# Characterisation of the pQTLs on inflammation

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## Abstract

BACKGROUND. METHODS. FINDINGS. INTERPRETATION.

## Introduction

Proteins play central role in many biological processes and large-scale protein-wide genomic analysis (PGWAS) became an important source of information as highlighted in a recent work by Sun et al. (2018). Unlike other GWAS, many aspects linking proteins remain unclear but could only be revealed via large-scale studies.

Through proteomic data on the Olink/INF1 panel within the SCALLOP consortium, we set to investigate pQTLs, the mechanistic basis of identified cis- and trans-pQTL by functional annotation, pQTL pleiotropic effects, the causal role on disease outcomes such as CHD as well as other downstream analysis.

## Data and analysis

### The SCALLOP consortium

The contributing cohorts are listed in Supplementary Table.

We report pQTLs associated with OLINK/INF1 panel, using cohorts in the SCAndinavian coLLaboration for Olink plasma Protein genetics (SCALLOP) consortium, a collaborative framework for discovery and follow-up of genetic associations with proteins on the Olink Proteomics platform.

### Proteins

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.

### SNPs

1000 genomes imputation, build 37 (hg19) positions. Quality control on aspects such as SNP/sample call rates, gender mismatch, abnormal inbreeding coefficient, failed cryptic relatedness test, ancestry outlier, heterozygosity and Hardy-Weinberg equilibrium test.

### 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

R package QCGWAS was used to generate cohort-level Q-Q and Manhattan plots, suggesting MAF cut-off. Meta-analysis were performed centrally using the inverse-variance weighted analysis of regression betas and standard errors, as implemented in the software METAL, version 28.8.2018. Filters such as MAF, HWE, minimum sample size and imputation quality filters were applied at the meta-analysis. Genomic control was not considered on the cohort level. Q-Q and Manhattan plots were generated from R package qqman while regional association plot from LocusZoom 1.4. The Bonferroni threshold for the genome-wide analyses is 5 x 10-10. The results were replicated in independent cohorts. Independent loci were assessed by PLINK and GCTA and cis/trans classifications were obtained using customised R functions. The reference panels for these analyses included 1000Genomes release 3 as well as INTERVAL-based UK10K+1000Genomes. Variants explained were approximated via 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.

## Heritability analysis

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

## Results

The list of variants is shown in Tables. The Q-Q, Manhattan, LocusZoom, and forest plots are shown in Supplementary Figures. The cis/trans classification is shown in Table 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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## Supplementary information

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>; 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**.

**COMBINE/RECOMBINE**.

**EGCUT**.

**INTERVAL.** See Sun et al. (2018).

**KORA**. 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. The total number of variants were 81,651,446.

**MadCam**.

**NSPHS**.

**ORCADES**.

**STABILITY**.

**STANLEY**.

**VIS**.