jang
PhD rotation project
Drug target identification through single cell eQTL mapping of immune response regulation in health and SLE
- Mar 2021 – May 2021  Isaac Garcia-Salinas
PhD rotation project
Determining putative causal genes of neuropsychiatric lupus through genotype and brain gene expression data
- Jan 2020 – Jun 2020  Martijn Vochteloo
Master thesis
Investigation of Cell Type Mediated eQTL Regulatory Effects in Psychiatric and Neurodegenerative Diseases
- Apr 2019 – Jun 2019  Fabian VogelPohl
Bachelor internship
Unraveling the brain specific molecular network of the SCGE gene, the major gene for myoclonus dystonia.
- Sep 2018 – Apr 2019  Omar El Garwany
Master thesis
Brain eQTLs show more enrichment for neuro-psychotic diseases than blood eQTLs

Teaching (continued)

- Feb – Jul 2017 ■ Anne Tjallingii
M.Sc. internship
Influence of a diabetes mellitus type II on the susceptibility of getting tuberculosis
- Jan – Jun 2016 ■ Carlos Urzua
M.Sc. internship
Allele-specific signals in gluten sensitive t-cell clones

Misc

- Jun 2022 ■ Marking students for M.Sc. course Genomics of complex disease
Cambridge University, United Kingdom
- Aug 2020, 2021 ■ External examiner for various bachelor thesis projects
H.A.N., Nijmegen, the Netherlands

Grants

- 07 Mar 2016 ■ One tool to interpret and assess impact of genetic variants and predict disease-causing genes using the BBMRI – BIOS data (Co-Applicant)
€ 60,000

Miscellaneous Experience

Conference poster presentations

- 17 October 2019 ■ eQTL analysis in brain cortex samples of 3,833 individuals and 31,684 blood samples reveals distinct regulatory effects of disease-associated genetic variants
ASHG (Poster)
- 17 June 2018 ■ Allele specific expression identifies rare variants as cause for extreme allelic imbalance
ESHG (Poster)
- 25 May 2016 ■ Genotyping of all public RNA-sequencing data for large scale trans-QTL and ASE studies
ESHG (Poster)
- 8 Sep 2014 ■ Connecting multiple gene expression signatures with candidate drugs for boosting heart regeneration potential
ECCB (Poster)

Other

- Okt 2019 – Dec 2019 ■ Research visit at Biogen – including invited talk
- Aug 2018 ■ Leena Peltonen Summer School
Summer school

Miscellaneous Experience (continued)

Jul 2016 ■ Microsoft Research PhD Summer School
Summer school

Research Publications (Reverse chronological order)

Journal Articles

- 1 Boulogne, F., Claus, L., Wiersma, H., Oelen, R., Schukking, F., de **Klein**, N., Li, S., Westra, H.-J., van der Zwaag, B., van Reekum, F., et al. (2023). Kidneynetwork: Using kidney-derived gene expression data to predict and prioritize novel genes involved in kidney disease. *medRxiv, in press European Journal of Human Genetics* 2023.
- 2 de **Klein***, N., Tsai*, E. A., Vochteloo*, M., Baird, D., Huang, Y., Chen, C.-Y., van Dam, S., Deelen, P., Bakker, O. B., El Garwany, O., et al. (2023). Brain expression quantitative trait locus and network analysis reveals downstream effects and putative drivers for brain-related diseases. *bioRxiv - in press Nature Genetics* 2023.
- 3 Bakker, O. B., Ramirez-Sanchez, A. D., Borek, Z. A., de **Klein**, N., Li, Y., Modderman, R., Kooy-Winkelaar, Y., Johannesen, M. K., Matarese, F., Martens, J. H., et al. (2021). Potential impact of celiac disease genetic risk factors on t cell receptor signaling in gluten-specific cd4+ t cells. *Scientific reports*, 11(1), 1–15.
- 4 Karabegovic, I., Portilla-Fernandez, E., Li, Y., Ma, J., Maas, S. C., Sun, D., Hu, E. A., Kuhnel, B., Zhang, Y., Ambatipudi, S., et al. (2021). Epigenome-wide association meta-analysis of dna methylation with coffee and tea consumption. *Nature communications*, 12(1), 1–13.
- 5 Schlosser, P., Tin, A., Matias-Garcia, P. R., Thio, C. H., Joehanes, R., Liu, H., Weihs, A., Yu, Z., Hoppmann, A., Grundner-Culemann, F., et al. (2021). Meta-analyses identify dna methylation associated with kidney function and damage. *Nature communications*, 12(1), 1–16.
- 6 Van Rheenen, W., Van Der Spek, R. A., Bakker, M. K., Van Vugt, J. J., Hop, P. J., Zwamborn, R. A., de **Klein**, N., Westra, H.-J., Bakker, O. B., Deelen, P., et al. (2021). Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nature genetics*, 53(12), 1636–1648.
- 7 Zhang, Z., van Dijk, F., de **Klein**, N., van Gijn, M. E., Franke, L. H., Sinke, R. J., Swertz, M. A., & van der Velde, K. J. (2021). Feasibility of predicting allele specific expression from dna sequencing using machine learning. *Scientific reports*, 11(1), 1–11.
- 8 Aguirre-Gamboa*, R., de **Klein***, N., di Tommaso*, J., Claringbould, A., van der Wijst, M. G., de Vries, D., Brugge, H., Oelen, R., Vosa, U., Zorro, M. M., et al. (2020). Deconvolution of bulk blood eqtl effects into immune cell subpopulations. *BMC bioinformatics*, 21(1), 1–23.
- 9 de **Klein***, N., van Dijk*, F., Deelen, P., Urzua, C. G., Claringbould, A., Vosa, U., Verlouw, J. A., Monajemi, R., AC't Hoen, P., Sinke, R. J., et al. (2020). Imbalanced expression for predicted high-impact, autosomal-dominant variants in a cohort of 3,818 healthy samples. *bioRxiv*.
- 10 Rodius, S., de **Klein**, N., Jeanty, C., Sanchez-Iranzo, H., Crespo, I., Ibberson, M., Xenarios, I., Dittmar, G., Mercader, N., Niclou, S. P., et al. (2020). Fisetin protects against cardiac cell death through reduction of ros production and caspases activity. *Scientific reports*, 10(1), 1–12.
- 11 Parmar, P., Lowry, E., Cugliari, G., Suderman, M., Wilson, R., Karhunen, V., Andrew, T., Wiklund, P., Wielscher, M., Guarrera, S., et al. (2018). Association of maternal prenatal smoking gfi1-locus and cardio-metabolic phenotypes in 18,212 adults. *EBioMedicine*, 38, 206–216.

- 12 Claringbould*, A., de **Klein***, N., & Franke, L. (2017). The genetic architecture of molecular traits. *Current Opinion in Systems Biology*, 1, 25–31.
- 13 Zhernakova, D. V., Deelen, P., Vermaat, M., Van Iterson, M., Van Galen, M., Arindrarto, W., Van't Hof, P., Mei, H., Van Dijk, F., Westra, H.-J., et al. (2017). Identification of context-dependent expression quantitative trait loci in whole blood. *Nature genetics*, 49(1), 139–145.
- 14 Graham, D. B., Lefkovith, A., Deelen, P., de **Klein**, N., Varma, M., Boroughs, A., Desch, A. N., Ng, A. C., Guzman, G., Schenone, M., et al. (2016). Tmem258 is a component of the oligosaccharyltransferase complex controlling er stress and intestinal inflammation. *Cell reports*, 17(11), 2955–2965.
- 15 Rodius, S., Androsova, G., Gotz, L., Liechti, R., Crespo, I., Merz, S., Nazarov, P. V., de **Klein**, N., Jeanty, C., Gonzalez-Rosa, J. M., et al. (2016). Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. *Scientific reports*, 6(1), 1–12.
- 16 de **Klein**, N., Ibberson, M., Crespo, I., Rodius, S., & Azuaje, F. (2015). A gene mapping bottleneck in the translational route from zebrafish to human. *Frontiers in Genetics*, 5, 470.
- 17 de **Klein**, N., Magnani, E., Banf, M., & Rhee, S. Y. (2015). Microprotein prediction program (mip3): A software for predicting microproteins and their target transcription factors. *International journal of genomics*, 2015.
- 18 Magnani, E., de **Klein**, N., Nam, H.-I., Kim, J.-G., Pham, K., Fiume, E., Mudgett, M. B., & Rhee, S. Y. (2014). A comprehensive analysis of microproteins reveals their potentially widespread mechanism of transcriptional regulation. *Plant physiology*, 165(1), 149–159.

* = shared first author

Books and Chapters

- 1 Fiume, E., de **Klein**, N., Rhee, S. Y., & Magnani, E. (2016). *A framework for discovering, designing, and testing microproteins to regulate synthetic transcriptional modules* (Vol. 1482). Humana Press, New York, NY.

References

Available on request