# Proteins quantitative trait loci on 91 Olink/inflammation proteins

Authors to be added here

## Contact information

For general questions about SCALLOP, please contact Anders Malarstig (anders.malarstig@ki.se). For technical issues about TRYGGVE, please contact Lasse Folkersen (lasfol@cbs.dtu.dk).

For questions regarding SCALLOP/INF, please contact Jing Hua Zhao (jhz22@medschl.cam.ac.uk) and James Peters ([jp549@medschl.cam.ac.uk](mailto:jp549@medschl.cam.ac.uk)).

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## Abstract

BACKGROUND. METHODS. FINDINGS. INTERPRETATION.

## Introduction

Proteins involve in many biological processes and much can be learnt about these and their relationship with diseases from and large-scale protein-wide genomic studies (PGWAS) with respect to the so-called quantitative trait loci with proteins (pQTLs), as highlighted in recent work by Sun et al. (2018), for which it is difficult to know otherwise.

Based on the SomaLogic platform, the INTERVAL study as reported in Sun et al. (2018) was able to render a broad landscape of human plasma proteome; proteins measured on specific functions are of particular interests whose focus here is Olink/INF1 panel, originally consisting of 91 proteins. Moreover, to increase power we also assembled data from a number of other cohorts within the SCAndinavian coLLaboration for Olink plasma Protein genetics (SCALLOP) consortium, including 966 individuals with sequence data.

In the following we report our findings on pQTLs, their their cis- and trans- effects through functional annotation, pleiotropic effects, as well as causal role on disease outcomes such as CHD and other downstream analysis.

## Data and analysis

### The INTERVAL study

The INTERVAL study was designed (Moore et al. 2014).

### The SCALLOP/INF1 consortium

The contributing cohorts in this study are listed in Supplementary Table S1. The original Olink INFlammation panel contained 92 proteins whose raw measurements, including those beyond lower limit of detection, were subject to a rank-based inverse normal transformation. Quality control on cohort level involves SNP/sample call rates, gender mismatch, abnormal inbreeding coefficient, failed cryptic relatedness test, ancestry outlier, heterozygosity and Hardy-Weinberg equilibrium test. 1000 genomes imputation, build 37 (hg19) positions. At the time of analysis, BDNF was dropped from the panel so will not be analysed.

### Association analysis

Multiple linear regression was conducted on protein data and genotypes as well as sex, age, principal components and other cohort specific covariates under an additive genetic model. As individual level data from KORA study rather than GWAS summary statistics were available, the protein normalization and association testing were done centrally.

Software which account for genotype uncertainty, such as SNPTEST were used but due to the relatively large number of proteins, results based on PLINK were also accepted, both amended with outputs from qctool –snp-stats.

## Meta-analysis

Prior to the meta-analysis, intensive work was done on quality control of the GWAS summary statistics based on information such as MAF, minimum sample size, HWE, and imputation score. Cohort-level Q-Q and Manhattan plots were generated with R package qqman and QCGWAS. Meta-analysis were performed using the inverse-variance weighted analysis of regression betas and standard errors, as implemented in the software METAL, version 28.8.2018. This was followed for meta-analysed summary statistics by Q-Q, Manhattan plots and regional association plots with LocusZoom 1.4. Independent loci were assessed by PLINK, using Bonferroni threshold for the genome-wide analyses approximately 5 x 10-10, and GCTA and cis/trans classifications were obtained using customised R functions. These were done iteratively to ensure validity of the findings. The reference panels for these analyses included 1000Genomes release 3 as well as INTERVAL-based UK10K+1000Genomes. Variants explained were approximated with where *T* is the total number of variants, the chi-squared statistic and the associate sample size, respectively (Giri, et al. 2019).

PhenoScanner was used for variant annotation. Positive controls were applied on OPG and TNFSF14. In particular, findings on OPG are in line with earlier report (Kwan et al. 2014).

The GWAS summary statistics were further used in finemapping experiment via several software including finemap and JAM using approximately independent LD blocks, as well as gene enrichment and pathway analysis.

## Finemapping

Attempt was made through approaches implemented in several software, including PLINK, GCTA and finemap.

## Pathway analysis

Attempt was also made for based on cis signals.

## Heritability analysis

Individual level data from the INTERVAL study were analysed with GCTA, to be followed by counterpart for GWAS summary statistics.

## Transcriptomewide association analysis

This mirrors work by Mancuso et al. (2017) and work on mQTL by McRae et al. (2018) and Yengo, et al. (2018).

## Results

The list of variants is shown in Tables xx. The Q-Q, Manhattan, LocusZoom, and forest plots are shown in Supplementary Figures xx. The cis/trans classification is shown in Supplementary Table x along with chord diagram in Figure.

## Discussions

We were able to assess the protein-genetic associations in the OLINK panel. The variants identified were further characterized on cis/trans effects, evidence of pleiotropy, utility as instruments for causal inference through Mendelian randomization, as well as biological pathways. By analogy to polygenic score and protein score (Ganz et al. 2016), an inflammation score could also be built.

We were also be able to develop relevant functions in Bash as well as R, some of which were made generic through R package gap.

## Acknowledgements

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## References

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McRae AF, et al. (2018). Identification of 55,000 Replicated DNA Methylation QTL. *Sci Rep.* 8(1):17605. doi: 10.1038/s41598-018-35871-w.

Sun BB, et al. (2018). Genomic atlas of the human plasma proteome. Nature 558: 73–79.

Yengo L, et al. (2018). Meta-analysis of genome-wide association studies for height and body mass index in ∼700000 individuals of European ancestry. *Hum Mol Genet*. 27(20):3641-3649. doi: 10.1093/hmg/ddy271.

## Supplementary information

## URLs

Additional information about this investigation is available from GitHub, <https://github.com/jinghuazhao/INF>.

URL: SCALLOP, <https://www.olink.com/scallop/>; METAL <https://github.com/statgen/METAL>; PLINK, <http://zzz.bwh.harvard.edu/plink>; KING, <http://people.virginia.edu/~wc9c/KING/>; LDetect-data (for approximately independent LD blocks), <https://bitbucket.org/nygcresearch/ldetect-data>; FUSION, <http://gusevlab.org/projects/fusion/>, LocusZoom, <https://github.com/statgen/locuszoom-standalone>; R. <https://cran.r-project.org>; Uniprot, [https://www.uniprot.org](https://www.uniprot.org/):

## Cohort information

**BioFinder**.

**EGCUT**.

**INTERVAL.** The INTERVAL study: NHSBT (11-01-GEN) and the NIHR-BTRU in Donor Health and Genomics (NIHR BTRU-2014-10024) at the University of Cambridge in partnership with NHSBT. This study was partially funded by Merck. The views expressed are those of the authors and not necessarily those of the NHS, the NIHR, the Department of Health of England, or NHSBT. The Cardiovascular Epidemiology Unit at the University of Cambridge: UK MRC (G0800270), BHF (SP/09/002), UK NIHR Cambridge Biomedical Research Centre, ERC (268834), and European Commission Framework Programme 7 (HEALTH-F2-2012-279233).

See Astle, et al. (2016), Sun, et al. (2018).

**KORA**. The KORA study was initiated and financed by the Helmholtz Zentrum München – German

Research Center for Environmental Health, which is funded by the German Federal Ministry of Education and Research (BMBF) and by the State of Bavaria. Furthermore, KORA research was supported within the Munich Center of Health Sciences (MC-Health), Ludwig-Maximilians-Universität, as part of LMUinnovativ and by the Competence Network Asthma and COPD (ASCONET), network COSYCONET (subproject 2, BMBF FKZ 01GI0882) funded by the German Federal Ministry of Education and Research (BMBF).

Genotypes were available on Affymetrix Axiom chips on 3788 individuals. The imputation was done through IMPUTE 2.3.2 with 1000Genomes phase 3 reference panel. A total of 1,070 individuals with both genotypes and protein data were used in association analysis via SNPTEST 2.5.2, where the per-sample missing proportion was obtained from qctool 2.0.1, and covariates were sex, age, and five PCs from GCTA 1.91.7beta. IBD information was obtained via KING 2.1.6. The total number of variants were 81,651,446.

**MadCam**. The MadCam trial samples were all from baseline but the patients included were moderate ulcerative cholitis. Several details on the trial are available from [Vermeire S](https://www.ncbi.nlm.nih.gov/pubmed/?term=Vermeire%20S%5BAuthor%5D&cauthor=true&cauthor_uid=28527704), et al. (2017).

**NSPHS**. Swedish Medical Research Council (K2007-66X-20270-01-3, 2011-5252, 2012-2884 and 2011-2354), the Foundation for Strategic Research (SSF). NSPHS as part of European Special Populations Research Network (EUROSPAN) was also supported by the European Commission FP6 STRP (01947, LSHG-CT-2006-01947).

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Imputation panel was HRC.

**RECOMBINE**.

**STABILITY**.

**STANLEY**. The study consists of lah1 and swe6 subcohorts.

**VIS**. CROATIA-Vis is a family-based, cross-sectional study in the isolated island of Vis, Croatia that included 1,056 examinees aged 18-93. It is a genetic epidemiology study that aims to discover genetic factors that influence traits (e.g. height) or the risk of common complex diseases. The cohort is very well characterised with detailed phenotyping and genotyping information available.

Imputation panel was HRC.

## References

[Vermeire S](https://www.ncbi.nlm.nih.gov/pubmed/?term=Vermeire%20S%5BAuthor%5D&cauthor=true&cauthor_uid=28527704), et al. (2017). Anti-MAdCAM antibody (PF-00547659) for ulcerative colitis (TURANDOT): a phase 2, randomised, double-blind, placebo-controlled trial. *Lancet* 390(10090):135-144. doi: 10.1016/S0140-6736(17)30930-3.

## Supplementary tables

S1. Study information

S2. Signals from the INTERVAL study

S3. cis/trans classification from the INTERVAL study

## Q-Q and Manhattan plots

## Regional association plots

## Forest plots

## Pathway analysis

## PheWAS results

## EWAS results