Prioritizing Sample Selection

1. **Sample size**
   a. Amalgamation of data from multiple cohorts
   b. Need quality phenotyping, but maybe not exquisite phenotype

2. **Broad phenotyping**
   a. The GWAS experience

3. Mixture of direct measurements, follow-up questionnaire, and health record linkage

4. Ongoing contact and longitudinal

5. Consent, including ability to re-contact

6. Breadth for initial discovery and then depth on as select individuals

   e.g. Detailed measures on those with rare LOF mutations

7. Population diversity

Unresolved issues

1. Families

2. Role of other –omics

3. Need for continued analytic involvment