Variable selection (KORA and TwinsUK)
Identify SNP-MET-LIP sets significant under Bonferroni correction

- **SNP**
  - 102 SNPs at 95 known lipid loci
- **MET**
  - 151 metabolites
- **LIP**
  - TC, LDL-C, HDL-C, TG

- **P<3.3x10^-6**
- **P<8.3x10^-5**

**Figure 1.**

- **Conditional Analysis (KORA)**
  - Measure the effect size decreases from SNP to LIP after adjusting for MET
- **Mendelian Randomization (KORA)**
  - Measure the significance of unconfounded effect from MET to LIP assuming MET→LIP
- **Structural Equation Modeling (KORA)**
  - Measure the model fit and select the best fitted path model among the models 4-10 in Figure2

**Conditional Analysis (TwinsUK) Replication**

**Mendelian Randomization (TwinsUK) Replication**

**Structural Equation Modeling (TwinsUK) Replication**