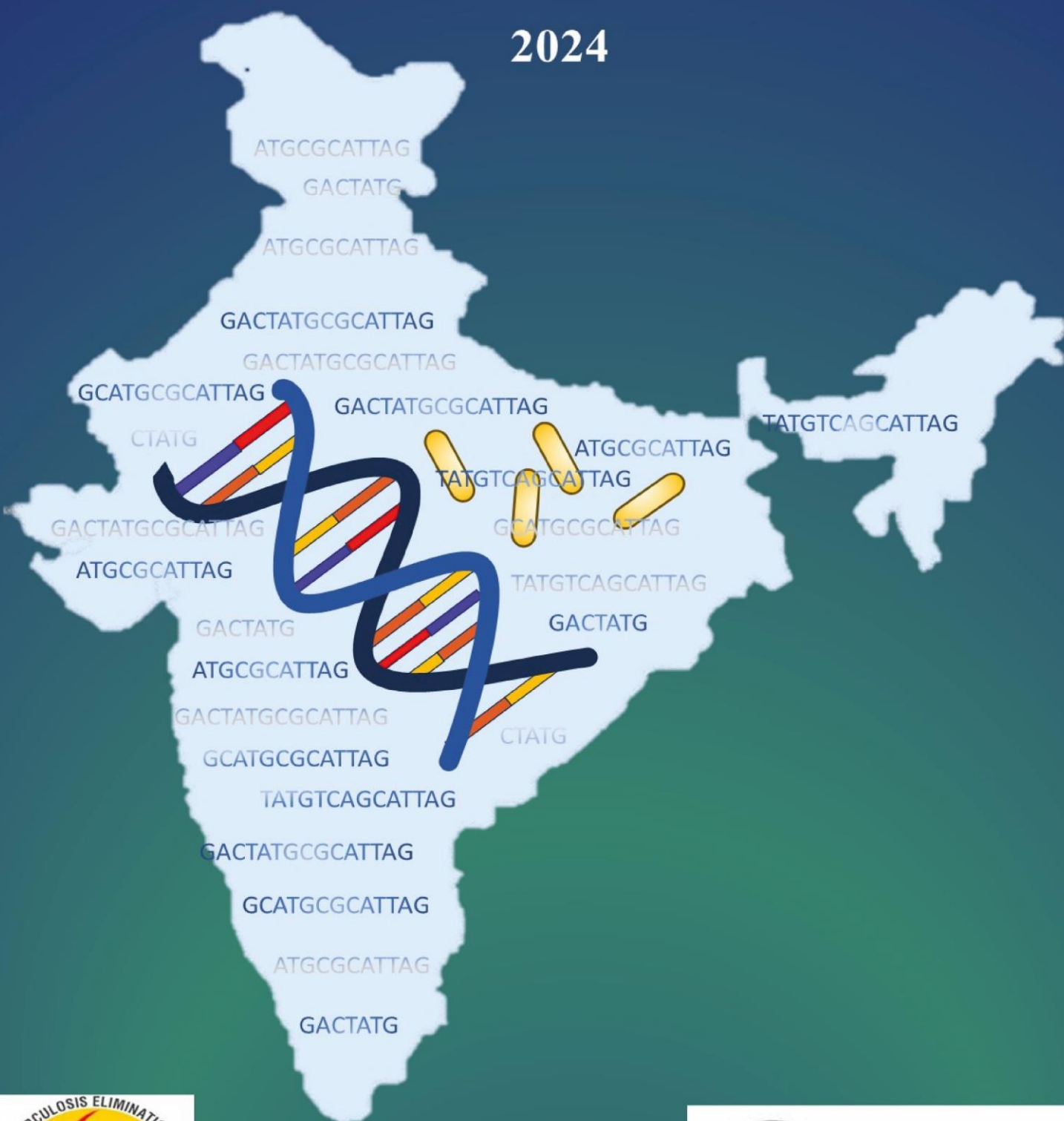


Indian Catalogue of *Mycobacterium tuberculosis* Mutations and their Association with Drug Resistance

Version 2.0

2024



Contents

Abbreviations	3
Drugs	4
Study Team	5
Introduction	6
Outline of the Indian Mutation Catalogue version 2	7
Catalogue Disclaimer Statement	7
Phenotypic and Genotypic Drug Susceptibility Testing Results	8
Diagnostic Testing of confidence-graded mutations for predicting phenotypic drug susceptibility	10
Catalogue Limitations	12
Mutation Catalogue Reckoner	13
Reading the tables	13
Initial Confidence Grading	15
Additional Grading Criteria	16
An illustrative example	16
Isoniazid	17
Rifampicin	32
Ethambutol	38
Fluoroquinolones – Levofloxacin, Ofloxacin and Moxifloxacin	39
Pyrazinamide	43
Linezolid	63
Para-amino salicylic acid	64
Amikacin, Streptomycin, Capreomycin and Kanamycin	65
Ethionamide	68
Methods and Approaches	89
Phenotypic Drug Susceptibility Testing	89
Genomic DNA Isolation	90
Whole Genome Sequencing	90
Quality Control	90
Variant Calling and Resistance Prediction	91
Statistical Analysis	91
Executive Summary	92
References	98

Abbreviations

CC	Critical Concentration
CI	Confidence Interval
CTAB	Cetyl TrimethylAmmonium Bromide
CRyPTIC	Comprehensive Resistance Prediction for Tuberculosis: an International Consortium
DNA	Deoxyribo Nucleic Acid
DST	Drug Susceptibility Testing
FDR	False Discovery Rate
FMR	The Foundation for Medical Research
gDST	Genotypic Drug Susceptibility Testing
indel	Insertion/ Deletion
lb	Lower Bound
MDR-TB	Multi-Drug Resistant TB
MGIT	Mycobacteria Growth Indicator Tube
MICs	Minimum Inhibitory Concentrations
MTB	<i>Mycobacterium tuberculosis</i>
MTBC	<i>Mycobacterium Tuberculosis</i> Complex
NA	Not Available
NGS	Next Generation Sequencing
NTEP	National Tuberculosis Elimination Program
OR	Odds Ratio
OR SOLO	Odds Ratio of SOLO Mutation
pDST	phenotypic Drug Susceptibility Testing
PPV	Positive Predictive Value
RRDR	Rifampicin Resistance-Determining Region
TB	Tuberculosis
ub	Upper Bound
WGS	Whole Genome Sequencing
WHO	World Health Organization

Drugs

AMK	Amikacin
CAP	Capreomycin
EMB	Ethambutol
ETO	Ethionamide
INH	Isoniazid
KAN	Kanamycin
LFX	Levofloxacin
LZD	Linezolid
MXF	Moxifloxacin
OFX	Ofloxacin
PAS	para-amino salicylic acid
PZA	Pyrazinamide
RIF	Rifampicin
STM	Streptomycin

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NTEP: National Tuberculosis Elimination Program

Introduction

Tuberculosis remains a significant global public health concern, profoundly impacting morbidity and mortality. According to the World Health Organization (WHO), in 2020, an estimated 10 million people worldwide contracted tuberculosis, with 1.4 million succumbing to the disease. Although substantial progress has been achieved in recent years, challenges such as drug-resistant tuberculosis and the repercussions of the COVID-19 pandemic have impeded disease control efforts. India, in particular, bears a substantial burden of tuberculosis cases, representing approximately 26% of the global incidence (1).

As indicated by TB surveillance efforts in India, the year 2022 marked a high record of 2.42 million cases, a 13% upsurge compared to 2021. This translates to a notification rate of approximately 172 cases per lakh population. In 2022, a total of 63,801 cases were diagnosed with MDR/RR in India. Furthermore, the presumptive TB examination rate (PTBER) for the country in 2022 increased to 1,281 per lakh population, a 68% increase from 763 in 2021 (2).

In 2021, the World Health Organization released the "Catalogue of Mutations in *Mycobacterium tuberculosis* Complex and Their Association with Drug Resistance" (WHO Mutation Catalogue). This catalogue synthesized and analyzed resistance profiles from a global collection of isolates, utilizing complementary whole-genome sequencing (WGS) and phenotypic drug susceptibility testing (DST) data (3, 4). The catalogue facilitates standardized interpretation of genotypic data for all currently recommended anti-tuberculosis drugs. However, it's worth noting that as the sources of data and *Mycobacterium tuberculosis* (MTB) strains in the WHO Mutation Catalogue are not evenly distributed globally, cataloged mutations may predominate regionally rather than globally or exhibit varying levels of association with drug-resistant tuberculosis (DR-TB). In 2022, following the WHO Mutation Catalogue, an Indian Mutation Catalogue was introduced, marking the first country-specific catalogue of its kind for *M. tuberculosis* (5). The study employed a quota sampling technique to obtain *M. tuberculosis* isolates from 25 states and four union territories. Subsequently, next-generation WGS and WHO-approved phenotypic DST were applied to these isolates. Employing a setting-adapted categorization scheme based on the WHO Mutation Catalogue and a validated bioinformatics workflow, genomic and phenotypic drug resistance profiles were compared and evaluated. This catalogue represents the first national Indian Catalogue of Mutations for drug-resistant tuberculosis (DR-TB). Currently, we have formulated another catalogue based on the CRyPTIC

consortium data representing the Indian region, which encompasses both drug-resistant and sensitive strains.

Outline of Indian Mutation Catalogue Version 2

In 2022, Indian Mutation Catalogue Version 1 was released by the honorable Minister of Health and Family Welfare and Chemicals and Fertilizers of India, Dr. Mansukh Mandaviya. This catalogue utilized a quota-based sampling frame for the collection of 3,167 isolates of the *M. tuberculosis* complex (MTBC) obtained from patients living in 25 States and 4 Union Territories. The sample collection mainly focused on MDR strains, with cultures obtained from processed sputum and directly from collection sites totaling 448 and 1,635, respectively, while 28 cultures had unavailable processing history, and one sample was of extrapulmonary origin. After quality filtering, matching WGS data were obtained for 2,112 isolates, which were then included for further analysis. This catalogue comprises descriptions of more than 8,000 mutations.

In 2023, a dataset of 6,782 isolates of the *M. tuberculosis* complex (MTBC) obtained from The Foundation for Medical Research (FMR) was further collated and included in the catalogue (Version 2.0). Among these 6,782 isolates, 50% were MDR and 30% were pan-sensitive isolates. In addition to the earlier catalogue (Version 1.0), descriptions of 3,033 mutations were obtained from the FMR data.

Thus, Version 2.0 is obtained by merging Version 1.0 with FMR data. This current version comprises 8,894 isolates, among which 2,444 (27%) were drug-sensitive TB isolates, with overall descriptions of 10,673 mutations. For a more detailed description of the collating process, please refer to the Methodology section of this catalogue.

Catalogue Disclaimer Statement

Next generation WGS is yet to be endorsed by the WHO or the Indian NTEP as a diagnostic or drug susceptibility testing method for clinical use. Hence, Indian Mutation Catalogue version 2.0 data shall not serve as a guide for clinical care of patients in India or elsewhere in the world. It should be noted that this catalogue is mainly collated and presented in order to support the DR-TB surveillance and disease control efforts in India.

Phenotypic and Genotypic Drug Susceptibility Testing Results

The current catalogue (Version 2.0) comprises 8,894 isolates, featuring mutations pertaining to 14 drugs. Among these 14 drugs, Phenotypic Drug Susceptibility Testing (pDST) data were available for all isolates only for 9 drugs. In the case of PAS, pDST data were available for 4,443 isolates. For the remaining drugs such as CAP, PZA, OFX, and STM, pDST data were available for only 2,112 isolates.

Genotypic Drug Susceptibility Testing (gDST) data were available for all 8,894 isolates studied. The total numbers and percentages of collected samples with pDST and gDST resistance results for each drug are outlined in **Table 1**. The prevalence of phenotypic resistance to first-line drugs INH and RIF was found to span 65.44% and 54.15% among the tested isolates, respectively. In the case of EMB and PZA, it was observed to be 34.46% and 42.61%, respectively. The prevalence of phenotypic resistance to AMK, KAN, CAP, LZD, and PAS ranged between 7–15% (**Table 1**). In the case of gDST, resistance to the first-line drugs RIF and INH was observed to be $\geq 60\%$ of isolates tested, whereas resistance to EMB was 57.71% (23% higher than reported using pDST) and PZA was observed in 36.77% of the isolates. Resistance to the fluoroquinolones (LFX, MFX, and OFX) was observed for 48.28% of isolates, while resistance to the second-line drugs AMK, KAN, CAP, LZD, and PAS ranged from 2.0 to 20.0%. Finally, the percentage of resistance detected to STM was observed to be high for both pDST and gDST, at 50.38% and 51.24%, respectively.

Table 1. Phenotypic and genotypic drug susceptibility testing results

Drug	Number of resistant isolates by pDST (n=8894)	Percentage (95% CI)	Number of resistant isolates by gDST (n=8894)	Percentage (95% CI)
RIF	4816	54.15(53.11-55.19)	5304	59.64(58.61-60.66)
INH	5820	65.44(64.44-66.43)	5783	65.02(64.02-66.01)
EMB	3065	34.46(33.47-35.46)	5133	57.71(56.68-58.74)
LFX	4307	48.43(47.38-49.47)	4294	48.28(47.24-49.32)
MFX	5298	59.57(58.54-60.59)	4294	48.28(47.24-49.32)
LZD	881	9.91(9.29-10.55)	189	2.13(1.84-2.45)
AMK	707	7.95(7.40-8.53)	775	8.71(8.14-9.32)
CAP	*163	7.72(6.62-8.94)	1766	19.97(19.14-20.81)
KAN	1326	14.91(14.18-15.67)	1144	12.86(12.17-13.58)
ETO	2444	27.48(26.55-28.42)	1590	17.88(17.09-18.69)
PAS	\$623	14.02(13.00-15.04)	470	5.28(4.83-5.77)

PZA	**900	42.61(40.49-44.76)	3270	36.77(35.76-37.78)
OFX	***1223	57.91(55.77-60.02)	4294	48.28(47.24-49.32)
STM	#1064	50.38(48.22-52.53)	4557	51.24(50.19-52.28)

* CAP – pDST available for only 2112 isolates

\$ PAS – pDST available for only 4443 isolates

**PZA – pDST available for only 2112 isolates

***OFX – pDST available for only 2112 isolates

#STM – pDST available for only 2112 isolates

Diagnostic Testing of confidence-graded mutations for predicting phenotypic drug susceptibility

Table 2. Numerical Split of grading of mutations based on analysis

Drug	1) Associated with Resistance	2) Associated with Interim Resistance	3) Uncertain Significance	4) Not Associated with Interim	5) Not Associated with Resistance
RIF	4	84	1652	1	392
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	96.12%(95.57%-96.67%) 86.2 %(85.2%-87.3%) 89.2%(88.37%-90.5%)	59.57%(58.96%-60.18%) 22.90%(21.70%-24.28%) 82.70%(82.15%-83.25%)			
INH	4	55	1730	0	107
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	96.12%(95.57%-96.67%) 86.2 %(85.2%-87.3%) 89.2%(88.37%-90.5%)	59.57%(58.96%-60.18%) 22.90%(21.70%-24.28%) 82.70%(82.15%-83.25%)			
EMB	4	13	432	0	822
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	79.60%(78.17%-81.03%) 78.03%(76.97%-79.09%) 65.56%(64.03%-67.09%)	33.10%(31.43%-34.77%) 91.58%(90.87%-92.29%) 67.38%(65.01%-69.75%)			
LFX	7	14	385	0	176
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	81.61%(80.45%-82.77%) 81.67%(80.55%-82.79%) 80.69%(79.52%-81.86%)	5.18%(4.52%-5.84%) 98.32%(97.95%-98.69%) 74.33%(69.39%-79.27%)			
MOX	6	16	398	0	159
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	63.82%(62.53%-65.11%) 74.46%(73.03%-75.89%) 78.65%(77.43%-79.87%)	19.83%(18.76%-20.90%) 79.61%(78.29%-80.93%) 58.91%(56.63%-61.19%)			
OFX	6	10	186	0	165
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	98.19%(97.46%-98.92%) 97.07%(95.96%-98.18%) 97.96%(97.18%-98.74%)	6.53%(5.15%-7.91%) 98.76%(98.03%-99.49%) 87.91%(81.21%-94.61%)			
LZD	2	0	373	0	455
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	14.25%(11.95%-16.55%) 99.20%(99.0%-99.40%) 66.32%(59.60%-73.04%)	NA			

AMK	2	1	82	0	355
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	60.65%(57.05%-64.25%) 98.24%(97.96%-98.52%) 74.91%(71.36%-78.46%)	0.42%(0.06%-0.90%) 99.95%(99.90%-1.%) 42.86%(6.20%-79.52%)			
CAP	2	3	10	0	219
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	80.12%(74.05%-86.19%) 98.87%(98.40%-99.34%) 85.81%(80.32%-91.30%)	4.82%(1.56%-8.08%) 100.00%(100.00%-100.00%) 100.00%(100.00%-100.00%)			
KAN	7	1	78	0	162
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	55.87%(53.20%-58.54%) 94.05%(93.48%-94.62%) 65.09%(62.32%-67.86%)	0.23%(0.03%-0.49%) 99.93%(99.87%-99.99%) 37.50%(3.95%-71.05%)			
ETH	4	161	547	2	283
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	47.71%(45.73%-49.69%) 94.79%(94.25%-95.33%) 77.64%(75.53%-79.75%)	13.%(11.67%-14.33%) 96.76%(96.33%-97.19%) 60.34%(56.16%-64.52%)			
PAS	4	4	131	1	248
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	42.74%(33.78%-51.70%) 99.45%(99.13%-99.77%) 81.97%(72.32%-91.62%)	7.69%(2.86%-12.52%) 99.80%(99.60%-1.%) 69.23%(44.14%-94.32%)			
PZA	2	304	107	1	153
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	10.54%(8.52%-12.56%) 99.25%(98.76%-99.74%) 91.26%(85.81%-96.71%)	72.50%(70.53%-74.47%) 30.13%(27.54%-32.72%) 63.%(61.02%-64.98%)			
STM	4	11	74	2	50
Sensitivity (95% CI), Specificity (95% CI), PPV (95% CI)	94.93%(93.61%-96.25%) 96.08%(94.90%-97.26%) 96.11%(94.94%-97.28%)	17.73%(15.44%-20.02%) 96.46%(95.34%-97.58%) 83.63%(78.81%-88.45%)			

Catalogue Limitations

This study has several inherent limitations. Firstly, Version 2.0 data combines quota-based sampling from Version 1.0 with a prospective-all sampling approach by the CRyPTIC Consortium. Although this version encompasses most Indian States and Union Territories, it does not statistically represent the entire locale or the nation as a whole. Our primary objective was to systematically gather *Mycobacterium tuberculosis* (MTB) strains to assess genetic diversity and characterize mutations linked with drug resistance in India. However, it is important to acknowledge that this method may not fully encompass the diversity, and certain analysis of resistance associations may lack statistical power to accurately evaluate association measures.

Secondly, the inclusion criteria of Version 1.0 focused on patients assumed to have drug-resistant TB, resulting in a bias toward the collection, testing, and analysis of DR-TB isolates and strains. Conversely, CRyPTIC data incorporated in Version 2.0 comprises all culture-positive clinical samples (prospective all) that were prospectively included. Version 2.0 encompasses drug-sensitive TB isolates, constituting approximately 27% of the final dataset. Despite representing a large volume of DR-TB strains nationwide, this may introduce bias to the dataset, potentially resulting in incomplete associations of detected mutations among drug-susceptible strains. This bias could lead to the overestimation of mutation-associated resistance for polymorphisms not previously recognized as resistance-associated. Thirdly, as the pDST data for Bedaquiline was not available for all the isolates, hence, we could not collate and report the corresponding resistance association analysis.

Mutation Catalogue reckoner

Reading the tables

The terms and abbreviations used in drug-specific subsections and tables below are listed in **Table 3** and mirror those used in the WHO Mutation Catalogue.

Table 3. Terms used in the report and their description

Terms Used in the Mutation Catalogue	Description
Assoc w R	Associated with resistance
Assoc w RI	Associated with resistance – interim
Inf	Infinity
NA	Not Available
Undef	Undefined (0/0)
Not Assoc w R	Not associated with resistance
Not Assoc w RI	Not associated with resistance – interim
Uncert. Sig.	Uncertain significance
WHO-endorsed gDST assay	WHO-endorsed genotypic drug susceptibility testing assay
Drug	Name of drug
Mutations	Mutation, with common name where relevant
Present in R (TP)	Number of resistant isolates with the mutation
Present in S (FP)	Number of susceptible isolates with the mutation
Absent in R (FN)	Number of resistant isolates without the mutation
Absent in S (TN)	Number of susceptible isolates without the mutation
Sensitivity	True positive rate of mutation
Specificity	True negative rate of mutation
PPV	Positive predictive value of mutation
PPV SOLO	Positive predictive value conditional on being solo
Initial confidence grading	Initial grouping of mutation
Dataset(s)	Dataset(s) used to derive the initial confidence grading
Additional grading criteria	Criterion for changing the initial confidence grading (e.g., previous WHO guidance or WHO-endorsed genotypic DST assays) to determine the final confidence grading
LoF	Loss of function
Final confidence grading	Final grouping of mutation after additional grading criteria were applied

Additional Variables Shown in the Catalogue	Description
Gene Name	Gene Name of Each Mutation
Gene ID	Gene ID for Every Variant
Present SOLO_R	Resistant isolates with the single (solo) mutation
Present SOLO_S	Sensitive isolates with the single (solo) mutation
Present SOLO_SR	Sum of resistant and susceptible isolates with the single (solo) Mutation
Sensitivity*	True positive rate of mutation
Specificity*	True negative rate of mutation
PPV*	Positive predictive value of mutation
LR+*	Positive likelihood ratio of mutation
LR-*	Negative likelihood ratio of mutation
OR*	Odds ratio of mutation
OR SOLO*	Odds ratio of solo mutation
OR SOLO_FE-sig	Fisher's exact test for the false discovery rate (FDR)-corrected P for the OR SOLO; TRUE = FDR-corrected $P \leq 0.05$, FALSE = FDR-corrected $P > 0.05$

* The lower bound (lb) and upper bound (ub) of the 95% CI are provided as additional columns in the Mutation Catalogue.

The tables in this report were simplified and abridged to fit the page space (i.e., all Group 3, Group 4 and Group 5 Mutations are not shown; full list available upon request).

A description of methods used to calculate and analyze data for the variables above is presented in the Statistical Analysis section of this document. The thresholds used to define the initial confidence grading are listed below; if they were met, the entry is highlighted in the colour denoted within parentheses.

Initial Confidence Grading

Group 1: Associated with resistance (**Red**)

1. Sum of resistant and susceptible isolates with the solo mutation (Present SOLO_SR) ≥ 5
2. Lower bound of 95% CI of PPV conditional on being solo (PPV | SOLO_lb) $\geq 25\%$
3. OR > 1 , which always applies if criterion 4 is met
4. OR | SOLO > 1
5. Statistical significance of OR | SOLO (OR SOLO_FE-sig) with Fisher exact FDR-corrected $P \leq 0.05$

Group 2: Associated with resistance – interim (**Orange**)

1. Resistant isolates with the solo mutation (Present SOLO_R) ≥ 2
2. PPV $\geq 50\%$

Group 3: Uncertain significance

Mutations that did not meet the criteria for inclusion in group 1, 2, 4 or 5.

Group 4: Not associated with resistance – Interim

1. PPV conditional on being solo (PPV | SOLO) $< 40\%$
2. Upper bound of 95% CI of PPV conditional on being solo (PPV | SOLO_ub) $< 75\%$

Group 5: Not associated with resistance

Mutations which have PPV less than 50% were considered as Not associated with resistance while WHO filtered those mutations which are less than 10%.

Additional Grading Criteria

Following the initial confidence grading, certain mutations originally categorized within Groups 3, 4, and 5 were reclassified into Group 2. This reclassification was guided by expert rules and precedents adhered to in the WHO Catalogue, and were motivated by the same reasons elucidated in the WHO Catalogue (Blue). Furthermore, it is worth noting that certain mutations with a robust association with resistance were not initially placed in Group 1 or Group 2 due to stringent statistical criteria. The rationales behind these reclassifications are provided in the tables (Blue). Finally, for the sake of thoroughness and precision, all the strains and mutations are presented in drug-specific tables below, regardless of their frequency.

An illustrative example

In the first example below, the drug considered is INH. The variant is in the *katG* gene, the amino acid change is at codon 315, and the amino acid change is from Serine to Threonine. This variant was found in 4877 phenotypically resistant isolates and in 203 susceptible isolates. The mutation was not found in 944 phenotypically resistant isolates and in 2869 susceptible isolates. The mutation Q190! of *katG* gene falls into Group-5 category by initial confidence grading based on its statistical classification. This mutation was moved to Group 2 (Associated with interim resistance) following the expert rule that any INDEL or premature stop codon mutation can confer INH resistance as described in WHO Mutation Catalogue (3).

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SO-LO	PPV SO-LO_lb	PPV SO-LO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional Grading Criteria	FINAL CONFIDENCE GRADING
S315T	katG	2294	2521	4877	203	944	2869	96%	92%	91%	93%	84%	93%	30.7132	Group-1		Group-1
Q190!	katG	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	Indel or premature stop codon	Group-2

The sensitivity, specificity, and PPV represent the performance of this mutation in the dataset. The next four columns indicate the statistical performance of this mutation when it occurs without other mutations (defined as ‘SOLO’) in the genomic regions selected when assessing INH resistance. The values given are the midpoint PPV with the corresponding lower bound (lb) and upper bound (ub), and the odds ratio for the solo mutation (OR SOLO). This template is as per the WHO Mutations Catalogue.

The initial confidence grading for *katG* S315T was group 1 (Assoc w R) because:

- Present_SOLO_SR (see Mutation Catalogue) was 2521 and, consequently, ≥ 5 .
- PPV|SOLO_lb of 90.7% was $\geq 25\%$.
- OR SOLO of 30.7 was > 1 and statistically significant.

Isoniazid

For Isoniazid, fifteen mutations were classified into Group-1 and Group-2 based on initial confidence grading. Then fourty-four mutations were moved to Group 2 based on Additional Grading Criteria (Indel or premature stop codon loss of function [LoF]) in *katG* gene. Promoter mutation was found at C-15T of *fabG1* (Group 1). Two *katG* mutations (S315T and S315N) were found in Group 1.

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional Grading Criteria	FINAL CONFIDENCE GRADING
C-15T	<i>fabG1</i> / promoter	83	87	1276	44	4547	3026	97%	65%	57%	74%	22%	99%	13.8089	Group-1		Group-1
S94A	<i>inhA</i>	4	6	65	2	5758	3068	97%	67%	29%	104%	1%	100%	1.0656	Group-1		Group-1
S315T	<i>katG</i>	2294	2521	4877	203	944	2869	96%	92%	91%	93%	84%	93%	30.7132	Group-1		Group-1
S315N	<i>katG</i>	13	13	39	0	5784	3070	100%	100%	100%	100%	1%	100%	Inf	Group-1		Group-1

D142G	<i>katG</i>	2	2	3	0	5820	3070	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
G-17T	<i>fabG1/</i> pro- moter	2	2	30	2	5793	3068	90%	50%	1%	99%	0%	100%	Inf	Group-2		Group-2
G406A	<i>embB</i>	2	2	112	7	5711	3063	94%	22%	0%	49%	2%	100%	Inf	Group-2		Group-2
G-48A	<i>ahpC</i> /prom oter	2	2	43	4	5780	3066	91%	33%	0%	71%	1%	100%	Inf	Group-2		Group-2
R268H	<i>ndh</i>	11	95	144	126	5679	2944	53%	8%	3%	13%	2%	96%	0.0678	Group-2		Group-2
S315I	<i>katG</i>	3	3	11	0	5812	3070	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
S315R	<i>katG</i>	4	4	52	3	5771	3067	95%	57%	20%	94%	1%	100%	Inf	Group-2		Group-2
T-8A	<i>fabG1/</i> pro- moter	4	4	24	2	5799	3068	92%	67%	29%	104%	0%	100%	Inf	Group-2		Group-2
T-8C	<i>fabG1/</i> pro- moter	2	2	125	4	5698	3066	97%	33%	0%	71%	2%	100%	Inf	Group-2		Group-2
R463L	<i>katG</i>	8	185	5105	2530	718	540	67%	0%	0%	1%	88%	18%	0.0339	Group-2		Group-2
S315T2	<i>katG</i>	2	2	15	0	1730	366	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
Q190!	<i>katG</i>	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	In- del or pre- ma- ture sto p co-	Group-2

																don	
!741C	<i>katG</i>	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	In- del or pre ma- ture sto p co- don	Group-2
GACA6 1GA	<i>katG</i>	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	IN DE L or pre ma- ture sto p co- don	Group-2
K554!	<i>katG</i>	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	In- del or pre ma- ture sto p co- don	Group-2
GCCCC 703GC CCCC	<i>katG</i>	0	0	0	1	1745	365	0%	0%	0%	0%	0%	100%	Undef	Group-5	IN DE L or pre ma-	Group-2

																ture sto p co- don	
CG97C GG	<i>katG</i>	0	0	1	0	4077	2704	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GTTT1 05GTT	<i>katG</i>	0	0	1	0	4077	2704	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2

GCCCC C372G CCCC	<i>katG</i>	0	0	3	0	1742	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
TC1003 TCC	<i>katG</i>	0	0	2	0	1743	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
TCC117 7TCCC	<i>katG</i>	0	0	2	0	1743	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GC1367 GCC	<i>katG</i>	0	0	2	0	1743	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or	Group-2

																pre ma- ture sto p co- don	
W728!	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	In- del or pre ma- ture sto p co- don	Group-2
CTTAC CGCTG TAACG 639C	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
ACC15 50ACC C	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co-	Group-2

																don	
TTGT1 734TTG TGT	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
CTT474 CT	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
AGG11 45AGG G	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
AC- CTT- GCCAC TGCCA	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or	Group-2

TCCTT GCC20 60ACC TTGCC																pre ma- ture sto p co- don	
AGCGC 1921AG CGCGC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
ACC13 34ACC CC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
TC1868 TCC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p	Group-2

																co- don	
ACC14 85ACC CC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
TGGG1 8TGGG G	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
TGCTT GGG- GAC- CAGC1 301TGC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GC1855 GCC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L	Group-2

																or pre ma- ture sto p co- don	
TC29T CC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
CCCGG CGCCG 369CCC G	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
CTCGG GTTCG GG867 CTCGG GTTCG GGTTC GGG	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto	Group-2

																p co- don	
CAC- GAC- GGGA C69CA C	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
W668!	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	In- del or pre ma- ture sto p co- don	Group-2
TCCC6 44TCC CCC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
CG486 CGG	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE	Group-2

																L or pre-mature stop co-don	
CA1614 CATA	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or pre-mature stop co-don	Group-2
W39!	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	Indel or pre-mature stop co-don	Group-2
W341!	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	Indel or pre-mature stop p	Group-2

																co- don	
GCCCC C372G CCCC C	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GACAC 1616GA CACAC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
C2106C A	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GC1920	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN	Group-2

GCC																DE L or pre ma- ture sto p co- don	
CGGG7 17CGG GG	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
AC2081 ACC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2

CCGGT GGTGG TTTCT GTAAT GGGTG GGTGT TGC41 CCGGT GGTGG TTTCT GTAAT GGGTG GGTGT TGCGG TGGTG GTTTC TGTA TGGGT GGGTG TTGC	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GCCC1 433GC C	<i>katG</i>	0	0	1	0	1744	366	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	IN DE L or pre ma- ture sto p co- don	Group-2
GCCC1 285GC C	<i>katG</i>	0	0	1	1	1744	365	50%	0%	0%	0%	0%	100%	Undef	Group-3	IN DE L or pre- ma-	Group-2

																ture sto p co- don	
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Rifampicin

In case of Rifampicin, four mutations (S450L, D435V, H445Y and H445D) were classified into Group 1, and eighty-four mutations were found to span in Group 2 (Associated with interim resistance), as per the final confidence grading criteria. Based on previous WHO Guidance, mutations outside the RRDR (I491F) were moved to Group-2 from Group-5. Sixty-four Group 2 mutations were all in the RRDR, and these were classified in accordance to the expert rule which implies that any RRDR mutation, except for synonymous mutations, it should be assumed to confer RIF resistance. It should also be noted that this expert rule was first introduced by WHO in 2018 and was reaffirmed in 2021 (4, 10).

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional GradingCriteria	FINAL CONFIDENCE GRADING
D435V	<i>rpoB</i>	64	76	294	62	4525	4013	83%	51%	42%	60%	6%	98%	4.7298	Group-1		Group-1
H445D	<i>rpoB</i>	32	36	163	30	4656	4045	84%	52%	39%	64%	3%	99%	6.9501	Group-1		Group-1

S450L	<i>rpoB</i>	727	834	3891	402	926	3675	91%	64%	62%	67%	81%	90%	26.9647	Group-1		Group-1
H445Y	<i>rpoB</i>	42	47	284	66	4535	4009	81%	39%	30%	48%	6%	98%	7.4257	Group-1		Group-1
H445L	<i>rpoB</i>	19	23	60	17	4759	4058	78%	53%	36%	69%	1%	100%	4.0503	Group-2		Group-2
D435Y	<i>rpoB</i>	31	49	555	275	4264	3800	67%	10%	7%	14%	12%	93%	1.5348	Group-2		Group-2
G332S	<i>rpoC</i>	3	4	760	124	4059	3951	86%	2%	0%	5%	16%	97%	2.9201	Group-2		Group-2
G433S	<i>rpoC</i>	2	2	565	75	4254	4000	88%	3%	0%	6%	12%	98%	Inf	Group-2		Group-2
H445N	<i>rpoB</i>	16	25	223	155	4596	3920	59%	9%	5%	14%	5%	96%	1.5162	Group-2		Group-2
H445R	<i>rpoB</i>	12	12	153	18	4666	4057	89%	40%	22%	58%	3%	100%	Inf	Group-2		Group-2
I491T	<i>rpoC</i>	3	3	542	73	4277	4002	88%	4%	0%	8%	11%	98%	Inf	Group-2		Group-2
I491V	<i>rpoC</i>	11	12	3400	421	1419	3654	89%	3%	1%	4%	71%	90%	28.3255	Group-2		Group-2
L430P	<i>rpoB</i>	24	60	1049	577	3770	3498	65%	4%	2%	6%	22%	86%	0.6185	Group-2		Group-2
L452P	<i>rpoB</i>	21	45	163	113	4656	3962	59%	16%	10%	22%	3%	97%	0.7445	Group-2		Group-2
L516P	<i>rpoC</i>	2	2	141	16	4678	4059	90%	11%	0%	26%	3%	100%	Inf	Group-2		Group-2
P1040R	<i>rpoC</i>	7	7	3093	315	1726	3760	91%	2%	1%	4%	64%	92%	Inf	Group-2		Group-2
Q432L	<i>rpoB</i>	5	5	46	12	4773	4063	79%	29%	8%	51%	1%	100%	Inf	Group-2		Group-2
S431T	<i>rpoB</i>	4	7	302	240	4515	3837	56%	2%	0%	3%	6%	94%	1.1331	Group-2		Group-2
S441L	<i>rpoB</i>	6	6	10	0	4809	4075	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
S450W	<i>rpoB</i>	16	21	123	65	4696	4010	65%	20%	11%	28%	3%	98%	2.7325	Group-2		Group-2

S493L	<i>rpoB</i>	2	2	7	0	4812	4075	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
V170F	<i>rpoB</i>	2	4	28	13	4791	4062	68%	13%	0%	31%	1%	100%	0.8478	Group-2		Group-2
V483A	<i>rpoC</i>	10	10	3023	333	1796	3742	90%	3%	1%	5%	63%	92%	Inf	Group-2		Group-2
H445P	<i>rpoB</i>	1	1	11	2	4808	4073	85%	33%	0%	87%	0%	100%	Inf	Group-4	RRDR	Group-2
P434A	<i>rpoC</i>	1	1	6	2	3416	3358	75%	33%	0%	87%	0%	100%	Inf	Group-4	RRDR	Group-2
I491F	<i>rpoB</i>	11	20	23	27	4796	4048	46%	29%	15%	43%	0%	99%	1.0316	Group-5	previous WHO Guidance	Group-2
Q432E	<i>rpoB</i>	0	0	0	1	3422	3359	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
S431G	<i>rpoB</i>	0	0	1	3	4818	4072	25%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
M434L	<i>rpoB</i>	0	0	0	1	1397	714	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
S441I	<i>rpoB</i>	0	0	0	2	1397	713	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
S441P	<i>rpoB</i>	0	0	0	3	1397	712	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
P454S	<i>rpoB</i>	0	0	0	1	1397	714	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
A451V	<i>rpoB</i>	0	0	0	1	1397	714	0%	0%	0%	0%	0%	100%	Undef	Group-5	RRDR	Group-2
D435A	<i>rpoB</i>	0	0	5	0	4814	4075	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	previous WHO guidance	Group-2
D435G	<i>rpoB</i>	1	3	92	16	4727	4059	85%	6%	0%	17%	2%	100%	0.4293	Group-3	previous WHO guidance	Group-2
D435N	<i>rpoB</i>	0	0	1	0	3421	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
F452C	<i>rpoC</i>	0	0	7	0	4812	4075	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2

F452L	<i>rpoC</i>	0	0	37	5	4782	4070	88%	0%	0%	0%	1%	100%	Undef	Group-3	RRDR	Group-2
F452S	<i>rpoC</i>	0	0	9	0	4810	4075	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
H445Q	<i>rpoB</i>	1	1	4	1	4815	4074	80%	50%	0%	119%	0%	100%	Inf	Group-3	RRDR	Group-2
K445R	<i>rpoC</i>	0	0	68	8	4751	4067	89%	0%	0%	0%	1%	100%	Undef	Group-3	RRDR	Group-2
L430R	<i>rpoB</i>	1	1	31	6	4788	4069	84%	14%	0%	40%	1%	100%	Inf	Group-3	RRDR	Group-2
L449V	<i>rpoC</i>	0	0	10	1	4809	4074	91%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
M434I	<i>rpoB</i>	0	0	19	7	4800	4068	73%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
M434V	<i>rpoB</i>	0	0	6	1	4813	4074	86%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
N437D	<i>rpoB</i>	0	0	26	25	4793	4050	51%	0%	0%	0%	1%	99%	Undef	Group-3	RRDR	Group-2
P434L	<i>rpoC</i>	0	0	7	2	4812	4073	78%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
P434Q	<i>rpoC</i>	0	0	7	2	4812	4073	78%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
P434R	<i>rpoC</i>	0	0	3	1	4816	4074	75%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
P454R	<i>rpoB</i>	0	0	1	0	3421	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
Q429H	<i>rpoB</i>	0	0	13	3	4806	4072	81%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
Q432H	<i>rpoB</i>	0	0	1	0	3421	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
Q432P	<i>rpoB</i>	0	1	37	19	4782	4056	66%	0%	0%	0%	1%	100%	0	Group-3	RRDR	Group-2
Q432R	<i>rpoB</i>	1	1	2	0	4817	4075	100%	100%	100%	100%	0%	100%	Inf	Group-3	RRDR	Group-2
S428A	<i>rpoC</i>	0	0	17	2	4802	4073	89%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2

S428C	<i>rpoB</i>	0	0	6	3	4813	4072	67%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
S428R	<i>rpoB</i>	0	0	33	17	4786	4058	66%	0%	0%	0%	1%	100%	Undef	Group-3	RRDR	Group-2
S428T	<i>rpoB</i>	0	0	17	12	4801	4064	59%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
S428T	<i>rpoC</i>	0	0	6	3	3416	3357	67%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
S431C	<i>rpoB</i>	0	0	24	18	4795	4057	57%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
S431R	<i>rpoB</i>	1	1	162	90	4655	3987	64%	1%	0%	3%	3%	98%	Inf	Group-3	RRDR	Group-2
S450*	<i>rpoB</i>	0	0	2	0	3420	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
S450A	<i>rpoB</i>	0	0	4	0	3418	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
S450P	<i>rpoB</i>	0	0	5	0	4814	4075	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
T427P	<i>rpoB</i>	0	0	1	0	3421	3360	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
V431M	<i>rpoC</i>	0	0	17	1	4802	4074	94%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
Q432K	<i>rpoB</i>	0	0	7	6	4812	4069	54%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2
T427I	<i>rpoB</i>	0	0	2	0	1395	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
S450!	<i>rpoB</i>	0	0	2	0	1395	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
K446Q	<i>rpoB</i>	0	0	2	0	1395	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
G433A	<i>rpoC</i>	0	0	2	0	1395	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
L452V	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
L452Q	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2

N437Y	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
T427A	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
H445S	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
L449R	<i>rpoC</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
Q436P	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
R448Q	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
F433L	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
G433D	<i>rpoC</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
N438T	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
Q435P	<i>rpoC</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
L446Q	<i>rpoC</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
P434S	<i>rpoC</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
L452R	<i>rpoB</i>	0	0	1	0	1396	715	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	RRDR	Group-2
H445C	<i>rpoB</i>	1	1	4	3	1393	712	57%	25%	0%	67%	0%	100%	Inf	Group-3	RRDR	Group-2
S428I	<i>rpoB</i>	0	0	1	1	1396	714	50%	0%	0%	0%	0%	100%	Undef	Group-3	RRDR	Group-2

Ethambutol

Four EMB resistance-associated mutations were classified into Group 1, and only thirteen were classified into Group 2. Out of these thirteen mutations associated with interim resistance, twelve were within the well-characterized *embB* gene, including its promoter region and remaining one was found *ubiA* gene.

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional Grading Criteria	FINAL CONFIDENCE GRADING
C-16T	<i>embA</i> /promoter	171	237	322	106	3461	7115	75%	62%	56%	67%	9%	99%	5.3262	Group-1		Group-1
M306L	<i>embB</i>	44	65	69	42	2994	5788	62%	51%	41%	62%	2%	99%	4.0505	Group-1		Group-1
M306V	<i>embB</i>	694	1156	1574	752	1491	5076	68%	48%	45%	51%	51%	87%	5.1140	Group-1		Group-1
Q497R	<i>embB</i>	367	669	473	381	2590	5449	55%	49%	45%	53%	15%	93%	2.5566	Group-1		Group-1
C-11A	<i>embA</i> /promoter	3	4	229	36	2114	4403	86%	8%	0%	16%	10%	99%	6.2483	Group-2		Group-2
C-12T	<i>embA</i> /promoter	2	6	69	40	2274	4399	63%	5%	0%	11%	3%	99%	0.9672	Group-2		Group-2
C-16A	<i>embA</i> /promoter	4	9	35	20	3028	5810	64%	17%	2%	32%	1%	100%	1.5350	Group-2		Group-2
C-16G	<i>embA</i> /promoter	2	4	15	16	3048	5814	48%	11%	0%	26%	0%	100%	1.9074	Group-2		Group-2
D1024N	<i>embB</i>	7	14	48	40	3015	5790	55%	15%	5%	25%	2%	99%	1.9203	Group-2		Group-2

D354A	<i>embB</i>	17	30	26	17	3037	5813	60%	50%	33%	67%	1%	100%	2.5030	Group-2		Group-2
G-43C	<i>embA/promoter</i>	6	14	37	17	2306	4422	69%	26%	8%	44%	2%	100%	1.4382	Group-2		Group-2
Q497K	<i>embB</i>	5	11	26	12	3037	5818	68%	29%	8%	51%	1%	100%	1.5964	Group-2		Group-2
T1082A	<i>embB</i>	6	32	391	245	2672	5585	61%	2%	1%	4%	13%	96%	0.4823	Group-2		Group-2
V188A	<i>ubiA</i>	2	2	3	0	2340	4439	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
Y319S	<i>embB</i>	8	13	15	5	3048	5825	75%	62%	35%	88%	0%	100%	3.0577	Group-2		Group-2
S347I	<i>embB</i>	2	3	15	6	3048	5824	71%	25%	0%	55%	0%	100%	3.8215	Group-2		Group-2
Y334H	<i>embB</i>	2	2	5	1	3058	5829	83%	67%	13%	120%	0%	100%	Inf	Group-2		Group-2

Fluoroquinolones – Levofloxacin, Ofloxacin and Moxifloxacin

There were Group-1 and Group-2 mutations in LFX(20), MFX (21) and OFX (13), as per the initial confidence grading. The expert rule for FLQ was applied following the WHO Mutation Catalogue criteria. This expert rule requires any *gyrA* or *gyrB* mutation associated with LFX resistance to also be classified as resistant to MFX and OFX. Hence, adhering to previous WHO catalogue, four mutations in one each from LFX, MFX and two from OFX were moved from Group-3 to Group-2, one from OFX in Group-5 was moved to Group-2, as per the expert criteria.

Drug	Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	ppv SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional Grading Criteria	FINAL CONFIDENCE GRADING
LFX	A90V	gyrA	675	892	884	256	3423	4331	78%	73%	70%	75%	21%	94%	3.9357	Group-1		Group-1
LFX	D94A	gyrA	204	298	301	114	4005	4474	73%	64%	59%	69%	7%	98%	2.4243	Group-1		Group-1
LFX	D94G	gyrA	1518	1825	1644	326	2663	4262	83%	82%	81%	84%	38%	93%	7.9136	Group-1		Group-1
LFX	D94H	gyrA	40	43	48	6	4258	4582	89%	87%	77%	97%	1%	100%	14.3478	Group-1		Group-1
LFX	D94N	gyrA	233	279	278	50	4028	4538	85%	82%	78%	87%	6%	99%	5.7065	Group-1		Group-1
LFX	D94Y	gyrA	182	216	199	39	4106	4550	84%	82%	77%	87%	5%	99%	5.9317	Group-1		Group-1
LFX	S91P	gyrA	124	166	160	50	4146	4538	76%	71%	65%	78%	4%	99%	3.2315	Group-1		Group-1
MFx	A90V	gyrA	600	893	812	328	4489	3266	71%	65%	62%	68%	15%	91%	1.4898	Group-1		Group-1
MFx	D94A	gyrA	207	298	308	107	4991	3488	74%	66%	61%	71%	6%	97%	1.5897	Group-1		Group-1
MFx	D94G	gyrA	1504	1826	1632	338	3668	3257	83%	82%	80%	83%	31%	91%	4.1474	Group-1		Group-1
MFx	D94N	gyrA	236	279	280	48	5018	3548	85%	83%	79%	87%	5%	99%	3.8805	Group-1		Group-1
MFx	D94Y	gyrA	176	216	193	45	5104	3551	81%	80%	74%	85%	4%	99%	3.0612	Group-1		Group-1
MFx	S91P	gyrA	122	166	158	52	5140	3544	75%	70%	63%	77%	3%	99%	1.9117	Group-1		Group-1
OFx	D94G	gyrA	509	513	565	6	662	879	99%	99%	98%	100%	46%	99%	168.9619	Group-1		Group-1
OFx	A90V	gyrA	251	259	342	7	885	877	98%	97%	95%	99%	28%	99%	31.0913	Group-1		Group-1
OFx	D94N	gyrA	84	85	106	1	1120	885	99%	99%	97%	101%	9%	100%	66.375	Group-1		Group-1
OFx	D94A	gyrA	72	80	107	8	1119	878	93%	90%	83%	97%	9%	99%	7.0616	Group-1		Group-1
OFx	D94Y	gyrA	61	61	72	2	1153	885	97%	97%	92%	101%	6%	100%	Inf	Group-1		Group-1
OFx	S91P	gyrA	39	41	57	2	1169	884	97%	95%	89%	102%	5%	100%	14.7459	Group-1		Group-1
LFX	D461N	gyrB	9	13	17	9	4289	4579	65%	50%	27%	73%	0%	100%	2.4021	Group-2		Group-2
LFX	D89N	gyrA	3	7	4	4	4302	4584	50%	43%	6%	80%	0%	100%	0.7991	Group-2		Group-2
LFX	D94V	gyrA	2	2	2	0	3213	3567	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
LFX	E501D	gyrB	11	29	52	24	4254	4564	68%	31%	16%	47%	1%	99%	0.6556	Group-2		Group-2

LFX	E501V	<i>gyrB</i>	2	3	2	1	4304	4587	67%	67%	13%	120%	0%	100%	2.1315	Group-2		Group-2
LFX	G88A	<i>gyrA</i>	6	9	14	3	4292	4585	82%	67%	36%	97%	0%	100%	2.1365	Group-2		Group-2
LFX	G88C	<i>gyrA</i>	20	25	21	5	4285	4583	81%	80%	64%	96%	0%	100%	4.2781	Group-2		Group-2
LFX	N499T	<i>gyrB</i>	7	13	29	12	4277	4576	71%	37%	15%	59%	1%	100%	1.2482	Group-2		Group-2
LFX	R446C	<i>gyrB</i>	3	5	15	3	4291	4585	83%	50%	10%	90%	0%	100%	1.6027	Group-2		Group-2
LFX	R446H	<i>gyrB</i>	4	7	9	3	4297	4585	75%	57%	20%	94%	0%	100%	1.4226	Group-2		Group-2
LFX	S447F	<i>gyrB</i>	2	4	8	4	4298	4584	67%	33%	0%	71%	0%	100%	1.0665	Group-2		Group-2
LFX	T500N	<i>gyrB</i>	4	7	26	6	4279	4583	81%	40%	10%	70%	1%	100%	1.4280	Group-2		Group-2
MFx	D461N	<i>gyrB</i>	7	13	14	12	5284	3584	54%	37%	15%	59%	0%	100%	0.7913	Group-2		Group-2
MFx	D89N	<i>gyrA</i>	5	7	6	2	5292	3594	75%	71%	38%	105%	0%	100%	1.6978	Group-2		Group-2
MFx	D94H	<i>gyrA</i>	39	43	47	7	5251	3589	87%	85%	74%	95%	1%	100%	6.6640	Group-2		Group-2
MFx	D94V	<i>gyrA</i>	2	2	2	0	4283	2497	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
MFx	E501D	<i>gyrB</i>	23	29	63	13	5235	3583	83%	64%	48%	80%	1%	100%	2.6236	Group-2		Group-2
MFx	E501V	<i>gyrB</i>	2	3	2	1	5296	3595	67%	67%	13%	120%	0%	100%	1.3576	Group-2		Group-2
MFx	G88A	<i>gyrA</i>	6	9	12	5	5286	3591	71%	55%	25%	84%	0%	100%	1.3586	Group-2		Group-2
MFx	G88C	<i>gyrA</i>	20	25	21	5	5277	3591	81%	80%	64%	96%	0%	100%	2.7220	Group-2		Group-2
MFx	N499T	<i>gyrB</i>	6	13	29	12	5269	3584	71%	33%	12%	55%	1%	100%	0.5830	Group-2		Group-2
MFx	R446C	<i>gyrB</i>	5	5	18	0	5280	3596	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
MFx	R446H	<i>gyrB</i>	4	7	8	4	5290	3592	67%	50%	15%	85%	0%	100%	0.9053	Group-2		Group-2
MFx	S447F	<i>gyrB</i>	2	4	9	3	5289	3593	75%	40%	0%	83%	0%	100%	0.6793	Group-2		Group-2
MFx	T500N	<i>gyrB</i>	4	7	26	6	5271	3591	81%	40%	10%	70%	0%	100%	0.9083	Group-2		Group-2
MFx	M291I	<i>gyrB</i>	3	79	770	660	4528	2936	54%	0%	0%	1%	15%	82%	0.0255	Group-2		Group-2
LFX	N499D	<i>gyrB</i>	4	5	9	2	4297	4586	82%	67%	29%	104%	0%	100%	4.2690	Group-2		Group-2
MFx	N499D	<i>gyrB</i>	4	5	9	2	5289	3594	82%	67%	29%	104%	0%	100%	2.7180	Group-2		Group-2
OFx	D94H	<i>gyrA</i>	14	14	21	0	1205	886	100%	100%	100%	100%	2%	100%	Inf	Group-2		Group-2
OFx	T500N	<i>gyrB</i>	2	2	12	0	1213	887	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
OFx	G88C	<i>gyrA</i>	7	7	7	0	1219	886	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
OFx	E501D	<i>gyrB</i>	2	7	15	5	1211	881	75%	29%	0%	62%	1%	99%	0.2909	Group-2		Group-2

OFX	N499D	<i>gyrB</i>	3	3	4	0	1222	886	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
OFX	D461N	<i>gyrB</i>	2	3	6	1	1220	885	86%	67%	13%	120%	0%	100%	1.4508	Group-2		Group-2
OFX	D89N	<i>gyrA</i>	2	5	3	3	1223	883	50%	40%	0%	83%	0%	100%	0.4813	Group-2		Group-2
OFX	E501V	<i>gyrB</i>	0	1	0	1	1226	885	0%	0%	0%	0%	0%	100%	0	Group-5	previous WHO guidance	Group-2
LFX	A504V	<i>gyrB</i>	1	1	15	1	4291	4587	94%	50%	0%	119%	0%	100%	Inf	Group-3	previous WHO guidance	Group-2
MFx	A504V	<i>gyrB</i>	1	1	15	1	5283	3595	94%	50%	0%	119%	0%	100%	Inf	Group-3	previous WHO guidance	Group-2
OFX	A504V	<i>gyrB</i>	0	0	8	0	1218	886	100%	Undef	Undef	Undef	1%	100%	Undef	Group-3	previous WHO guidance	Group-2
OFX	G88A	<i>gyrA</i>	0	1	4	1	1222	885	80%	0%	0%	0%	0%	100%	0	Group-3	Previous WHO guidance	Group-2

Pyrazinamide

About 48 mutations were classified into Group-1 and Group-2 category, as per the initial grading criteria and application of expert rule which implies that any nonsense mutation and indel in the coding region of *pncA*, as well as all non-synonymous mutations are presumed to cause loss of function resistance phenotypes (unless disproven) in rifampicin-resistant isolates, 258 mutations of Group-3, Group-4 and Group-5 were moved to Group-2 in final grading resulting in 306 mutations in Group-1 and Group-2 category. There were two promoter region mutations: A-11G and A-11C observed in *pncA* gene. In addition, a single mutation(R212R) in *rpsA* gene was also classified into Group-1 based on the initial confidence grading criteria.

Mutation	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional Grading Criteria	FINAL CONFIDENCE GRADING
V139A	<i>pncA</i>	6	8	42	2	850	1206	95%	75%	45%	105%	5%	100%	4.2564	Group-1		Group-1
A-11G	<i>pncA</i> /promoter	8	12	52	7	839	1202	88%	53%	28%	79%	6%	99%	2.8653	Group-1		Group-1
R212R	<i>rpsA</i>	19	182	500	191	392	1017	72%	9%	5%	13%	56%	84%	0.3024	Group-2		Group-2
I5S	<i>pncA</i>	2	3	36	2	856	1206	95%	50%	1%	99%	4%	100%	2.8177	Group-2		Group-2
ACC392 ACCCC	<i>pncA</i>	3	4	26	4	866	1204	87%	43%	6%	80%	3%	100%	4.1709	Group-2		Group-2
V139G	<i>pncA</i>	5	5	11	0	881	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
T76P	<i>pncA</i>	3	4	12	1	880	1207	92%	75%	33%	117%	1%	100%	4.1147	Group-2		Group-2
V128G	<i>pncA</i>	3	3	9	0	883	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
W68G	<i>pncA</i>	3	3	8	0	884	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
W68R	<i>pncA</i>	5	5	7	0	885	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2

F94L	<i>pncA</i>	5	5	5	0	887	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
L4W	<i>pncA</i>	2	2	5	0	887	1208	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
G97D	<i>pncA</i>	3	3	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
P62L	<i>pncA</i>	3	3	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
V7G	<i>pncA</i>	4	4	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
A-11C	<i>pncA/pr omoter</i>	2	2	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
Q141P	<i>pncA</i>	2	2	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
V180F	<i>pncA</i>	5	5	5	1	887	1207	83%	83%	54%	113%	1%	100%	Inf	Group-2		Group-2
K96R	<i>pncA</i>	5	6	5	1	887	1207	83%	83%	54%	113%	1%	100%	6.8038	Group-2		Group-2
D12A	<i>pncA</i>	2	3	6	2	886	1206	75%	50%	1%	99%	1%	100%	2.7223	Group-2		Group-2
ACC392 ACCC	<i>pncA</i>	2	3	6	2	886	1206	75%	50%	1%	99%	1%	100%	2.7223	Group-2		Group-2
F58L	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
G162R	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
P62T	<i>pncA</i>	3	3	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
Q10K	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
T135P	<i>pncA</i>	3	3	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
P54R	<i>pncA</i>	3	3	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
P54L	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
A3P	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
S67P	<i>pncA</i>	2	2	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
L35P	<i>pncA</i>	2	3	4	1	888	1207	80%	67%	13%	120%	0%	100%	2.7184	Group-2		Group-2
TCC473 TCCC	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
TGGTA	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2

TCGG50 2TGGT ATCGG TATCG G																	
V180L	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
K96T	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
CCGAC CACAT CGACC 395CCG ACC	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
T47I	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
A46T	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
AT408A TT	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
TGG91T G	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
A171E	<i>pncA</i>	2	2	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
A146T	<i>pncA</i>	2	2	3	1	889	1207	75%	67%	13%	120%	0%	100%	Inf	Group-2		Group-2
T47A	<i>pncA</i>	2	2	5	3	887	1205	63%	40%	0%	83%	1%	100%	Inf	Group-2		Group-2
Q10P	<i>pncA</i>	2	3	4	2	888	1206	67%	50%	1%	99%	0%	100%	2.7162	Group-2		Group-2
G132D	<i>pncA</i>	2	3	3	2	889	1206	60%	50%	1%	99%	0%	100%	2.7131	Group-2		Group-2
T76I	<i>pncA</i>	2	3	2	1	890	1207	67%	67%	13%	120%	0%	100%	2.7123	Group-2		Group-2
GC418G CC	<i>pncA</i>	2	2	2	1	890	1207	67%	67%	13%	120%	0%	100%	Inf	Group-2		Group-2
Q10!	<i>pncA</i>	2	2	2	2	890	1206	50%	50%	1%	99%	0%	100%	Inf	Group-2		Group-2

G108R	<i>pncA</i>	1	1	10	2	882	1206	83%	33%	0%	87%	1%	100%	Inf	Group-4	pncA_mutation	Group-2
S67W	<i>pncA</i>	1	1	2	2	890	1206	50%	33%	0%	87%	0%	100%	Inf	Group-4	pncA_mutation	Group-2
Y103H	<i>pncA</i>	1	2	1	2	891	1206	33%	33%	0%	87%	0%	100%	1.3535	Group-4	pncA_mutation	Group-2
S65S	<i>pncA</i>	12	444	171	519	721	689	25%	2%	1%	4%	19%	57%	0.0265	Group-5	pncA_mutation	Group-2
I187W	<i>pncA</i>	0	1	1	2	891	1206	33%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
F58V	<i>pncA</i>	0	0	1	3	891	1205	25%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
C138F	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
C138C	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
V155L	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
E181D	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
V169A	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
V183L	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
E174Q	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
C184G	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
S179C	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
V183V	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
A170P	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
A170A	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2

H137R	<i>pncA</i>	0	2	0	2	892	1206	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
F94V	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
Q141I	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
M1K	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
D63A	<i>pncA</i>	0	2	0	2	892	1206	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
L27R	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
TGGTA GTCCG CCGCT TCGGC CAGGT AGTC12 5TGGT AGTC	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
CGGCC G496CG GCCGG GCCG	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
TCC239 TC	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
L35L	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
AG172A GG	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
S66L	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
P62Q	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
TC167T CC	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2

P69L	<i>pncA</i>	0	1	0	2	892	1206	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
CAATA400CAATAATA	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
CG385C GG	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
TGG170 TGGGG	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
D63G	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
CAA413 CAAA	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
CTT288 CT	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
V130M	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
T168I	<i>pncA</i>	0	2	0	2	892	1206	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
AC307A	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
D63E	<i>pncA</i>	0	1	0	2	892	1206	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
S59F	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
L116M	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
L116Q	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
G17A	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
Y41D	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
GCGAGCC55GC GAGCC	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2

CGAGC C																	
G24V	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
S65P	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
G55V	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
CTGGC G536C	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
CGGG8 6CGG	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
GC526G CC	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
V21A	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
P77L	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
D49V	<i>pncA</i>	0	0	0	1	892	1207	0%	0%	0%	0%	0%	100%	Undef	Group-5	pncA_mutation	Group-2
S59Y	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
T153I	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
A28T	<i>pncA</i>	0	1	0	1	892	1207	0%	0%	0%	0%	0%	100%	0	Group-5	pncA_mutation	Group-2
L27P	<i>pncA</i>	1	1	91	1	801	1207	99%	50%	0%	119%	10%	100%	Inf	Group-3	pncA_mutation	Group-2
G132A	<i>pncA</i>	1	2	91	4	801	1204	96%	20%	0%	55%	10%	100%	1.5031	Group-3	pncA_mutation	Group-2
L182S	<i>pncA</i>	0	0	17	0	875	1208	100%	Undef	Undef	Undef	2%	100%	Undef	Group-3	pncA_mutation	Group-2
T177P	<i>pncA</i>	0	0	15	2	877	1206	88%	0%	0%	0%	2%	100%	Undef	Group-3	pncA_mutation	Group-2
D136G	<i>pncA</i>	1	1	9	0	883	1208	100%	100%	100%	100%	1%	100%	Inf	Group-3	pncA_mutation	Group-2

A3E	<i>pncA</i>	0	0	8	0	884	1208	100%	Undef	Undef	Undef	1%	100%	Undef	Group-3	pncA_mutation	Group-2
L172P	<i>pncA</i>	1	1	7	0	885	1208	100%	100%	100%	100%	1%	100%	Inf	Group-3	pncA_mutation	Group-2
C138R	<i>pncA</i>	1	1	7	0	885	1208	100%	100%	100%	100%	1%	100%	Inf	Group-3	pncA_mutation	Group-2
D49G	<i>pncA</i>	1	1	5	0	887	1208	100%	100%	100%	100%	1%	100%	Inf	Group-3	pncA_mutation	Group-2
A134V	<i>pncA</i>	1	1	5	0	887	1208	100%	100%	100%	100%	1%	100%	Inf	Group-3	pncA_mutation	Group-2
H71Y	<i>pncA</i>	0	1	8	2	884	1206	80%	0%	0%	0%	1%	100%	0	Group-3	pncA_mutation	Group-2
G78V	<i>pncA</i>	0	0	4	0	888	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
D49A	<i>pncA</i>	1	1	4	0	888	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
CG394C GG	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
GA18G AA	<i>pncA</i>	0	0	3	0	889	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
H57Y	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L4S	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
T160A	<i>pncA</i>	0	0	3	0	889	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
A146V	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
MII	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
M175V	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
A46V	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
S104R	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

H51P	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H51R	<i>pncA</i>	1	1	3	0	889	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
C14!	<i>pncA</i>	0	0	4	1	888	1207	80%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T142A	<i>pncA</i>	0	1	4	1	888	1207	80%	0%	0%	0%	0%	100%	0	Group-3	pncA_mutation	Group-2
D12G	<i>pncA</i>	1	2	4	1	888	1207	80%	50%	0%	119%	0%	100%	1.3592	Group-3	pncA_mutation	Group-2
E91K	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
AG451A GG	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G97S	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H51Y	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
F106L	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T47P	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
R121P	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
W119!	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L120R	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L159R	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H57R	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L120P	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H51Q	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

A146E	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
G17D	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
Y41!	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
!187R	<i>pncA</i>	0	0	2	0	890	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L85R	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H57D	<i>pncA</i>	1	1	2	0	890	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
T167I	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
V125F	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
T100P	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
D49E	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
V7A	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
F106C	<i>pncA</i>	0	0	2	1	890	1207	67%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CG54CGG	<i>pncA</i>	0	1	2	1	890	1207	67%	0%	0%	0%	0%	100%	0	Group-3	pncA_mutation	Group-2
H82R	<i>pncA</i>	1	2	2	1	890	1207	67%	50%	0%	119%	0%	100%	1.3561	Group-3	pncA_mutation	Group-2
Q10R	<i>pncA</i>	0	1	2	1	890	1207	67%	0%	0%	0%	0%	100%	0	Group-3	pncA_mutation	Group-2
ACATC GACCT CATCG AC389A CATCG AC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

TG183T	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CGTGT 261CGT GTGT	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
P69R	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
CCGCT GTCAG G484CC GCTGT CAGGC GCTGT CAGG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
CG419C GG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
TG16TG G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GCC455 GCCCC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GCC315 GCCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
GGT475 GGTGT	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
ATGTG GAAGT CCTTG1 55ATG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
ACC396 ACCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
GCC339 GCCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
I6L	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
GCATA CGTCC ACCAT	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2

ACGT4 GCATA CGT																	
TA296T	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
C522CA	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
AAACC AACTC GA550A A	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
TGCGC 529TGC GCGC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
CA292C AA	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
V169I	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G162S	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GGCAC CCTTG T294G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GCC72G CCCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
TGGCC A457TG GCCAG GCCA	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TCC257 TCCC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GCC315 GCCCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L4!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
AGG295 AGGG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

TG259T GG	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CG97C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
G97V	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TGG457 TGGGG	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CGGG2 32CGG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
ACCC48 6ACC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GCCGC TGTAC GCTCC G315GC CG	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TCC119 TCCCC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GC420G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TCCAG ACTGG GATGG AAG257 TCCAG ACTGG GATGG AAGCC AGACT GGGAT GGAAG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
TCACC 167TC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
K48T	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2

K48N	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
E107Q	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TCC239 TCCC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V9A	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
R140G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CAA400 CAAA	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
D12D	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T142M	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G132S	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T114P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L159P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
C72Y	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
S59P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
W119R	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
C14G	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
CG342C	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V155G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
D12E	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2

T142P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H137P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V139M	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
A171V	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
H71R	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
A102P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
D136E	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T135N	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
E91I	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
I133T	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
TC407T CC	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G97R	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CGAGG A198C	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
K48E	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L116V	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L85P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L116P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
T160P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2

TGG422 TGGG	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G17V	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
E127!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
W68!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
G132C	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
A143G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V131G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
Y34D	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
A134G	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
D8G	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
S164P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
H43P	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
Q10H	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
I5T	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
GGCAA TACCG 402GG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
GC528G CC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
ATAGT CCGGT GT192A T	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

GGCCA GCGCG GCGCC ACCGG TTACC GCCAG CG84G GCCAG CG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
CGACG G508C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
G132V	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
AG56A	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
S164!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
GCC107 GCCCC	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
Q10E	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
CGAGG AATAG TCCGG TGTGC CGGAG AAGTG GTCAC CCGGG TCGAT GTGGA 198CGA	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
G105R	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
H71P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i> <i>utation</i>	Group-2
C138G	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	<i>pncA_m</i>	Group-2

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S88!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V7F	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
M1T	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
F58C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
W119C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
V163A	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
V155M	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H82D	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
V93G	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
D136Y	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
V130A	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
L19P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
A46P	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
Y103C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
G97C	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
C138!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
H57Q	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2

CGG532 CGGG	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
H71Q	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
G97A	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
S104G	<i>pncA</i>	1	1	1	0	891	1208	100%	100%	100%	100%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
E37!	<i>pncA</i>	0	0	1	0	891	1208	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	pncA_mutation	Group-2
!187G	<i>pncA</i>	0	0	3	3	889	1205	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V157A	<i>pncA</i>	1	1	1	1	891	1207	50%	50%	0%	119%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
K96E	<i>pncA</i>	1	2	1	1	891	1207	50%	50%	0%	119%	0%	100%	1.3546	Group-3	pncA_mutation	Group-2
G105D	<i>pncA</i>	1	1	1	1	891	1207	50%	50%	0%	119%	0%	100%	Inf	Group-3	pncA_mutation	Group-2
T61P	<i>pncA</i>	1	2	1	1	891	1207	50%	50%	0%	119%	0%	100%	1.3546	Group-3	pncA_mutation	Group-2
P62S	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
P69S	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CGG76C GGG	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
CGACG AGGAA TAG201 C	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
P54S	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
L156P	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
A102V	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2

C14R	<i>pncA</i>	0	0	1	1	891	1207	50%	0%	0%	0%	0%	100%	Undef	Group-3	pncA_mutation	Group-2
V9G	<i>pncA</i>	0	1	1	1	891	1207	50%	0%	0%	0%	0%	100%	0	Group-3	pncA_mutation	Group-2

Linezolid

Only two mutations (C154R, G2814T) in the linezolid resistance-associated genes, *rplC* and *rrl* were classified as Group 1.

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional GradingCriteria	FINAL CONFIDENCE GRADING
C154R	<i>rplC</i>	102	159	108	56	776	7953	66%	65%	57%	72%	12%	99%	18.3398	Group-1		Group-1
G2814T	<i>rrl</i>	13	21	18	8	866	8001	69%	62%	41%	83%	2%	100%	15.0134	Group-1		Group-1

para-aminosalicylic acid

In total, eight mutations were found in three PAS resistance-associated genes (*thyA*, *folC* & *ribD*). Four mutations (*thyA* T22A, *folC* I43T, *ribD* TCCCCC83TCCCC, and *folC* R49W) were classified as Group 1, including one deletion. Four mutations (*thyA* R126G, R99! and T22N, as well as *folC* E40G) were classified as Group 2, which includes a nonsense mutation.

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional GradingCriteria	FINAL CONFIDENCE GRADING
T22A	<i>thyA</i>	30	37	30	7	87	1988	81%	81%	68%	94%	26%	100%	97.9310	Group-1		Group-1
I43T	<i>folC</i>	6	10	9	4	108	1991	69%	60%	30%	90%	8%	100%	27.6527	Group-1		Group-1
TCCCCC83TCCCC	<i>ribD</i>	6	6	6	0	111	1995	100%	100%	100%	100%	5%	100%	Inf	Group-1		Group-1
R49W	<i>folC</i>	5	5	5	0	112	1995	100%	100%	100%	100%	4%	100%	Inf	Group-1		Group-1
R126G	<i>thyA</i>	3	5	3	2	114	1993	60%	60%	17%	103%	3%	100%	26.2236	Group-2		Group-2
E40G	<i>folC</i>	2	2	2	0	115	1995	100%	100%	100%	100%	2%	100%	Inf	Group-2		Group-2
R99!	<i>thyA</i>	2	3	2	1	115	1994	67%	67%	13%	120%	2%	100%	34.6782	Group-2		Group-2
T22N	<i>thyA</i>	2	3	2	1	115	1994	67%	67%	13%	120%	2%	100%	34.6782	Group-2		Group-2

Amikacin, Streptomycin, Capreomycin and Kanamycin

In case of Amikacin resistance genes, only two mutations were found to span in Group-1 as per the initial confidence grading (A1401G and G1484T) and other mutation namely, C1402T was moved from Group-5 to Group-2 based on expert final grading criteria. For, capreomycin resistance genes, five mutations were classified as Group-1 and Group-2 mutation. Kanamycin resistance genes, featured eight mutations in Group-1 and Group-2 category. And streptomycin resistance genes harboured sixteen mutations in Group-1 and Group-2 category.

Drug	Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	PPV SOLO_lb	PPV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional GradingCriteria	FINAL CONFIDENCE GRADING
AMK	A1401G	<i>Rrs</i>	265	522	417	120	291	8066	78%	69%	64%	73%	59%	99%	28.581	Group-1		Group-1
KAN	C-12T	<i>eis</i> /promoter	91	211	121	151	1207	6538	44%	38%	32%	44%	9%	98%	4.1076	Group-1		Group-1
KAN	C-14T	<i>eis</i> /promoter	30	34	39	9	1289	6491	81%	77%	64%	90%	3%	100%	37.7676	Group-1		Group-1
KAN	G-10A	<i>eis</i> /promoter	43	55	48	16	1280	6494	75%	73%	62%	84%	4%	100%	18.1798	Group-1		Group-1
KAN	G-10C	<i>eis</i> /promoter	61	94	63	34	1265	6515	65%	64%	55%	74%	5%	99%	9.5200	Group-1		Group-1
KAN	A1401G	<i>Rrs</i>	425	509	446	91	881	6760	83%	82%	79%	86%	34%	99%	38.8222	Group-1		Group-1
KAN	C1402T	<i>Rrs</i>	6	6	7	0	1321	6466	100%	100%	100%	100%	1%	100%	Inf	Group-1		Group-1

AMK	G1484T	<i>Rrs</i>	23	30	13	24	696	8161	35%	49%	35%	63%	2%	100%	38.5269	Group-1	Group-1
CAP	A1401G	<i>Rrs</i>	128	151	128	22	38	1922	85%	85%	80%	91%	77%	99%	281.4828	Group-1	Group-1
CAP	G1484T	<i>Rrs</i>	5	5	5	0	161	1944	100%	100%	100%	100%	3%	100%	Inf	Group-1	Group-1
KAN	G-37T	<i>eis</i> /promoter	15	21	18	7	1310	6473	72%	68%	49%	88%	1%	100%	12.3530	Group-1	Group-1
STM	K43R	<i>rpsL</i>	654	662	755	9	311	1037	99%	99%	98%	100%	71%	99%	272.5876	Group-1	Group-1
STM	K88R	<i>rpsL</i>	69	69	82	0	985	1045	100%	100%	100%	100%	8%	100%	Inf	Group-1	Group-1
STM	C517T	<i>Rrs</i>	27	28	27	1	1040	1044	96%	96%	90%	103%	3%	100%	27.1038	Group-1	Group-1
STM	A514C	<i>Rrs</i>	23	25	27	2	1040	1043	93%	92%	81%	103%	3%	100%	11.5332	Group-1	Group-1
KAN	C-15G	<i>eis</i> /promoter	3	5	3	5	1325	6464	38%	38%	4%	71%	0%	100%	7.3177	Group-2	Group-2
CAP	C1402T	<i>Rrs</i>	4	4	4	0	162	1944	100%	100%	100%	100%	2%	100%	Inf	Group-2	Group-2
CAP	GT293G	<i>Gid</i>	2	2	2	0	164	1944	100%	100%	100%	100%	1%	100%	Inf	Group-2	Group-2
CAP	E121Q	<i>Gid</i>	2	2	2	0	164	1944	100%	100%	100%	100%	1%	100%	Inf	Group-2	Group-2
STM	A1401G	<i>Rrs</i>	21	48	121	29	946	1016	81%	42%	28%	56%	11%	97%	0.8353	Group-2	Group-2

STM	A906G	<i>Rrs</i>	16	19	19	3	1048	1042	86%	84%	68%	101%	2%	100%	5.3028	Group-2		Group-2
STM	A908C	<i>Rrs</i>	9	10	11	1	1056	1044	92%	90%	71%	109%	1%	100%	8.8977	Group-2		Group-2
STM	K88M	<i>rpsL</i>	8	8	8	0	1059	1045	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
STM	C905G	<i>Rrs</i>	5	5	6	0	1061	1045	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
STM	P75R	<i>Gid</i>	5	5	5	0	1062	1045	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
STM	K88T	<i>rpsL</i>	5	5	5	0	1062	1045	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
STM	A908G	<i>Rrs</i>	2	2	4	0	1063	1045	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
STM	A514T	<i>Rrs</i>	4	5	5	1	1062	1044	83%	80%	45%	115%	0%	100%	3.9322	Group-2		Group-2
STM	A134E	<i>Gid</i>	2	2	2	0	1065	1045	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
STM	L79S	<i>Gid</i>	2	5	3	3	1064	1042	50%	40%	0%	83%	0%	100%	0.6529	Group-2		Group-2
AMK	C1402T	<i>Rrs</i>	0	5	3	4	706	8181	43%	0%	0%	0%	0%	100%	0	Group-5	W H O- en d. gD ST	Group-2

Ethionamide

In case of Ethionamide, twenty-eight mutations were classified as Group-1 and Group-2 based on initial confidence grading. One hundred and thirty-seven mutations were moved to Group-2 based on expert criteria, wherein any premature stop codon and indel in *ethA* is considered to be associated with ETO resistance. L203L in *fabG1* gene was moved to Group-2 adhering to WHO catalogue criteria. Thus, finally four mutations were classified as Group-1 and one hundred and sixty-one mutations were classified into Group-2, as per the final confidence grading.

Mutations	Gene Name	Present SOLO_R	Present SOLO_SR	Present in R (TP)	Present in S (FP)	Absent in R (FN)	Absent in S (TN)	PPV	PPV SOLO	ppV SOLO_lb	ppV SOLO_ub	Sensitivity	Specificity	OR SOLO	INITIAL CONFIDENCE GRADING	Additional GradingCriteria	FINAL CONFIDEN CE GRADING
C-15T	<i>fabG1</i> /promoter	906	1182	1034	285	1412	6163	78%	76%	74%	78%	42%	96%	14.3277	Group-1		Group-1
S94A	<i>inhA</i>	18	27	40	15	1784	4943	73%	55%	38%	72%	2%	100%	5.5415	Group-1		Group-1
T-8C	<i>fabG1</i> /promoter	58	84	68	30	1756	4928	69%	66%	56%	76%	4%	99%	6.2604	Group-1		Group-1
T-8C	<i>ethA</i>	7	13	25	6	596	1485	81%	54%	27%	81%	4%	100%	2.9069	Group-1		Group-1
G-17T	<i>fabG1</i> /promoter	11	19	11	10	1813	4948	52%	52%	31%	74%	1%	100%	3.7526	Group-2		Group-2
S266R	<i>inhA</i>	9	65	60	59	561	1432	50%	13%	5%	21%	10%	96%	0.4102	Group-2		Group-2
L203L	<i>inhA</i>	10	19	18	9	603	1482	67%	53%	30%	75%	3%	99%	2.7308	Group-2		Group-2
Y84D	<i>ethA</i>	11	13	11	2	2434	6447	85%	85%	65%	104%	0%	100%	14.5679	Group-2		Group-2
S94A	<i>ethA</i>	3	4	10	2	611	1489	83%	60%	17%	103%	2%	100%	7.311	Group-2		Group-2
G-17T	<i>ethA</i>	4	7	8	3	613	1488	73%	57%	20%	94%	1%	100%	3.2365	Group-2		Group-2
A341V	<i>ethA</i>	4	4	21	8	2424	6441	72%	33%	7%	60%	1%	100%	Inf	Group-2		Group-2

CTTT3 65CTT TT	<i>ethA</i>	4	4	4	0	617	1491	100%	100%	100%	100%	1%	100%	Inf	Group-2		Group-2
R207C	<i>ethA</i>	3	4	5	1	616	1490	83%	75%	33%	117%	1%	100%	7.2565	Group-2		Group-2
CAAA A1243 CAAA	<i>inhA</i>	7	14	10	7	611	1484	59%	50%	24%	76%	2%	100%	2.4288	Group-2		Group-2
T342A	<i>ethA</i>	2	2	6	2	2439	6447	75%	50%	1%	99%	0%	100%	Inf	Group-2		Group-2
W455!	<i>ethA</i>	2	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
Y276!	<i>ethA</i>	2	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
S390F	<i>ethA</i>	3	5	3	2	2442	6447	60%	60%	17%	103%	0%	100%	3.9600	Group-2		Group-2
G43S	<i>ethA</i>	4	9	4	5	2441	6444	44%	44%	12%	77%	0%	100%	2.1119	Group-2		Group-2
T88I	<i>ethA</i>	2	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
TGTA GGTG GG634 TGTA GGTG GGGT AGGT GGG	<i>ethA</i>	2	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
TGCG C141T GCGC GC	<i>ethA</i>	2	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-2		Group-2
C137R	<i>ethA</i>	3	5	3	2	618	1489	60%	60%	17%	103%	0%	100%	3.6141	Group-2		Group-2
L134R	<i>ethA</i>	2	3	3	2	2442	6447	60%	50%	1%	99%	0%	100%	5.2800	Group-2		Group-2
W21!	<i>ethA</i>	2	2	2	1	619	1490	67%	67%	13%	120%	0%	100%	Inf	Group-2		Group-2
G42D	<i>ethA</i>	2	3	2	1	619	1490	67%	67%	13%	120%	0%	100%	4.8142	Group-2		Group-2

G182D	<i>ethA</i>	2	2	2	2	619	1489	50%	50%	1%	99%	0%	100%	Inf	Group-2		Group-2
GTTT T342G TTT	<i>ethA</i>	1	3	2	2	619	1489	50%	33%	0%	87%	0%	100%	1.2027	Group-4	INDEL or premat ure stop codon	Group-2
Y143!	<i>ethA</i>	1	2	1	2	620	1489	33%	33%	0%	87%	0%	100%	2.4016	Group-4	INDEL or premat ure stop codon	Group-2
TGGG 241TG G	<i>ethA</i>	1	1	1	2	620	1489	33%	33%	0%	87%	0%	100%	Inf	Group-4	INDEL or premat ure stop codon	Group-2
GGCG C756G GCGC GC	<i>ethA</i>	0	1	1	2	620	1489	33%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
GTT10 35GT	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
W109!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
TGG7 61TG	<i>ethA</i>	0	2	0	2	621	1489	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
C253!	<i>ethA</i>	0	0	0	5	621	1486	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or	Group-2

																premature stop codon	
CGG977CG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
TGG88TG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
ATT281AT	<i>ethA</i>	0	0	0	2	621	1489	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2
CAGC CA687 CAGC CAAG CCA	<i>ethA</i>	0	2	0	2	621	1489	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
TC1033T	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
AGG631AG	<i>ethA</i>	0	2	0	2	621	1489	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
Y140!	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2

ATGT 1394A TGTG T	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
GT131 GTT	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
GT75 GTT	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
G441G A	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
AGGA TGGG 245AG G	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
Q215!	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TGG8 12TG	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TA816 T	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure	Group-2

																stop codon	
Q359!	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
CA62 C	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
GCC5 02GC	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
Q347!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
GAA9 06GA	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
GT633 GTT	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TGA3 16TG AGA	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
AG104	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or	Group-2

3A																premature stop codon	
Q269!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
AGG1037AGGG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
GTC1392GTC TC	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
GGTG T948GTGT GT	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2
GAA300GA	<i>ethA</i>	0	2	0	2	621	1489	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premature stop codon	Group-2
AGG1037AG	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2
CAAA141CA A	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2

Y286!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
CTTC TCG67 2C	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
Y382!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
E274!	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
TGGG G1308 TGGG GG	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TGGG 628TG GGG	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
AG94 AGG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
CCA8 67C	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure	Group-2

																stop codon	
TGTC GATT CC286 T	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
GCCC 33GC C	<i>ethA</i>	0	1	0	2	621	1489	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
TGCG C555T GCGC GC	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TGG3 05TG GG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
TAA1 223TA	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
GCCC 33GC CCC	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premat ure stop codon	Group-2
TCG16 7TCG CG	<i>ethA</i>	0	1	0	1	621	1490	0%	0%	0%	0%	0%	100%	0	Group-5	INDEL or premat ure stop codon	Group-2
GT12	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or	Group-2

G																premature stop codon	
GCC743GCC	<i>ethA</i>	0	0	0	1	621	1490	0%	0%	0%	0%	0%	100%	Undef	Group-5	INDEL or premature stop codon	Group-2
L203L	<i>fabG1</i>	0	0	36	27	1788	4931	57%	0%	0%	0%	2%	99%	Undef	Group-3	WHO catalogue	Group-2
ATCG GCCC GACG AAAT CCTC CGAG CCGG CGAA TCTC GGC4 82ATC GGC	<i>ethA</i>	0	0	64	9	2381	6440	88%	0%	0%	0%	3%	100%	Undef	Group-3	INDEL or premature stop codon	Group-2
TAGT TCTG ATTG AG138 2TAG	<i>ethA</i>	0	0	3	0	618	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premature stop codon	Group-2
AAC1301AACAC	<i>ethA</i>	1	1	4	0	2441	6449	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premature stop codon	Group-2
TC313TCC	<i>ethA</i>	0	0	2	0	619	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premature stop codon	Group-2

TG374 TGG	<i>ethA</i>	0	0	2	0	619	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
AGGC CG61 AGGC CGGC CG	<i>ethA</i>	0	0	2	0	619	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GTAG CCA1 158G	<i>ethA</i>	0	0	2	0	619	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
AGGG 1291A GG	<i>ethA</i>	1	1	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
W69!	<i>ethA</i>	1	2	2	0	619	1491	100%	100%	100%	100%	0%	100%	2.4087	Group-3	INDEL or premat ure stop codon	Group-2
TC115 4TCC	<i>ethA</i>	1	1	2	0	619	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
ACCC C826A CCC	<i>ethA</i>	1	2	2	1	619	1490	67%	50%	0%	119%	0%	100%	2.4071	Group-3	INDEL or premat ure stop codon	Group-2
AGC6 74AG CGC	<i>ethA</i>	1	2	2	1	619	1490	67%	50%	0%	119%	0%	100%	2.4071	Group-3	INDEL or premat ure	Group-2

																stop codon	
CAAA AA104 8CAA AAAA	<i>ethA</i>	1	2	2	1	619	1490	67%	50%	0%	119%	0%	100%	2.4071	Group-3	INDEL or premat ure stop codon	Group-2
GTTT T342G TTTT T	<i>ethA</i>	0	1	2	1	619	1490	67%	0%	0%	0%	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2
S308!	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
ACC3 71AC CC	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TCGC CG106 3TCG	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
TGG3 08TG GG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
CAAA AA104 8CAA AA	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TGAG	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or	Group-2

624TG AGGAG																	premat ure stop codon	
GACA GACA AAC1 210G	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
Y92!	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2	
GAA3 00GA AA	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2	
AGCG C581A GCGC GC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
GTCT C695G TCTC TC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
CGG1 72CG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2	
TGG6 97TG GG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2	

GC568 GCC	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
K370!	<i>ethA</i>	0	1	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2
TGG7 10TG GG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TCGC 676TC GCGC	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
ATCG GCAC TGAT CACC TT324 ATCG GCAC TGAT CACC TTCG GCAC TGAT CACC TT	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GTT86 1GT	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop	Group-2

																codon	
ATCT TC788 ATC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
Q271!	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
Y235!	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TCGC 1263T CGCG C	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
TC118 7TCC	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GC81 G	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
C27!	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
CG215	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or	Group-2

C																premat ure stop codon	
GCC1 128GC CCC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
CGGG 84CG G	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TC139 1TCC	<i>ethA</i>	0	0	9	1	2436	6448	90%	0%	0%	0%	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
AGG9 02AG GG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TGCG 1038T GCGC G	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TG101 5TGG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TGGG G1308 TGGG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2

TG778 TGG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GT138 7G	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GAA9 06GA AA	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
CA687 CAA	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
TGGG CG143 3TG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TG218 TGG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
ACGC G1356 ACGC GCG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
CA801 CAA	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure	Group-2

																stop codon	
GCC1 142GC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
W391!	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
ACCC C826A CCCC C	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
AG581 AGG	<i>ethA</i>	0	0	1	0	620	1491	100%	Undef	Undef	Undef	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
G1152 GC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
CT129 9CTT	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
TGG8 72TG	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
GA606	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or	Group-2

G																	premat ure stop codon	
GCC5 9GCC C	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
GA727 G	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
GTT10 36GTT T	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
Q363!	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
GCCC 345GC C	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
ACAA CGTC GAGG T23A	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	
GCC1 288GC	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2	

Y351!	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
Q246!	<i>ethA</i>	1	1	1	0	620	1491	100%	100%	100%	100%	0%	100%	Inf	Group-3	INDEL or premat ure stop codon	Group-2
C131!	<i>ethA</i>	1	2	1	1	620	1490	50%	50%	0%	119%	0%	100%	2.4032	Group-3	INDEL or premat ure stop codon	Group-2
Y461!	<i>ethA</i>	0	0	1	1	620	1490	50%	0%	0%	0%	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
CTTT T111C TTTA	<i>ethA</i>	0	1	1	1	620	1490	50%	0%	0%	0%	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2
AT779 A	<i>ethA</i>	0	0	1	1	620	1490	50%	0%	0%	0%	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
GC673 GCC	<i>ethA</i>	0	1	1	1	620	1490	50%	0%	0%	0%	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2
AGGG G865A GGG	<i>ethA</i>	0	0	1	1	620	1490	50%	0%	0%	0%	0%	100%	Undef	Group-3	INDEL or premat ure	Group-2

																stop codon	
W289!	<i>ethA</i>	0	0	1	1	620	1490	50%	0%	0%	0%	0%	100%	Undef	Group-3	INDEL or premat ure stop codon	Group-2
TC111 7TCC	<i>ethA</i>	0	1	1	1	620	1490	50%	0%	0%	0%	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2
TCCC 137TC CCC	<i>ethA</i>	0	1	1	1	620	1490	50%	0%	0%	0%	0%	100%	0	Group-3	INDEL or premat ure stop codon	Group-2

Methods and Approaches:

Across India, MTB isolates and processed sputum specimens were collected and their phenotype-genotype correlation data were utilized to develop this catalogue. The developing process is as follows:

- a) Raw high-quality whole genome sequencing reads were produced using an Illumina MiSeq instrument
- b) A comprehensive and a validated bioinformatics pipeline (CamNIRTResPred) and customized python/shell scripts were used for generation of variant sequencing data interrogation, annotation, resistance determination, and lineage prediction (7)
- c) Phenotypic culture and DST data were generated using WHO-endorsed methods (LJ solid culture and BACTEC MGIT 960 liquid culture)
- d) Sequencing and phenotypic DST testing for strains with initial discordance between gDST and pDST were repeated for any anti-TB drug
- e) Based on the WHO Mutation Catalogue, the procedures outlined in the above-mentioned Initial Confidence Grading and Additional Confidence Grading sections, the variants were classified into “Associated with resistance” and “Not associated with resistance” categories.

Phenotypic Drug Susceptibility Testing

Mycobacterial Growth Indicator Tubes (MGIT) in BACTEC™ MGIT™ 960 system (BD, Franklin Lakes, NJ, USA) following the WHO-recommended critical concentrations for the year 2018 [Rifampicin (1.0µg/ml), Isoniazid (0.1µg/ml), Ethambutol (5.0µg/ml), Pyrazinamide (100µg/ml), Levofloxacin (1.5µg/ml), Moxifloxacin (0.5µg/ml), Ofloxacin (2.0µg/ml), Linezolid (1.5µg/ml), Amikacin (1.0µg/ml), Capreomycin (2.5µg/ml), Kanamycin (2.5µg/ml), Streptomycin (1.0µg/ml), Ethionamide (5.0µg/ml), and P-aminosalicylic acid (4.0µg/ml)] were used for generating Phenotypic DST. Before the release of the updated ‘2021 WHO Technical Report on critical concentrations for drug susceptibility testing of isoniazid and the rifamycins (rifampicin, rifabutin and rifapentine)’, the critical concentrations from 2018 report were used for phenotypic DST. Future MGIT-based DST will use the updated critical concentrations to maximize detection of phenotypic susceptibility and resistance. For instance, if genotypic and phenotypic results were discordant, pDST was repeated.

Genomic DNA Isolation

A conventional CTAB method was used for isolation of genomic DNA from LJ-amplified isolates of MTB. Genomic DNA Clean and Concentrator kit (ZYMO Research, Irvine, CA, USA) was used for DNA purification. Quality-checking and quantification of isolated genomic DNA were analyzed using NanoDrop (Thermo Fisher Scientific, Waltham, MA, USA) and the Qubit dsDNA Assay (Invitrogen, Waltham, MA, USA) respectively.

Whole Genome Sequencing

NexteraXT DNA Library Preparation and Index kits (Illumina, San Diego, CA, USA) were used for generating DNA libraries. The Bioanalyzer 2100 System (Agilent Technologies, Santa Clara, CA, USA) was used for measuring library sizes which tends to be ~850 bp on an average and were normalized in equimolar concentrations. The 2×251 cycles of paired-end read sequencing was generated using MiSeq Reagent Kit v3 (Illumina, San Diego, CA, USA) and Miseq sequencer (Illumina, San Diego, CA, USA).

Quality Control

The Sequencing data were then aligned to the H37Rv reference genome (NC_000962.3) and their coverage, depth and breadth were calculated. To identify the primary species for each isolate and their percentage of relatedness to other species, Kraken tool was used (6). Besides applying filter quality in variant calling, as depicted in the Variant Calling and Resistance Prediction section below, the following criteria were employed to eliminate low-quality isolates from downstream analysis:

- ❖ Sequences with breadth coverage less than 85% were excluded from further analysis, as these isolates were deemed to be contaminated.
- ❖ Isolates exhibiting contamination with genomes from other species during Kraken analysis were also excluded from downstream analytics to ensure MTB-specific genomes were scrutinized for variant calling and resistance determination.

Variant Calling and Resistance Prediction

The filtered genomes were subjected to analysis using CamNIRTResPred, an in-house, validated genomic analytics pipeline (7). A total of 6,782 whole genome sequences passed quality control, with reads having at least 60 base pairs and a minimum base quality of 20. Further the sequences were trimmed using Trimmomatic software v0.36 (LEADING:20 TRAILING:20 SLIDINGWINDOW:4:20 MINLEN:60) (8). Genome index for the H37Rv reference genome was build using bwa v0.7.12, and the samtools faidx option (v1.3.1) (9, 10). The bwa v0.7.12 mem with default parameters was used for alignment of the reads to the H37Rv reference genome. Picard v2.2.4 and GATK v3.5 were used for sorting, duplicate removal, and indel mapping correction (11, 12).

Variants were called using Samtools and bcftools v1.3.1 with the following parameters (samtools mpileup -d 8000 -t DP -B -u -g -m 4 and bcftools call -m -v -o) respectively (13). The variant quality filter metrices such as base quality >50, mapping quality >30, read depth >5, and at least one read mapping in either direction was further applied. Homozygous and heterozygous sites were classified by variants with >75% of the mapped reads and by variants with <75% of the mapped reads. RD-analyzer was used to predict the lineages of the isolates (14).

At the end, to predict the variants association with resistance, the filtered variants were annotated and compared against a database of mutations containing published resistance-associated mutations for first- and second-line antituberculosis drugs.

Statistical Analysis

The number of drug-resistant and drug-susceptible samples with and without mutations were determined using genotype and phenotype comparisons and were merged into 2x2 contingency tables (refer **Table 4**). Sensitivity, Specificity, Positive Predictive Values (PPVs), and Odds Ratios (ORs) were calculated with corresponding Confidence Intervals (CIs). Fisher's exact test was used to determine p-values based on the hypergeometric distribution. A Benjamini-Hochberg correction procedure with a False Discovery Rate (FDR) of 5% was used to handle multiple testing (15). Isolates with a single (SOLO) mutation were included in the count of SOLO mutations instead of including all isolates with a given mutation and were compared with the corresponding

numbers of isolates without mutation. To calculate the PPVs and ORs for SOLO mutations (PPV SOLO and OR SOLO) as per the WHO Mutations Catalogue, the same statistical procedure was applied as represented below:

- **PPV SOLO** $= \frac{\text{Present SOLO}_R}{\text{Present SOLO}_R + \text{Present in S}}$
- **OR SOLO** $= \frac{\text{Present SOLO}_R}{\text{Absent in R}} / \frac{\text{Present SOLO}_S}{\text{Absent in S}}$

Table 4. Phenotype - Genotype Comparison Conditions

Diagnostic List	Phenotype Results	Genotype Results
True Positive (TP)	R	R
False Positive (FP)	S	R
False Negative (FN)	R	S
True Negative (TN)	S	S

The above-said analyses were performed using R v.4.1.0 and MedCalc, v.19.2.6 (16, 17).

Executive Summary

To summarize, this mutation catalogue version 2.0 is a collation of MTB-specific mutations that are graded into five categories based on TB drug-resistance association. This was achieved by comparing genotypic and phenotypic data for a vast collection of strains collected throughout India. Based on the availability of high-quality genotypic (whole genome sequencing) and phenotypic (TB culture) drug susceptibility testing data, a total of 8894 MTBC isolates were chosen for the investigation. Based on the 2021 WHO Mutations Catalogue approach (3), which includes categorizing mutations into "Groups" according to the strength of their evidence-based link with TB treatment resistance, the downstream analysis was performed which resulted in 10,673 variants. Following the first version, the second version will serve as a standard reference for the interpretation of mutations linked to drug-resistant tuberculosis in India, guiding national activities for disease prevention and surveillance.

The Version 2.0 catalogue has been enhanced with descriptions of 52 mutations, in addition to those documented in catalogue version 1.0. The key contributor gene is *rpoC*, with 25 mutations. Additionally, the current version includes new genes: *ndh*, *ubiA*, *rrl*, and *fabG1*, for which mutations were not reported in Version 1.0. A general comparative analysis of both catalogues and the differences in terms of genes and number of mutations are tabulated in Table 5a. Furthermore, in Version 2.0, additional mutations in isoniazid resistance genes, namely *inhA*, *embB*, and *ndh* (new addition in Version 2.0), were observed. Similarly, concerning rifampicin, ethambutol, linezolid, and ethionamide, Version 2.0 features additional genes: *rpoC*, *ubiA*, *rrl*, and *fabG1*, respectively. The contrast of differences in mutations between Version 1.0 and Version 2.0 is tabulated in Table 5b. In summary, out of 14 drugs studied in Version 2.0, additional drug-resistant mutations were reported for 11 drugs. In Version 2.0, we observed 3 indels in *katG*, *fabG1*, and *ethA* genes.

Table 5a: The General comparative analysis of mutations in Version 1.0 and Version-2.0

Drugs	Version 1.0		Version 2.0	
	Genes	No of Mutations	Genes	No of Mutations
Rifampicin			<i>rpoB</i>	63
	<i>rpoB</i>	60	<i>rpoC</i>	25
Isoniazid	<i>katG</i>	46	<i>katG</i>	51
	<i>fabG1</i>		<i>fabG1</i> //promoter	4
	/promoter	1	<i>inhA</i>	1
	<i>ahpC</i> /promoter	1	<i>embB</i>	1
			<i>ahpC</i> //promoter	1
			<i>ndh</i>	1
Ethambutol	<i>embB</i>	6	<i>embB</i>	10
	<i>embA</i> //promoter	1	<i>embA</i>	6
			<i>ubiA</i>	1
Levofloxacin	<i>gyrA</i>	10	<i>gyrA</i>	11
	<i>gyrB</i>	5	<i>gyrB</i>	10
Moxifloxacin	<i>gyrA</i>	10	<i>gyrA</i>	11
	<i>gyrB</i>	5	<i>gyrB</i>	11
Ofloxacin	<i>gyrA</i>	9	<i>gyrA</i>	10
	<i>gyrB</i>	4	<i>gyrB</i>	6
Linezolid	<i>rplC</i>	1	<i>rplC</i>	1
			<i>rrl</i>	1

Amikacin	<i>rrs</i>	2	<i>rrs</i>	3
Capreomycin	<i>rrs</i>	3	<i>rrs</i>	3
	<i>gid</i>	4	<i>gid</i>	2
Kanamycin	<i>eis</i> /promoter	5	<i>eis</i> /promoter	6
	<i>rrs</i>	3	<i>rrs</i>	2
Ethionamide	<i>fabG1</i> / promoter	1	<i>fabG1</i> /promoter	3
	<i>inhA</i>	3	<i>inhA</i>	4
	<i>ethA</i>	159	<i>ethA</i>	157
	<i>ethR</i>	8		
	<i>mshA</i>	8	<i>fabG1</i>	1
Para-aminosalicylic acid	<i>thyA</i>	4	<i>thyA</i>	4
	<i>folC</i>	3	<i>folC</i>	3
	<i>ribD</i>	1	<i>ribD</i>	1
Pyrazinamide	<i>pncA</i>	297	<i>pncA</i>	303
	<i>pncA</i> /promoter	2	<i>pncA</i> /promoter	2
	<i>rpsA</i>	1	<i>rpsA</i>	1
Streptomycin	<i>rpsL</i>	4	<i>rpsL</i>	4
	<i>rrs</i>	8	<i>rrs</i>	8
	<i>gid</i>	8	<i>gid</i>	3

Table 5b. Details of unique genes and mutations between version 1.0 and version 2.0

Drugs	Genes	Mutations												
Rifampicin	<i>rpoB</i>	S493L	Q432E	P454S	D435N	P454R	Q432H	S450*	S450A	T427P	H445S			
		G433S	I491T	I491V	L516P	P1040R	V483A	P434A	F452C	F452L	F452S	K445R	L449V	
	<i>rpoC</i>	P434L	P434Q	P434R	S428A	S428T	V431M	G433A	L449R	G433D	Q435P	L446Q	P434S	G332S
isoniazid	<i>katG</i>	D142G	S315I	S315R	CG97CGG	GTTT105								
	<i>fabG1/pr</i>	G-17T	T-8A	T-8C		GTT								
	<i>inhA</i>	S94A												
	<i>embB</i>	G406A												
	<i>ahpC/pr</i>	C-81T/G48A												
	<i>ndh</i>	R268H												
ethambutol	<i>embB</i>	S347I	Y334H	T1082A	M306L									
	<i>embA</i>	C-11A	C-12T	C-16A	C-16G	G-43C								
	<i>ubiA</i>	V188A												
linezolid	<i>rrl</i>	G2814T												
Amikacin	<i>rrs</i>	C1402T												
capreomycin		GCCCCC1	GCCCCC3											
	<i>gid</i>	03GCCCC	52GCCCC											
kanamycin	<i>eis/prom</i>	C-12T	C-15G	CG-7C										
	<i>rrs</i>	G1484T												
Streptomycin	<i>gid</i>	Q125I	Q127I	E103I	S136I	E40I								
P-aminosalicylic acid	No additions													
levofloxacin	<i>gyrA</i>	D94V												
	<i>gyrB</i>	N499T	R446C	R446H	S447F	T500N								
moxifloxacin	<i>gyrA</i>	D94V												
	<i>gyrB</i>	N499T	R446C	R446H	S447F	M291I	T500N							
ofloxacin	<i>gyrA</i>	G88A												
	<i>gyrB</i>	E501V	A504V											
	<i>fabG1/pr</i>	T-8C	G-17T	C-15T										
	<i>inhA</i>	S94A												
	<i>fabG1</i>	L203L												
		GC753GC		AGGG386		G103GC	TGG710T							
	<i>ethR</i>	C	W116I	AGGGG	TC694TCC	G103GC	GGGG	GA286G	S186I					
Ethinoamide	<i>mshA</i>	GCC193G	CGG509C											
Pyrazinamide		GGG	y155I											
	<i>pncA</i>	S65S	C138C	V183V	A170A	L35L	D12D							

	Genes/Mutations present in Version 1.0 but not in Version 2.0
	Newly reported mutations for existing genes (Version 1.0) in Version 2.0
	Genes reported first time with respect to specific drug in Version 2.0

Grouping of mutations in version 2.0:

According to the additional grading criteria adopted in this study, the mutations were reclassified in Version 2.0. The number of mutations spanning each group for Version 1.0 and 2.0 are tabulated in Table 6. It should be noted that, in the case of Version 1.0, it comprised 45 mutations in Group 1 and 638 mutations in Group 2. Moreover, in Version 2.0, 14 new mutations were added in Group 1 and 38 were added in Group 2.

Table 6. Summary of mutation grouping details in Version 1.0

Drugs		Group 1:V1	Group 1:V2	Group 2:V1	Group 2:V2	Group 3:V1	Group 3:V2	Group 4:V1	Group 4:V2	Group 5:V1	Group 5:V2
RIF	Rifampicin	3	4	57	84	767	1652	121	1	850	392
INH	Isoniazid	2	4	46	55	1336	1730	26	0	106	107
EMB	Ethambutol	0	4	7	13	70	432	26	0	893	822
LFX	Levofloxacin	5	7	10	14	115	385	9	0	228	176
MOX	Moxifloxacin	6	6	9	16	112	398	10	0	230	159
OFX	Ofloxacin	7	6	6	10	118	186	10	0	226	165
LZD	Linezolid	1	2	0	0	304	373	10	0	477	455
AMK	Amikacin	2	2	0	1	48	82	0	0	383	355
CAP	Capreomycin	2	2	5	3	5	10	0	0	222	219
KAN	Kanamycin	5	7	3	1	23	78	0	0	103	162
ETH	Ethionamide	2	4	177	161	233	547	1	2	312	283
PAS	Para-aminosalicylic Acid	4	4	4	4	72	131	2	1	306	248
PZA	Pyrazinamide	2	2	298	304	47	107	0	1	220	153
STM	Streptomycin	4	4	16	11	34	74	4	2	83	50

Comparative analysis of WHO catalogue vs. Version 2.0:

In Version 2.0, we observed a total of 716 mutations and compared them with the 2023 WHO mutation catalogue. We found that 32% of drug resistant were common to those reported by WHO. The remaining mutations were confined to the Indian mutation catalogue Version 2.0. These 2 mutations correspond to 10 drugs and 16 genes/promoter. The most prevalent drug resistance mutations between WHO and Version 2.0 were observed for rifampicin, pyrazinamide, and fluoroquinolones. Moreover, 19 new mutations in Version 2.0, which were not reported in Version 1.0 but were common with WHO, were observed. These 19 mutations correspond to 8 genes/promoter feature resistance to 6 drugs (see Table 7).

Table 7. List of additional mutations in version 2.0 which are common to WHO catalogue with corresponding confidence grading

Drug	Gene name	Mutation	Final confidence grading version 2.0
Ethambutol	<i>embA</i> /Promoter	C-12T	Group 2
	<i>embB</i>	M306L	Group 1
	<i>embB</i>	T1082A	group 2
Linezolid	<i>rrl</i>	G2814T	Group 1
Rifampicin	<i>rpoC</i>	E1092D	Group 2
	<i>rpoC</i>	G594E	Group 2
	<i>rpoC</i>	A172V	Group 2
	<i>rpoC</i>	P601L	Group 2
	<i>rpoC</i>	P906A	Group 2
	<i>rpoC</i>	A621T	Group 2
	<i>rpoC</i>	D271G	Group 2
	<i>rpoC</i>	R69P	Group 2
	<i>rpoC</i>	E784Q	Group 2
Isoniazid	<i>inhA</i>	S94A	Group 1
	<i>katG</i>	D142G	Group 2
	<i>katG</i>	S315I	Group 2
	<i>katG</i>	S315R	Group 2
	<i>ndh</i>	R268H	Group 2
Ethionamide	<i>inhA</i>	S94A	Group 1
Pyrazinamide	<i>pncA</i>	V139A	Group 1

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