880 bacterial whole genome sequences

- phylogenetic classification, drug resistance mutations, KvarQ hits per SNP, KvarQ scanning time

- **subset i:**
  - direct comparison of KvarQ SNP calls with calls from BWA-pipeline

- **subset ii:**
  - comparison with previous phylogenetic interpretation

- **subset iii:**
  - drug resistance data interpretation

- **subset iv:**
  - "blind" FastQ set: phylogenetic classification and drug resistance mutations

- 206 MTB WGS with previous BWA/SAMtools SNP-calls
- 321 MTB WGS with *a priori* phylogenetic information (lab assay, other genotyping method, other data)
- 19 MTB WGS with annotated drug resistance mutation data from BWA pipeline
- 388 MTB WGS from Walker et al. (EBI ENA / Sanger Inst.)

overlapping