**PROCESSED AT :** FOCUS TB D-37/1,TTC MIDC,Turbhe, Navi Mumbai -400 703



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REPORT

Patient sample details, ID etc

NAME
REF. BY
TEST ASKED

PATIENTID

: KY16749597

. KRITIKA V YADAV (9Y/F)

: TB XDR SCREEN (LPA)

: RGMC TU 05 NID 18509219

**HOME COLLECTION :** KALWA HEALTH CENTRE, CSMH HOSPITAL, KALWA NAKA,

KALWA W SCT 29-4-21 - 400605

TGS Genome Analysis Report

#### **Clinical summary**

Mycobacterium tuberculosis detected	Yes	Coverage	0.99
Lineage	Beijing	% of reads	99.24

# Drug susceptibility profile

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

### Report summary for Patient ID

Mycobacterium tuberculosis was Detected.

The WGS analysis has categorized the sample as Extensively Drug-Resistant tuberculosis (XDR-TB). Drug resistance has been identified for 7 drugs.

Co-infections identified are NA.

Mixed infections identified are NA.

Sample Collected on (SCT) Sample Received on (SRT) Report Released on (RRT) Sample Type Labcode Barcode



: 03 May 2021 09:00 : 04 May 2021 10:02

- : 04 May 2021 14:07
- : CULTURE MGIT

Dr. Chaitali Nikam, Ph.D

Dr.Caesar Sengupta MD(Micro)

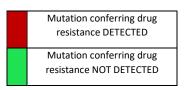
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# Antibiogram





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





Ref allele	Alternate allele	Туре	Frequency	Coverage	Substitution	Gene Symbol	Gene Name	Drug	Pubmed ID	Mutation Confidence
A	G	SNP	99.17	113	Lys43Arg (aag/aGg)	Rv0682	rpsL	SM	22646308	Yes
С	Т	SNP	100.00	51	Ser450Leu (tcg/tTg)	Rv0667	rpoB	RMP	7759399	Yes
С	G	SNP	100.00	44	Gly132Ala (ggt/gCt)	Rv2043c	pncA	PZA	25336456	Yes
С	G	SNP	100.00	81	Ser315Thr (agc/aCc)	Rv1908c	katG	INH	8878604	Yes
G	С	SNP	100.00	42	Gly88Ala (ggc/gCc)	Rv0006	gyrA	FQ	24055765	Yes
С	Т	SNP	98.90	48	Ala90Val (gcg/gTg)	Rv0006	gyrA	FQ	21300839	Yes
A	G	SNP	100.00	102	Met306Val (atg/Gtg)	Rv3795	embB	EMB	21300839	Yes
A	G	SNP	97.60	49	-	Rvnr01	-	AMK,KAN,CAP	21300839	Yes
	allele A C C C C G G A	alleleAGCTCGCGCTAG	allelealleleAGSNPCTSNPCGSNPCGSNPGCSNPCAGSNP	allele	allele  A  allele  A  SNP  99.17  113    A  G  SNP  99.17  113    C  T  SNP  100.00  51    C  G  SNP  100.00  44    C  G  SNP  100.00  44    C  G  SNP  100.00  42    G  C  SNP  100.00  42    A  G  SNP  100.00  102	allele  allede  allede<	allele  allele  Symbol  Symbol    A  G  SNP  99.17  113  Lys43Arg (aag/aGg)  Rv0682    C  T  SNP  100.00  51  Ser450Leu (tcg/tTg)  Rv0667    C  G  SNP  100.00  51  Ser450Leu (tcg/tTg)  Rv0667    C  G  SNP  100.00  44  Gly132Ala (ggt/gCt)  Rv2043c    C  G  SNP  100.00  81  Ser315Thr (agc/aCc)  Rv1908c    G  C  SNP  100.00  42  Gly88Ala (gg/gCt)  Rv0006    G  C  SNP  100.00  48  Ala90Val (gg/gCt)  Rv0006    C  T  SNP  98.90  48  Ala90Val (gg/gTg)  Rv0006    A  G  SNP  100.00  102  Met306Val (atg/Gtg)  Rv3795	allele  allele  x <th< td=""><td>alleleAGNNNameAGSNP99.17113Lys43Arg (aag/aGg)Rv0682rpsLSMCTSNP100.0051Ser450Leu (tcg/tTg)Rv0667rpoBRMPCGSNP100.0044Gly132Ala (ggt/gCt)Rv2043cpncAPZACGSNP100.0081Ser315Thr (agc/aCc)Rv1908ckatGINHGCSNP100.0042Gly88Ala (gg/gCc)Rv0006gyrAFQGCSNP100.0048Ala90Val (gg/gTg)Rv0006gyrAFQAGSNP100.00102Met306Val (atg/Gtg)Rv3795embBEMB</td><td>allele  allele  allele&lt;</td></th<>	alleleAGNNNameAGSNP99.17113Lys43Arg (aag/aGg)Rv0682rpsLSMCTSNP100.0051Ser450Leu (tcg/tTg)Rv0667rpoBRMPCGSNP100.0044Gly132Ala (ggt/gCt)Rv2043cpncAPZACGSNP100.0081Ser315Thr (agc/aCc)Rv1908ckatGINHGCSNP100.0042Gly88Ala (gg/gCc)Rv0006gyrAFQGCSNP100.0048Ala90Val (gg/gTg)Rv0006gyrAFQAGSNP100.00102Met306Val (atg/Gtg)Rv3795embBEMB	allele  allele<

## List of variants used to call resistance

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

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Multidrug resistant tuberculosis (MDR-TB)	Tuberculosis caused by <i>Mycobacterium tuberculosis</i> strains that and 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 Resistance	No Resistance for the anti-TB drugs detected





# Sample summary

Sample ID	Patient ID	Client ID	################	Test ID	##############
Sample Type	gDNA	Sample Receipt Date	ddmmyyyy	Sample Temperature on Receipt	XyzºC
Sample Source	Culture	Sample QC Date	ddmmyyyy	Sample QC	28 ng/µl

### Genome sequencing summary

Library Type	Whole Genome. PE x 150	Library Date	ddmmyyyy	Library QC	Pass
Genome Sequencer	Illumina NextSeq 500	Run Date	ddmmyyy	Machine/ Lane ID	#######################################

### **Genomic Analysis Application Summary**

Application	ΩΤΒ ver 2.0.1	Run Date	ddmmyyyy	QC check	Pass	Application Run By	
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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.

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