

SUPPLEMENTARY MATERIAL

This file contains the supplementary material from the research article **Optimizing Diagnostics for Drug-resistant Tuberculosis: A Comparative Study of Phenotypic and Genotypic Methods**

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Table SM1. Phenotypic results.

MGIT					MIC 7H9 (mg/L)							MIC OK (mg/L)						
ID	Str	Inh	Rif	Emb	Inh	Rif	Lfx	Mfx	Lzd	Pa	Bdq	Inh	Rif	Lfx	Mfx	Lzd	Pa	Bdq
RS-Ra	S	S	S	S	0.025	≤0.016	0.25	0.06	0.5	0.03	≤0.03	≤0.05	≤5	0.5	≤0.12	0.5	1	>1
RS-Rv	S	S	S	S	0.05	0.12	0.5	0.25	0.5	0.12	0.12	≤0.05	10	0.5	0.5	1	2	>1
RS-IR	S	R	S	S	>0.4	0.12	0.5	0.25	0.5	≤0.016	0.06	>1	10	0.5	0.25	0.5	2	>1
RS-RR	S	S	R	S	0.05	>2	0.5	0.25	0.5	0.12	0.12	≤0.05	>80	0.5	0.25	0.25	2	>1
CI-01	R	R	R	R	>0.4	>2	0.25	0.12	0.5	ND	0.12	>1	>80	0.5	0.25	0.5	ND	>1
CI-02	R	R	R	R	>0.4	>2	0.25	0.25	0.25	ND	0.12	>1	>80	1	1	0.5	ND	>1
CI-03	R	R	R	R	>0.4	>2	0.25	0.12	0.25	ND	0.5	>1	>80	0.5	0.5	0.5	ND	>1
CI-04	R	R	R	R	>0.4	>2	4	>1	0.25	ND	0.06	>1	>80	>8	>4	0.25	ND	>1
CI-05	S	S	S	S	0.05	0.25	0.12	0.12	0.25	ND	0.06	≤0.05	10	0.5	0.5	0.5	ND	>1
CI-06	S	R	R	S	>0.4	>2	0.12	0.06	1	ND	0.06	>1	>80	0.5	0.5	0.5	ND	ND
CI-07	S	S	S	S	0.012	0.5	0.12	0.12	0.25	≤0.016	ND	≤0.05	20	0.5	0.25	1	1	ND
CI-08	S	S	S	S	0.025	0.5	0.25	0.25	0.25	ND	0.12	≤0.05	10	0.5	0.5	0.5	ND	ND
CI-09	S	S	S	S	0.025	0.12	0.25	0.12	0.25	ND	0.12	≤0.05	≤5	0.5	0.5	0.5	ND	ND
CI-10	S	R	R	S	>0.4	>2	0.25	0.12	0.5	0.06	ND	1	>80	1	0.5	1	2	ND
CI-11	R	R	R	S	>0.4	>2	0.25	0.25	0.5	0.06	ND	>1	>80	0.5	1	1	1	ND
CI-12	S	S	S	S	0.012	0.12	0.25	0.06	0.25	ND	≤0.03	≤0.05	10	≤0.25	0.25	0.5	ND	ND
CI-13	S	S	S	S	0.025	0.25	0.25	0.25	0.25	ND	0.12	≤0.05	10	0.5	0.5	0.5	ND	ND
CI-14	S	S	S	S	0.025	0.25	0.25	0.25	0.5	ND	0.12	≤0.05	≤5	0.5	0.5	1	ND	ND
CI-15	S	R	R	S	>0.4	>2	0.25	0.12	1	ND	0.06	1	>80	1	0.5	1	ND	ND
CI-16	S	R	S	S	0.2	0.25	0.12	0.06	0.5	ND	0.12	0.25	10	0.5	0.25	0.5	ND	>1
CI-17	S	R	R	S	>0.4	>2	0.25	0.12	0.25	ND	0.12	>1	>80	0.5	0.25	0.25	ND	ND
CI-18	S	S	S	S	0.025	0.25	0.25	0.25	0.25	ND	0.12	≤0.05	≤5	0.5	0.25	0.25	ND	ND
CI-19	S	S	S	S	0.025	0.25	0.25	0.12	0.25	ND	0.12	≤0.05	≤5	0.5	0.5	0.5	ND	ND
CI-20	S	R	R	S	>0.4	>2	4	>1	0.25	0.03	ND	>1	>80	>8	>4	1	2	ND
CI-21	S	S	S	S	0.025	0.5	0.25	0.25	0.5	ND	0.12	≤0.05	10	0.5	0.5	0.5	ND	ND
CI-22	S	S	S	S	0.025	0.12	0.25	0.12	1	ND	0.06	≤0.05	10	0.5	0.5	0.5	ND	ND
CI-23	S	S	S	S	0.025	0.25	0.25	0.12	0.5	ND	0.12	≤0.05	10	1	0.5	0.5	ND	ND
CI-24	S	S	S	S	0.025	0.12	0.25	0.12	0.25	ND	0.12	≤0.05	≤5	1	0.5	0.5	ND	ND
CI-25	S	R	R	S	>0.4	>2	0.25	0.06	0.12	ND	≤0.03	>1	>80	0.5	0.25	0.25	ND	ND
CI-26	S	S	S	S	0.025	0.06	0.25	0.12	0.25	ND	≤0.03	≤0.05	≤5	0.5	0.25	0.25	ND	ND
CI-27	S	S	S	S	0.025	0.12	0.25	0.12	0.5	≤0.016	ND	≤0.05	10	0.5	0.25	1	1	ND
CI-28	S	S	S	S	0.025	0.25	0.25	0.12	0.5	ND	0.12	≤0.05	≤5	1	0.5	0.5	ND	ND
CI-29	S	S	S	S	0.05	0.12	0.12	0.06	0.25	ND	0.06	≤0.05	10	0.5	0.25	0.5	ND	ND
CI-30	S	R	R	S	>0.4	2	0.25	0.25	0.5	≤0.016	ND	>1	80	0.5	0.5	1	0.5	ND
CI-31	S	S	S	S	0.05	0.25	0.25	0.25	0.5	≤0.016	ND	≤0.05	≤5	0.5	0.5	0.5	1	ND
CI-32	S	S	S	S	0.025	0.25	0.25	0.25	0.5	≤0.016	ND	≤0.05	≤5	0.5	0.5	1	1	ND
CI-33	S	R	R	S	>0.4	>2	0.25	0.12	0.25	ND	0.06	1	>80	1	0.5	0.5	ND	ND
CI-34	R	R	R	S	>0.4	1	0.25	0.25	0.5	0.03	ND	>1	40	0.5	0.5	1	1	ND
CI-35	R	R	S	S	>0.4	2	0.5	0.25	0.5	0.06	ND	>1	40	1	1	1	2	ND
CI-36	S	S	S	S	0.05	0.25	0.25	0.25	0.5	0.12	ND	≤0.05	10	0.5	0.5	1	4	ND
CI-37	R	R	R	S	>0.4	>2	0.25	0.12	0.25	≤0.016	ND	>1	>80	0.5	0.5	0.5	1	ND
CI-38	S	R	R	S	>0.4	>2	0.25	0.25	0.25	>2	ND	1	>80	0.5	0.5	0.5	>8	ND
CI-39	R	R	R	S	>0.4	>2	0.25	0.25	0.5	0.03	ND	>1	>80	0.5	0.5	1	1	ND
CI-40	S	R	R	S	0.2	>2	0.25	0.25	0.25	≤0.016	ND	0.25	>80	0.5	0.5	0.5	0.5	ND
CI-41	S	R	R	S	>0.4	>2	0.12	0.12	0.25	≤0.016	ND	1	>80	0.5	0.5	0.5	2	ND
CI-42	S	R	R	S	>0.4	>2	0.25	0.12	0.5	0.03	ND	>1	>80	1	0.5	1	2	ND

CI-43	R	R	S	S	>0.4	1	0.5	0.5	0.5	0.06	ND	>1	80	1	1	1	2	ND
CI-44	R	R	R	S	>0.4	>2	0.25	0.25	0.25	0.03	ND	>1	>80	1	1	1	1	ND
CI-45	R	R	R	R	>0.4	>2	0.5	0.25	0.5	0.03	ND	>1	>80	1	0.5	1	1	ND
CI-46	S	R	S	S	>0.4	0.12	2	0.5	0.25	ND	0.12	1	10	4	2	0.5	ND	>1
CI-47	S	S	S	S	0.05	0.12	0.25	0.12	0.25	0.03	ND	≤0.05	10	0.5	0.5	1	2	ND
CI-48	S	S	S	S	0.025	0.03	0.25	0.12	0.25	ND	0.06	≤0.05	≤5	0.5	0.25	0.5	ND	ND
CI-49	S	S	S	S	0.025	0.06	0.25	0.12	0.25	ND	0.06	≤0.05	≤5	0.5	0.5	0.5	ND	ND
CI-50	R	R	R	S	>0.4	>2	0.25	0.25	0.5	0.06	ND	>1	>80	0.5	0.5	1	2	ND
CI-51	S	S	S	S	0.05	0.12	0.25	0.12	0.25	ND	≤0.03	≤0.05	≤5	0.5	0.25	0.5	ND	ND
CI-52	S	R	R	S	0.2	>2	0.12	0.12	0.5	>2	ND	1	>80	0.5	0.5	0.5	>8	ND
CI-53	S	S	S	S	0.025	0.12	0.25	0.12	0.5	ND	0.06	≤0.05	≤5	0.5	0.5	1	ND	ND
CI-54	S	R	R	S	>0.4	>2	0.25	0.25	0.5	0.06	ND	>1	>80	0.5	0.5	0.5	2	ND
CI-55	S	S	S	S	0.025	0.12	0.25	0.12	0.25	ND	≤0.03	≤0.05	≤5	0.5	0.5	0.5	ND	ND
CI-56	S	R	R	S	0.1	>2	0.12	0.06	0.25	≤0.016	ND	0.2	>80	0.5	0.25	0.5	0.5	ND
CI-57	S	S	S	S	0.025	0.03	0.25	0.12	1	ND	0.06	≤0.05	≤5	0.5	0.5	0.5	ND	ND
CI-58	S	R	S	S	>0.4	0.5	0.25	0.25	0.25	≤0.016	ND	>1	>80	0.5	0.5	0.5	0.5	ND
CI-59	R	R	R	S	>0.4	>2	0.25	0.25	0.5	0.12	ND	>1	>80	0.5	0.5	1	4	ND
CI-60	S	R	R	S	>0.4	>2	0.25	0.12	0.25	ND	0.06	>1	>80	0.5	0.25	0.5	ND	ND
CI-61	S	R	S	S	0.2	0.25	0.25	0.12	0.5	ND	0.25	0.25	10	0.5	0.25	0.5	ND	>1

MGIT: Mycobacteria Growth Indicator Tube; MIC: minimum inhibitory concentration; 7H9: Middlebrook 7H9 broth (EUCAST reference method); OK: Ogawa-Kudoh; ID: identification number; Str: streptomycin; Inh: isoniazid; Rif: rifampicin; Emb: ethambutol; Lfx: levofloxacin; Mfx: moxifloxacin; Lzd: linezolid; Pa: pretomanid; Bdq: bedaquiline; RS: Reference strain; Ra: Mtb H37Ra ATCC®25177™; Rv: Mtb H37Rv ATCC®27294™; IR: Mtb H37Rv-INH-R ATCC®35822™; RR: Mtb H37Rv-RIF-R ATCC®35838™; CI: clinical isolate; S: sensitive; R: resistant; ND: not done.

Table SM2. Genotypic results.

Xpert				MTBDR _{plus}				MTBDR _{sl}	
ID	Rif	Inh	Rif	WT probes	MUT probes	FLQ	AMG	WT probes	MUT probes
RS-Ra	S	S	S	APD	NPD	S	S	APD	NPD
RS-Rv	S	S	S	APD	NPD	S	S	APD	NPD
RS-IR	S	R	S	-katG (deleted gene)	NPD	S	S	APD	NPD
RS-RR	R	S	R	rpoB -WT8	rpoB +MUT3	S	S	APD	NPD
CI-01	R	R	R	rpoB -WT7 katG -WT inhA -WT1	rpoB +MUT2A katG +MUT1 inhA +MUT1	S	S	APD	NPD
CI-02	R	R	R	rpoB -WT3;-WT4;-WT8 katG -WT inhA -WT1	rpoB +MUT3 katG +MUT1	S	S	APD	NPD
CI-03	I	R	R	rpoB -WT3;-WT4 katG -WT inhA -WT1	katG +MUT1 inhA +MUT1	S	S	APD	NPD
CI-04	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	R	S	gyrA -WT3	gyrA +MUT3C
CI-05	S	S	S	APD	NPD	S	S	APD	NPD
CI-06	R	R	R	rpoB -WT7 katG -WT	rpoB +MUT2A katG +MUT1	S	S	APD	NPD
CI-07	R	S	R	rpoB -WT8	NPD	S	S	APD	NPD
CI-08	S	S	S	APD	NPD	S	S	APD	NPD
CI-09	S	S	S	APD	NPD	S	S	APD	NPD
CI-10	R	R	R	rpoB -WT7 inhA -WT1	rpoB +MUT2B inhA +MUT1	S	S	APD	NPD
CI-11	R	R	R	rpoB -WT3;-WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-12	R	S	R	rpoB -WT7	NPD	S	S	APD	NPD
CI-13	S	S	S	APD	NPD	S	S	APD	NPD
CI-14	S	S	S	APD	NPD	S	S	APD	NPD
CI-15	S	R	R	inhA -WT1	rpoB +MUT1 inhA +MUT1	S	S	APD	NPD
CI-16	S	R	S	inhA -WT1	inhA +MUT1	R	S	gyrA -WT2	NPD
CI-17	R	S	R	ropB -WT8	rpoB +MUT3	S	S	APD	NPD
CI-18	S	S	S	APD	NPD	S	S	APD	NPD
CI-19	R	S	R	ropB -WT2	NPD	S	S	APD	NPD
CI-20	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	R	S	gyrA -WT3	gyrA +MUT3C
CI-21	R	S	R	ropB -WT2	NPD	S	S	APD	NPD
CI-22	S	S	S	APD	NPD	S	S	APD	NPD
CI-23	R	S	R	ropB -WT2	NPD	S	S	APD	NPD
CI-24	S	S	S	APD	NPD	S	S	APD	NPD
CI-25	R	S	R	ropB -WT8	rpoB +MUT3	S	S	APD	NPD
CI-26	S	S	S	APD	NPD	S	S	APD	NPD
CI-27	S	S	S	APD	NPD	S	S	APD	NPD
CI-28	S	S	S	APD	NPD	S	S	APD	NPD
CI-29	S	S	S	APD	NPD	S	S	APD	NPD
CI-30	R	R	R	rpoB -WT7 katG -WT	katG MUT1	S	S	APD	NPD
CI-31	S	S	S	APD	NPD	S	S	APD	NPD
CI-32	S	S	S	APD	NPD	S	S	APD	NPD

CI-33	S	R	S	inhA -WT1	inhA +MUT1	S	S	APD	NPD
CI-34	S	R	S	APD	katG +MUT1	S	S	APD	NPD
CI-35	R	R	R	rpoB -WT3; -WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-36	S	S	S	APD	NPD	S	S	APD	NPD
CI-37	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	S	S	APD	NPD
CI-38	R	R	R	rpoB -WT8 inhA -WT1	rpoB +MUT3 inhA +MUT1	S	S	APD	NPD
CI-39	R	R	R	rpoB -WT3; -WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-40	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3	S	S	APD	NPD
CI-41	R	R	R	rpoB -WT8 inhA -WT1	rpoB +MUT3 inhA +MUT1	S	S	APD	NPD
CI-42	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	S	S	APD	NPD
CI-43	R	R	R	rpoB -WT3; -WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-44	R	R	R	rpoB -WT3; -WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-45	R	R	R	rpoB -WT3; -WT4 katG -WT	katG +MUT1	S	S	APD	NPD
CI-46	S	S	S	APD	NPD	R	S	gyrA -WT2	gyrA +MUT1
CI-47	S	S	S	APD	NPD	S	S	APD	NPD
CI-48	R	S	R	ropB -WT7	NPD	S	S	APD	NPD
CI-49	R	S	R	ropB -WT7	NPD	S	S	APD	NPD
CI-50	R	R	R	rpoB -WT7 katG -WT inhA -WT1	katG +MUT1	S	S	APD	NPD
CI-51	R	S	R	ropB -WT7	NPD	S	S	APD	NPD
CI-52	R	R	R	rpoB -WT8	rpoB +MUT3 inhA +MUT1	S	S	APD	NPD
CI-53	S	S	S	APD	NPD	S	S	APD	NPD
CI-54	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	S	S	APD	NPD
CI-55	R	S	R	ropB -WT7	NPD	S	S	APD	NPD
CI-56	R	S	R	ropB -WT8	rpoB +MUT3	S	S	APD	NPD
CI-57	R	S	R	ropB -WT7	NPD	S	S	APD	NPD
CI-58	R	S	S	APD	NPD	S	S	APD	NPD
CI-59	S	R	R	katG -WT	rpoB +MUT2A katG +MUT1	S	S	APD	NPD
CI-60	R	R	R	rpoB -WT8 katG -WT	rpoB +MUT3 katG +MUT1	S	S	APD	NPD
CI-61	S	R	S	inhA -WT1	inhA +MUT1	R	S	gyrA -WT2	NPD

ID: identification number; Inh: isoniazid; Rif: rifampicin; WT: wild type; MUT: known mutation; FLQ: fluoroquinolones; AMG: aminoglycosides; RS: Reference strain; Ra: Mtb H37Ra ATCC®25177™; Rv: Mtb H37Rv ATCC®27294™; IR: Mtb H37Rv-INH-R ATCC®35822™; RR: Mtb H37Rv-RIF-R ATCC®35838™; CI: clinical isolate; S: sensitive; R: resistant; I: indeterminate; APD: all probes detected; NPD: no probes detected; *rpoB*: DNA-directed RNA polymerase subunit beta gene; *inhA*: NADH-dependent enoyl-[ACP] reductase gene; *katG*: catalase-peroxidase gene; *gyrA*: DNA gyrase subunit A gene; - WT: wild type probe not detected; +MUT: mutation probe detected.

Table SM3. Susceptibility profiles for rifampicin.

N	Susceptibility profile	MIC RIF 7H9 [mg/L]						1	2	>2
		≤0.016	0.03	0.06	0.12	0.25	0.5			
24	pWT, gWT	1		1	10	10	2			
3	pWT, <i>rpoB</i> mutated (510-513)					2	1			
6	pWT, <i>rpoB</i> mutated (526-529)		2	1	3					
1	pWT, <i>rpoB</i> mutated (530-533)						1			
2	pNWT, gWT							1		1
7	pNWT, <i>rpoB</i> mutated (513-517) and mutated (516-519)							1	1	5
1	pNWT, <i>rpoB</i> D516V									1
2	pNWT, <i>rpoB</i> mutated (526-529)								1	1
3	pNWT, <i>rpoB</i> H526Y									3
1	pNWT, <i>rpoB</i> H526D									1
14	pNWT, <i>rpoB</i> S531L									14
1	pNWT, <i>rpoB</i> mutated (513-517), mutated (516-519) and S531L									1

MIC: minimum inhibitory concentration; RIF: rifampicin; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; pNWT: phenotypically non-wild type; gWT: genotypically wild type; *rpoB*: DNA-directed RNA polymerase subunit beta gene; Number sequences in parenthesis indicates the localization of non-specific mutations on the gene, e.g. (510-513) indicates that the sequence from codon 510 to codon 513 is different from the wild type sequence; D516V: mutation at codon 516 that changes aspartic acid to valine; H526Y: mutation at codon 526 that changes histidine to tyrosine; H526D: mutation at codon 526 that changes histidine to aspartic acid; S531L: mutation at codon 531 that changes serine to leucine; Red line indicates the MIC breakpoint.

Table SM4. Susceptibility profiles for isoniazid.

N	Susceptibility profile	MIC INH 7H9 [mg/L]								
		≤0.003	0.006	0.012	0.025	0.05	0.1	0.2	0.4	>0.4
31	pWT, gWT			2	20	8	1			
4	pNWT, gWT									4
8	pNWT, <i>inhA</i> c-15t							3		5
16	pNWT, <i>katG</i> S315T (agc/acc)									16
1	pNWT, <i>katG</i> deletion									1
2	pNWT, <i>katG</i> S315T (agc/acc) and <i>inhA</i> c-15t									2
2	pNWT, <i>katG</i> S315T (agc/acc) and <i>inhA</i> mutated (c-15;a-16)									2
1	pNWT, <i>katG</i> mutated (S315)							1		

MIC: minimum inhibitory concentration; INH: isoniazid; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; pNWT: phenotypically non-wild type; gWT: genotypically wild type; *inhA*: NADH-dependent enoyl-[ACP] reductase gene; *katG*: catalase-peroxidase gene; c-15t: mutation at nitrogenous base -15 (negative number indicates it is in promotor region) that changed cytosine to thymine; S315T: mutation at codon 315 that changes serine to threonine; (agc/acc): mutation at codon 315 that changed the sequence adenine-guanine-cytosine (translated as serine) to adenine-cytosine-cytosine (translated as threonine); (c-15;a-16): indicates the localization of non-specific mutation on the promotor region of *inhA* gene, meaning that the sequence from cytosine -15 to adenine -16 is different from the wild type sequence; Red line indicates the MIC breakpoint.

Table SM5. Susceptibility profiles for levofloxacin.

N	Susceptibility profile	MIC LFX 7H9 [mg/L]								
		≤0.03	0.06	0.12	0.25	0.5	1	2	4	>4
60	pWT, gWT			7	47	6				
2	pWT, <i>gyrA</i> mutated (89-93)			1	1					
1	pNWT, <i>gyrA</i> A90V							1		
2	pNWT, <i>gyrA</i> D94G								2	

MIC: minimum inhibitory concentration; LFX: levofloxacin; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; pNWT: phenotypically non-wild type; gWT: genotypically wild type; *gyrA*: DNA gyrase subunit A gene; (89-93): indicates that the sequence from codon 89 to codon 93 is different from the wild type sequence; A90V: mutation at codon 90 that changes alanine to valine; D94G: mutation at codon 94 that changes aspartic acid to glycine; Red line indicates the MIC breakpoint.

Table SM6. Susceptibility profiles for moxifloxacin.

N	Susceptibility profile	MIC MFX 7H9 [mg/L]								
		≤0.008	0.016	0.03	0.06	0.12	0.25	0.5	1	>1
59	pWT, gWT				6	28	25			
2	pWT, <i>gyrA</i> mutated (89-93)				1	1				
1	pNWT, gWT							1		
1	pNWT, <i>gyrA</i> A90V							1		
2	pNWT, <i>gyrA</i> D94G									2

MIC: minimum inhibitory concentration; MFX: moxifloxacin; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; pNWT: phenotypically non-wild type; gWT: genotypically wild type; *gyrA*: DNA gyrase subunit A gene; (89-93): indicates that the sequence from codon 89 to codon 93 is different from the wild type sequence; A90V: mutation at codon 90 that changes alanine to valine; D94G: mutation at codon 94 that changes aspartic acid to glycine; Red line indicates the MIC breakpoint.

Table SM7. Susceptibility profiles for linezolid.

		MIC LZD 7H9 [mg/L]								
N	Susceptibility profile	≤0.03	0.06	0.12	0.25	0.5	1	2	4	>4
65	pWT			1	31	29	4			

MIC: minimum inhibitory concentration; LZD: linezolid; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; Red line indicates the MIC breakpoint.

Table SM8. Susceptibility profiles for pretomanid.

N	Susceptibility profile	MIC Pa 7H9 [mg/L]						1	2	>2
		≤0.016	0.03	0.06	0.12	0.25	0.5			
29	pWT	11	8	6	4					
2	pNWT									2

MIC: minimum inhibitory concentration; Pa: pretomanid; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; pNWT: phenotypically non-wild type; Red line indicates the MIC breakpoint.

Table SM9. Susceptibility profiles for bedaquiline.

N	Susceptibility profile	BDQ CIM 7H9 [mg/L]						2	4	>4
		≤0.03	0.06	0.12	0.25	0.5	1			
38	pWT	6	13	17	1	1				

MIC: minimum inhibitory concentration; BDQ: bedaquiline; 7H9: Middlebrook 7H9 broth (EUCAST reference method); N: number of strains for each profile; pWT: phenotypically wild type; Red line indicates the MIC breakpoint.