

Nick Hirschmüller

PhD Candidate in Human Genetics & Genomic Epidemiology · University of Cambridge

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SUMMARY

PhD candidate in human genetics at the University of Cambridge, working with AstraZeneca on the genetic validation of drug targets. Six years of computational research at Cambridge, EMBL, Novartis and DKFZ, spanning statistical genetics (Mendelian randomization, molecular QTLs, colocalization) and single-cell transcriptomics.

PROFESSIONAL EXPERIENCE

PhD Candidate, BHF Cardiovascular Epidemiology Unit

Oct 2023 – present

Butterworth Group, University of Cambridge · Cambridge, UK

MRC DTP iCASE Studentship with AstraZeneca

- Leading the genetic validation of an AstraZeneca cardiovascular target: *cis*-Mendelian randomization across efficacy and safety outcomes to estimate predicted therapeutic benefit and on-target liabilities; first-author manuscript in preparation
- Map baseline and oxLDL-response eQTLs in iPSC-derived macrophages from more than 180 donors, colocalizing them with cardiovascular GWAS to prioritise candidate effector genes
- Build reproducible workflows on SLURM-based HPC and the UK Biobank Research Analysis Platform trusted research environment
- Present findings regularly to AstraZeneca scientists

Master's Thesis Researcher, then Research Assistant

Jul 2022 – Jul 2023

Huber Group, European Molecular Biology Laboratory (EMBL) · Heidelberg, Germany

Master's thesis Jul 2022 – Mar 2023; Research Assistant Apr 2023 – Jul 2023

- Integrated more than 10 large-scale single-cell RNA-seq experiments to study stem-cell regulation in the *Drosophila* intestine, identifying an autoinhibitory feedback mechanism that preserves intestinal stem-cell maintenance and fate commitment
- Prioritised candidate genes for follow-up *in vivo* experiments and built an R Shiny dashboard for interactive visualisation and exploration of the results

Translational Data Science Intern

Jan 2022 – Jun 2022

Novartis Institutes for BioMedical Research · Basel, Switzerland

- Analysed transcriptomic profiles of more than 2,000 patients with ALS to characterise molecular heterogeneity and nominate candidate biomarkers of disease progression
- Curated public transcriptomic studies into a reusable internal resource and contributed core functionality to an R package supporting standardised RNA-seq analysis

EARLIER RESEARCH EXPERIENCE

- Research Intern · Huber Group, **EMBL** May 2021 – Aug 2021
Built a GATK-based germline variant-calling pipeline and performed a pilot GWAS of proliferative drive in chronic lymphocytic leukaemia
- Research Intern · Goncalves Group, **German Cancer Research Center (DKFZ)** Nov 2020 – Mar 2021
Developed a method to quantify somatic selection across more than 100 premalignant mouse and naked mole-rat skin biopsies
- Research Assistant (part-time) · Jäger Group, **National Center for Tumor Diseases (NCT)** Apr 2020 – Dec 2021
Built a neoantigen-prediction pipeline used in the NCT MASTER precision-oncology programme and cut the runtime of somatic variant calling from cell-free DNA 4-fold

EDUCATION

- PhD, Cardiovascular Epidemiology Unit, University of Cambridge** Expected 2027
- MSc Cancer Biology, DKFZ & Heidelberg University** 2023 · Grade 1.0, best possible grade
- BSc Molecular Biotechnology, Heidelberg University** 2019 · Grade 1.2

PUBLICATIONS

- Redhai S*, **Hirschmüller N***, Wang T, *et al.* Autoinhibitory feedback preserves intestinal stem cell maintenance and fate commitment. *The EMBO Journal* 45, 4636–4669 (2026). *co-first authors
- Jiang X, **Hirschmüller N**, Taylor H, *et al.* Liver fat accumulation contributes to discordant genetic risk between coronary artery disease and type 2 diabetes. *medRxiv* (2026).
- Behm M, Baeza-Centurión P, ..., **Hirschmüller N**, ..., Frye M. Regenerative cell turnover coupled to a tumor-hostile niche protects naked mole-rats from cancer. *bioRxiv* (2023).

SKILLS

Human & statistical genetics: GWAS, Mendelian randomization, colocalization, fine-mapping, eQTL and response-QTL mapping

Genomics & multi-omics: single-cell and bulk RNA-seq, differential expression, trajectory inference, variant calling

Programming & infrastructure: R, Bioconductor, Python, bash, Git, Snakemake, SLURM HPC, UK Biobank Research Analysis Platform

Languages: Native German, fluent English

SELECTED PRESENTATIONS, AWARDS & LEADERSHIP

- Poster (accepted), ASHG Annual Meeting, Montreal · 2026
- Poster, ESHG Conference, Gothenburg · 2026
- Poster, HDR UK Conference, Glasgow · 2025
- Wolfson College Travel Grant, University of Cambridge · 2026
- Peer review: co-reviewed a manuscript for *Nature Communications* · 2026
- MRC DTP Student Representative, University of Cambridge · 2023 – 2026
- Chair & Lead Organiser, Cambridge MRC DTP Student Symposium · 2025