

Sample Summary					
Sample ID	#####	Client ID	#####	Test ID	#####
Sample Type	gDNA	Sample Receipt Date	ddmmyyyy	Sample Temperature on Receipt	XYZ°C
Sample Source	Culture	Sample QC Date	ddmmyyyy	Sample QC	260/280 = 1.8 Concentration = 28 ng/μl

Genome Sequencing Summary					
Library Type	Whole Genome. PE x 150	Library Date	ddmmyyyy	Library QC	Good (4nm)
Genome Sequencer	Illumina NextSeq 500	Run Date	ddmmyyy	Machine ID Lane ID	##### \$\$\$\$\$\$\$\$

Genomic Analysis Application Summary							
Application	ΩTB ver 2.0.1	Run Date	ddmmyyyy	QC check	Pass	Application Run By	

Clinical summary

<i>Mycobacterium tuberculosis</i> detected	Yes	Coverage	0.99
Lineage	Beijing	% of genome covered	99.24

Drug susceptibility profile

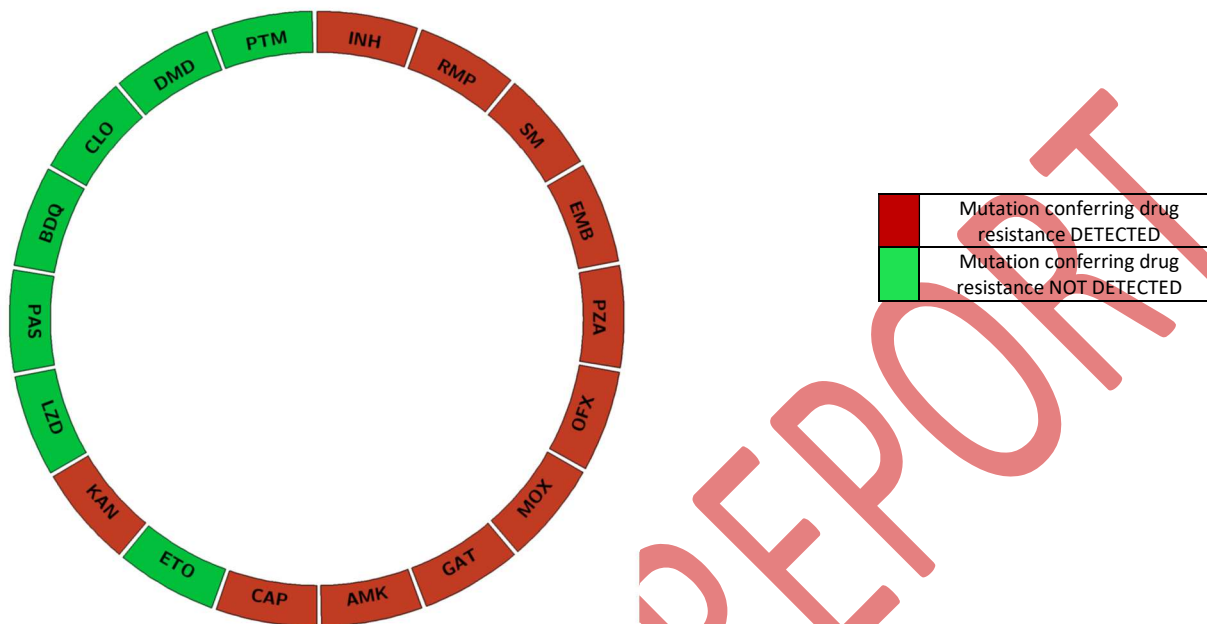
Antibiotic	Presence of Drug-Resistant Mutation
Rifampicin (RMP)	Detected
Isoniazid (INH)	Detected
Ethambutol (EMB)	Detected
Pyrazinamide (PZA)	Detected
Streptomycin (SM)	Detected
Capreomycin (CAP)	Detected
Kanamycin (KAN)	Detected
Amikacin (AMK)	Detected
Moxifloxacin (MOX)	Detected
Ofloxacin (OFX)	Detected
Gatifloxacin (GAT)	Detected
Ethionamide (ETO)	Not Detected
Linezolid (LZD)	Not Detected
Para-aminosalicylic acid (PAS)	Not Detected
Bedaquiline (BDQ)	Not Detected
Clofazimine (CLO)	Not Detected
Delamanid (DMD)	Not Detected
Pretomanid (PTM)	Not Detected

Clinical Recommendation

- **Tuberculosis antibiotic profile:** Extremely Drug Resistant Tuberculosis (XDR-TB)^a
- **Mixed infection:** Heterozygous calls detected
- **Other pathogens:** NA

Disclaimer: This is an automated report. The data reported here is based on statistical prediction of variants in the whole genome of the sample processed here. This report is not a phenotypic test of drug resistance. The variants used to predict antibiotic resistance and strain classification are based on genomic variants reported in peer reviewed publications.

Antibiogram



RIF: Rifampicin, INH: Isoniazid, EMB: Ethambutol, PZA: Pyrazinamide, STR: Streptomycin, CAP: Capreomycin, KAN: Kanamycin, AMK: Amikacin, MOX: Moxifloxacin, OFX: Ofloxacin, GAT: Gatifloxacin, ETO: Ethionamide, LZD: Linezolid, PAS: Para-aminosalicylic acid, BDQ: Bedaquiline, CLO: Clofazimine, DMD: Delamanid

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List of variants used to call resistance

Position	Ref allele	Alternate allele	Type	Frequency	Coverage	Substitution	Gene Symbol	Gene Name	Drug	Pubmed ID	Mutation Confidence
781687	A	G	SNP	99.17	113	Lys43Arg (aag/aGg)	Rv0682	rpsL	SM	22646308	Yes
761155	C	T	SNP	100.00	51	Ser450Leu (tcg/tTg)	Rv0667	rpoB	RMP	7759399	Yes
2288847	C	G	SNP	100.00	44	Gly132Ala (ggg/gCt)	Rv2043c	pncA	PZA	25336456	Yes
155168	C	G	SNP	100.00	81	Ser315Thr (agc/aCc)	Rv1908c	katG	INH	8878604	Yes
7564	G	C	SNP	100.00	42	Gly88Ala (ggc/gCc)	Rv0006	gyrA	FQ	24055765	Yes
7570	C	T	SNP	98.90	48	Ala90Val (gcg/gTg)	Rv0006	gyrA	FQ	21300839	Yes
247429	A	G	SNP	100.00	102	Met306Val (atg/Gtg)	Rv3795	embB	EMB	21300839	Yes
1473246	A	G	SNP	97.60	49	-	Rvnr01	-	AMK,KAN,CAP	21300839	Yes

Mutation confidence: Confidence of mutation for calling drug resistance as per WHO guidelines

Pubmed ID: Identification of peer reviewed study demonstrating mutation associated with drug resistance

ΩTB Drug resistance classification criteria

Multidrug resistant tuberculosis (MDR-TB)	Tuberculosis caused by <i>Mycobacterium tuberculosis</i> strains that is resistance to at least Isoniazid and Rifampicin.
Pre-extensively drug-resistant tuberculosis (Pre-XDR-TB)	Tuberculosis caused by <i>Mycobacterium tuberculosis</i> strains that fulfil the definition of MDR/Rifampicin Resistant-TB and that are also resistant to any Fluoroquinolones
Extensively drug-resistant tuberculosis (XDR-TB)	Tuberculosis caused by <i>Mycobacterium tuberculosis</i> strains that fulfil the definition of MDR/Rifampicin Resistant-TB and that are also resistant to any Fluoroquinolones and at least one additional Group A drug (The Group A drugs are currently Levofloxacin or Moxifloxacin, Bedaquiline and Linezolid)
Drug resistance detected	Tuberculosis caused by <i>Mycobacterium tuberculosis</i> (<i>M. tuberculosis</i>) strains that is resistant to anti-TB drugs and do not fall in the above-mentioned categories
Not Drug Resistant	No resistance to the anti-TB drugs detected

Mixed infection classification criteria

>25% showing heterozygous calls

Co-infection classification criteria

>20% coverage of genome mapping to co-infected pathogen

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SAMPLE REPORT

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