# SCALLOP sequence-based meta-analysis

Analyst call

**Date**: 19 October 2020/28 October 2020 (US)

**Chair**: Grace

**Notes:** Grace

**Present**:

Grace Png

Arthur Gilly

Andrei Barysenka

Anette Kalnapenkis

Åsa Johansson

Jinghua Zhao

Lucija Klaric

Urmo Võsa

Jeff Haessle

Chen Yao

Shih-Jen Hwang

## Action items

* Grace to set up Slack workspace - this has been done. Please click the link to join: <https://join.slack.com/t/scallop-seq/shared_invite/zt-iocn2n0w-pyPPsXnaXk4vVFMGor6rkw>
* All teams to send details on how their phenotypes have been transformed
* All teams to check for traits with multimodal distributions in CVD2 and CVD3
* All teams to send over prepared variant files (see Phase 1 in analysis plan) by **20 November 2020**

## Agenda

1. Slides in attachment
2. Fine tuning of analysis plan
   * We will go ahead with CVD2 and CVD3 first – these panels have the most samples
   * Lucija has done some comparisons between transformation before covariate adjustment vs. after covariate adjustment in ORCADES. Correlation plots have been sent round via email. There is also a paper explaining problems with the latter: 10.1038/s41431-018-0159-6 [Thanks Lucija!!!]
   * Regarding multimodal traits: different observations are likely to be made for different cohorts. Lucija has identified 1 protein (GH) with a bimodal distribution in ORCADES (also in email). All cohorts should also check for these proteins in the CVD2/3 panels
   * Most important is to standardise the phenotype preparation protocol. We will likely go with the most convenient approach (with the least amount of redoing). To be discussed more when all cohorts have sent details on how they have done their phenotype prep
3. Deadlines
   * Single point association: **15 January 2021**
   * RVA – Sending over of variant files (Phase 1): **20 November 2020**
4. Next meeting
   1. Scheduled for early December