# SCALLOP sequence-based meta-analysis

**Date**: 28 September 2020

**Chair**: Ele

**Notes:** Grace

**Present**:

Ele Zeggini

Grace Png

Åsa Johansson

Charles Kooperberg

Jim Wilson

Tõnu Esko

Urmo Võsa

## What happened

* Ele gave an introduction to the project and the motivation behind it
* Grace went through the analysis plan (slides and plan attached). The rare variant analysis pipeline is also described in more detail on <https://github.com/hmgu-itg/burden_testing/wiki>.

## Action items

1. All cohorts to nominate analysts to take part in analyst calls
2. Grace to have a meeting with analysts from each group to go through analysis plan and decide on a realistic timeline
3. Grace to circulate table containing information on which cohorts have what panels for how many samples, all cohorts to update. This is useful info to expedite future analyses and confirm which panels to analyse first
4. Grace to check/fill in paper proposals for WHI
5. Grace to discuss data sharing options with Arthur/analysts
6. Grace to check file sizes and runtimes

## Discussion points for follow-up

1. MAF cut-off for single point and rare variant analysis (currently includes all variants with MAF<5%)
   1. Should we have different cut-offs for single point and rare variant analysis
   2. Might 5% be too generous for rare variant analysis?
2. Phenotype preparation: Rank-based inverse normal transformation may not be the most appropriate for binomial traits and traits with true outliers. We should also consider alternatives