

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

206 MTB WGS
with previous
BWA/SAMtools
SNP-calls

subset ii:

comparison with previous
phylogenetic interpretation

321 MTB WGS
with *a priori*
phylogenetic information
(lab assay, other genotyping
method, other data)

subset iii:

drug resistance data
interpretation

19 MTB WGS
with annated drug
resistance mutation data
from BWA pipeline

subset iv:

„blind“ FastQ set:
phylogenetic classification
and drug resistance mutations

388 MTB WGS
from Walker et al.
(EBI ENA / Sanger Inst.)

overlapping