### Additional file 3. Characteristics of the four bioinformatics software for predicting drug resistance from *Mtb* genome sequences

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | TBProfiler | MyKrobe | KVarQ | PhyResSE |
| Types of data | Fastq; bam | Fastq; bam | Fastq | Fastq |
| User interfaces available | Web; Command line | Command line; Desktop apps | Command line;  Desktop apps (GUI) | Web; Pipelines documentations |
| TB identifications | No | Yes | No | No |
| Basis of resistance prediction | SNPs and indels | SNPs | SNPs | SNPs and indels |
| Sample quality report? | No | No | No | Yes |
| Drugs   |  | | --- | | Isoniazid | | Rifampicin | | Pyrazinamide | | Ethambutol | | Streptomycin | | Amikacin | | Kanamycin | | Capreomycin | | Quinolones/Fluoroquinolones | | Ethionamide | | PAS | | Aminoglycosides | | Bedaquiline | | Clofazimine | | Linezolid | | |  | | --- | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | |  | | --- | | X | | X | | X | | X | | X | | X | | X | | X | | X | | O | | O | | O | | O | | O | | O | | |  | | --- | | X | | X | | X | | X | | X | | X | | X | | O | | X | | O | | O | | O | | O | | O | | O | | |  | | --- | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | X | | O | | O | | O | | O | |

For KVarQ, Kanamycin and Amikacin were predicted as one entity.