# SCALLOP consortium - analysis plan for INF panel proteins

***Adapted from SCALLOP/CVD1 analysis plan, Cambridge 8/11/2018***

## 1. Background

The SCAndinavian coLLaboration for Olink plasma Protein genetics (SCALLOP) consortium, https://www.olink.com/scallop/, is a collaborative framework for discovery and follow-up of genetic associations with proteins on the Olink Proteomics platform. A meta-analysis has been conducted on data Olink CVD1 panel from participating cohorts and consequent contributions have been made on Olink INF panel. This document therefore follows closely the SCALLOP/CVD1 analysis plan for the analysis, and in particular highlights relevant information required to facilitate the meta-analysis.

## 2. Aims

As with the CVD1 meta-analysis, the tasks will involve

* Identification of pQTLs in SCALLOP discovery cohorts
* Replication of pQTLs in SCALLOP replication cohorts
* Investigation of the mechanistic basis of identified cis- and trans-pQTL by functional annotation
* Investigation of pleiotropic effects of the pQTLs
* Evaluation over the causal role of INF proteins disease outcomes such as CHD and stroke
* Other downstream analysis

among others.

## 3. Data analysis

### Proteins

The Olink INFlammation panel of 92 proteins, e.g, https://github.com/jinghuazhao/INF/blob/master/doc/olink.inf.panel.annot.tsv.

### SNPs

* 1000 genomes imputation
* SNPs will be filtered for imputation quality at time of meta-analysis, but please filter out SNPs with IMPUTE INFO quality less than 0.2
* Standard QC, including call rate < 95% or failed Illumina genotype calling, gender mismatch, abnormal inbreeding coefficient, failed cryptic relatedness test, ancestry outlier, sample call rate < 95%, Bonferroni corrected Hardy-Weinberg Equilibrium test.

### Association analysis

* Rank-based inverse normal transformation on the raw measurement of proteins including those below lower limit of detection, e.g., invnormal function from https://github.com/jinghuazhao/R/tree/master/gap,
* invnormal <- function(x)  
   qnorm((rank(x,na.last="keep")-0.5)/sum(!is.na(x)))
* Multiple linear regression for all samples including sex, age, principal components and other cohort specific covariates.
* Additive genetic model

### Stratification

* Analyse patients and controls separately – results will be merged at meta-analysis stage

## 4. Descriptive statistics

Please fill out the spreadsheet and use the naming convention:

* STUDY.descriptives.DATE.xls
* Where STUDY is a short (14 characters or less) identifier for the population studied, which is the same for all files provided by your study.
* DATE is the date on which the file was prepared, in the format “YYYYMMDD”.

## 5. File formats for GWAS results

### SNP table for GWAS results

Please include the following columns. Missing values are coded as “NA”.

|  |  |  |
| --- | --- | --- |
| No | Variable name | Description |
| 1 | SNPID | SNP ID as rs number |
| 2 | CHR | Chromosome number (1-22) |
| 3 | POS | Physical position for the reference sequence (please indicate NCBI build in descriptive file) |
| 4 | STRAND | Indicator of strand direction. Please specify “+” if positive or forward strand and “-” if negative or reverse strand. |
| 5 | N | Number of non-missing observations |
| 6 | EFFECT\_ALLELE | Allele for which the effect (beta coefficient) is reported. For example, in an A/G SNP in which AA = 0, AG=1, and GG=2, the coded allele is G. |
| 7 | REFERENCE\_ALLELE | Second allele at the SNP (the other allele). In the example above, the non-coded allele is A. |
| 8 | CODE\_ALL\_FQ | Allele frequency for the coded allele – “NA” if not available |
| 9 | BETA | Effect size for the coded allele, beta estimate from the genotype-phenotype association, with at least 5 decimal places. Note: if not available, please report “NA” for this variable. |
| 10 | SE | Standard error of the beta estimate, to at least 5 decimal places - “NA” if not available. |
| 11 | PVAL | p-value of Wald test statistic – “NA” if not available |
| 12 | RSQ | Residual phenotypic variance explained by SNP. “NA” if not available |
| 13 | RSQ\_IMP | Observed divided by expected variance for imputed allele dosage. |
| 14 | IMP | Please specify whether the SNP was imputed or genotyped: 1: imputed SNP, 0: directly genotyped SNP |

### File-naming convention

It is recommended to use format STUDY\_inf1\_protein\_UniProtID\_date.gz, see https://www.uniprot.org/ for additional information on UniProt IDs.

### Notes on PLINK

Due possibly to the large number of proteins for GWAS, some cohorts employed PLINK to expedite analysis with which one may see the following information:

|  |  |  |  |
| --- | --- | --- | --- |
| No | Name | Description | Comment |
| 1 | BP | Position in base pairs |
| 2 | CHR | Chromosome |
| 3 | SNP | SNP name/chr:pos\_a1\_a2 |
| 4 | HWE | Hardy-Weinberg equilibrium P-value |
| 5 | MAF | Minor allele frequency | Please indicate if this is the effect allele frequency |
| 6 | A1 | Allele 1 | Please indicate if this is the effect allele |
| 7 | N | Sample size |
| 8 | BETA | Regression coefficient |
| 9 | STAT | Regression test statistic |
| 10 | P | P value |

In this case, please provide for each SNP information on strand, effect allele, effect allele frequency, and the information measures for imputation -- the information measure can be on the genotype level rather than from phenotype-genotype regression through software such as SNPTEST. SNP and sample based statistics can greatly be facilitated with software qctool, http://www.well.ox.ac.uk/~gav/qctool\_v2/.

## 6. Meta-analysis

Meta-analysis will be performed using the inverse-N weighted analysis of regression betas and standard errors, as implemented in the software METAL (https://github.com/statgen/METAL).

We will apply genomic control and the appropriate marker filters at this stage (i.e. please provide unfiltered results).

* Marker exclusion filters: we will apply imputation quality filters at the meta-analysis stage, so provide unfiltered results.
* Genomic control (GC): genomic control will be applied to each study at the meta-analysis stage (single GC), so GC-correction is needed for each cohort.
* Significance: the threshold for the genome-wide analyses will be set at 5 x 10-10. The results will be replicated in independent cohorts.

## 7. Uploading of results

See CVD1 analysis plan.

## 8. Contact information

For questions about SCALLOP, please contact Anders Malarstig (anders.malarstig@ki.se). For technical issues regarding 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).