# Genomic analysis of 91 Olink/inflammation proteins

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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.

In contrast to the a broad landscape of human plasma proteome as reported in Sun et al. (2018) based on the SomaLogic platform in the INTERVAL study, our focus here is on proteins measured on specific functions in the inflammation panel of Olink originally consisting of 92 proteins. Moreover, to gain more statistical 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, particularly 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.

## 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 identify and validate protein-specific genetic associations in the OLINK/INF panel, which were further characterised with respect to their cis/trans effects, pleiotropic roles, 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.

## Methods

## Olink/INF panel

The inflammation panel is among many focused on a specific area of disease, targeting 92 established and/or exploratory biomarkers.

### 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 studies. The 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, extensive effort were paid on quality control of the GWAS summary statistics with available information such as MAF, HWE, and imputation score. To facilitate this, 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 and the results were additionally visualized with regional association plots from LocusZoom 1.4. Independent loci were assessed by PLINK clumping, using Bonferroni threshold for the genome-wide analyses approximately 5 x 10-10, 1000Genomes release 3 data as reference panel, and different degrees of linkage disequilibrium. cis/trans classifications were obtained using customised bash and R functions. A similar analysis was performed via GCTA. The above were done iteratively to ensure validity of the findings. Eventually, the reference panels for these analyses was INTERVAL-based imputed genotypes from UK10K+1000Genomes reference panel, and approximately independent LD-blocks were used. Genomic heritability was also assessed with GCTA. 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).

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## 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.**

See Moore, et al. (2014), Astle, et al. (2016), Sun, et al. (2018).

The KORA studies (Cooperative Health Research in the Region of Augsburg) are a series of independent population based studies from the general population living in the region of Augsburg, Southern Germany. The **KORA S3** study including 4,856 individuals was conducted in 1994/95. Spirometry was measured during a follow up in 1997/98 for all participants younger than 60 years who did not smoke or use inhalers one hour before the test. **KORA F4** including 3,080 individuals was conducted from 2006-2008 as a follow-up study to KORA S4 (1999-2001). 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).

**Northern Sweden Population Health Study** (NSPHS) represents a cross-sectional study conducted in the communities of Karesuando (samples gathered in 2006) and Soppero (2009) in the subarctic region of the County of Norrbotten, Sweden. Spirometry was performed in sitting position without noseclips using a MicroMedicalSpida 5 spirometer (http://www. medisave.co.uk). Three consecutive 28 lung function measurements per participant were done and the maximum value per measured lung function parameter was used for further analysis. Relatedness was taken into account by applying the "polygenic" linear mixed effects model. Genome-wide association analysis was performed using a score test, a family-based association test27 which uses the residuals and the variance-covariance matrix from the polygenic model and the SNP fixed effect coded under an additive model.

**Orkney Complex Disease Study** (ORCADES) is an ongoing family-based, cross-sectional study in the isolated Scottish archipelago of Orkney. Spirometry was performed in the sitting position without nose clips, using a Spida handheld spirometer. Measurements were repeated once and the better reading was used for analysis.

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

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## Supplementary tables

Studies. Study information

INT1. Signals from the INTERVAL study for r2=0 clumping

INT2. cis/trans classification on INT1

INT3. Signals from the INTERVAL study for r2=0.1 clumping

INT4. cis/trans classification on INT3

INF1.snp-stats. Basic summary statistics by cohort

INF1. Signals from the SCALLOP/INF1 for r2=0 clumping

INF2. cis/trans classification on INF1

INF3. Signals from SCALLOP/INF1 for r2=0.1 clumping

INF4. cis/trans classification on INF3

INF5. Signals from SCALLOP/INF1 for r2=0.1 cojo analysis

INF6. cis/trans classification on INF5

## Q-Q and Manhattan plots

## Regional association plots

## Forest plots

## Pathway analysis

## PheWAS results

## EWAS results