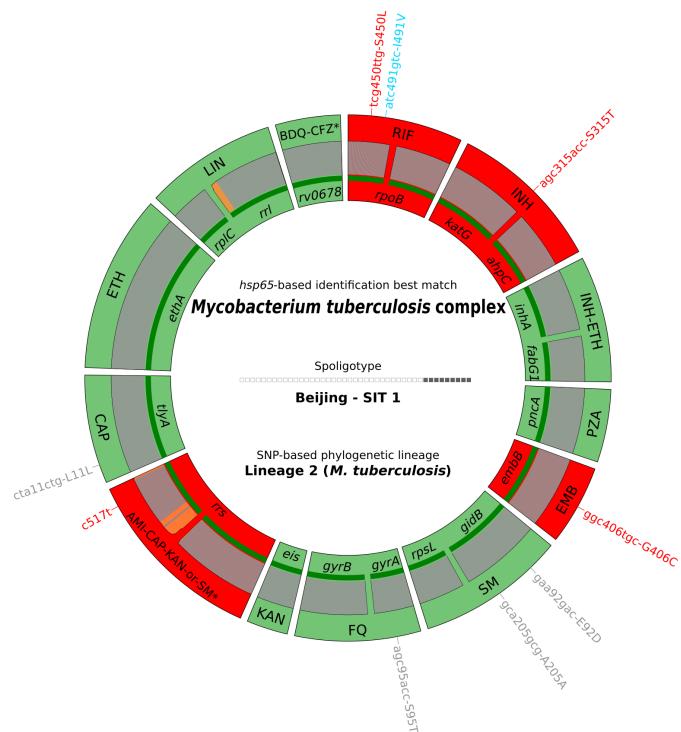
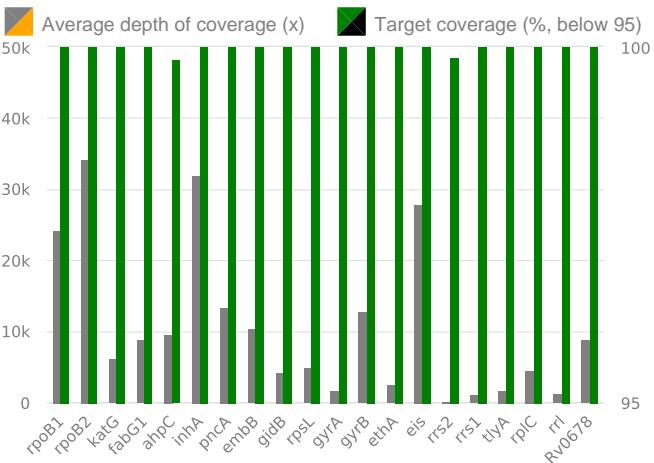


**SAMPLE ID: R30368**

Date of submission	Sep, 4 2024 21:48:33
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	
Experiment set	

Legend<sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
<b>Sample:</b>	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>99.992%</b>
Median depth of coverage *	<b>7365x</b>
(min. rrs2: 224x; max. rpoB2: 34182x)	

**hsp65-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
4760.8	400.0	100.000	0.0	<i>Mycobacterium tuberculosis complex</i>

### Drug resistance associated variants<sup>3</sup>

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247729	ggc406tgc	99.880	3140.00	G406C	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>katG</i>	2155168	agc315acc	99.930	350.00	S315T	INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761155	tcg450ttg	99.900	6100.00	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1472362	c517t	100.000	67.00	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>

### Uncharacterized and uncertain significance variants<sup>3</sup>

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rpoB</i>	761277	atc491gtc	4.500	308.25	I491V	RIF	Uncertain significance	<a href="#">WHO 2021</a>

### Spoligotype

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
000000000003771	18858.0	1	5800	Beijing
0011111111				

### SNP-based phylogenetic lineage

Lineage 2 ( *M. tuberculosis* )

### Potential mixed infection

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

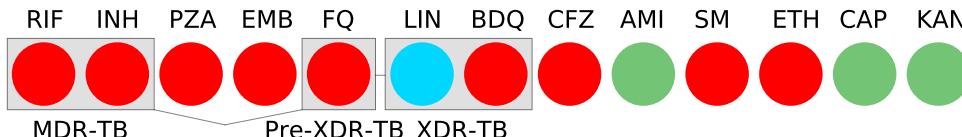
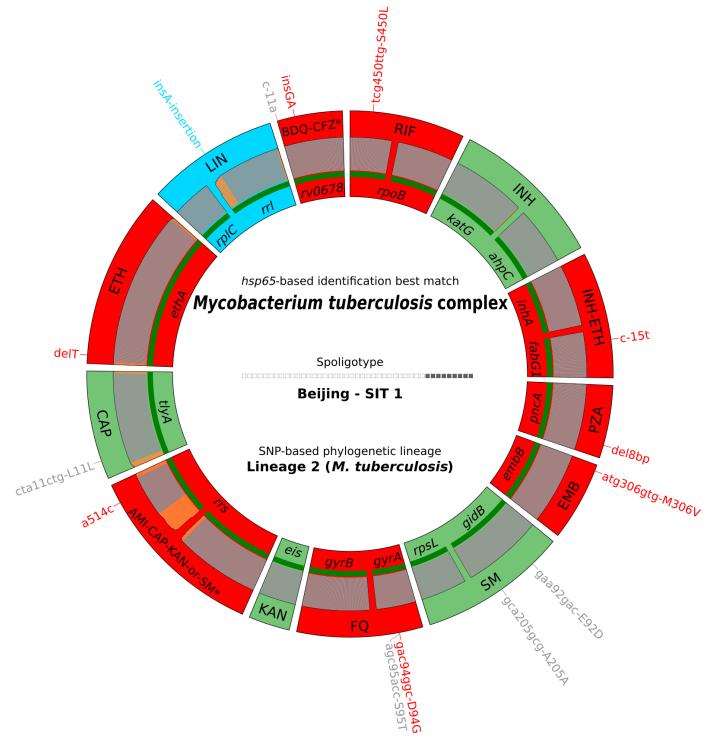
**Not detected.**



## DEEPLEX® Myc-TB Report

### SAMPLE ID: R27657

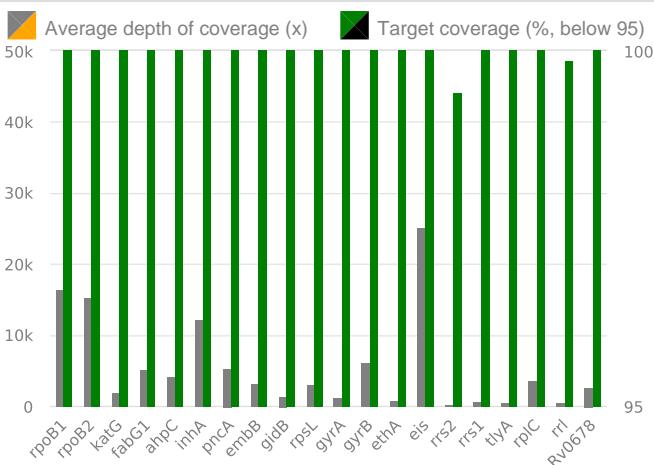
Date of submission	Sep, 4 2024 21:48:33
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	



Legend <sup>1</sup>

### Sample controls and metrics<sup>2</sup>

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>2233x</b>
(min. rrs2: 138x; max. eis: 25139x)	



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
3971.1	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247429	atg306gtg	99.920	322.25	M306V	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>gyrA</i>	7582	gac94ggc	99.790	359.25	D94G	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>fabG1</i>	1673425	c-15t	99.930	1837.50	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761155	tcg450ttg	99.940	4276.25	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1472359	a514c	100.000	42.25	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>ethA</i>	4327409	delT	99.790	0.00	frameshift	n/a	n/a	Resistant	n/a
<i>pncA</i>	2288777-84	del8bp	85.060	0.00	frameshift	n/a	n/a	Resistant	n/a
<i>rv0678</i>	779127	insGA	89.680	0.00	frameshift	n/a	n/a	Resistant	n/a

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rrl</i>	1476009	insA	7.870	0.00	insertion	n/a	Uncharacterised	n/a

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
0000000000003771	30614.6	1	5800	Beijing
0011111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

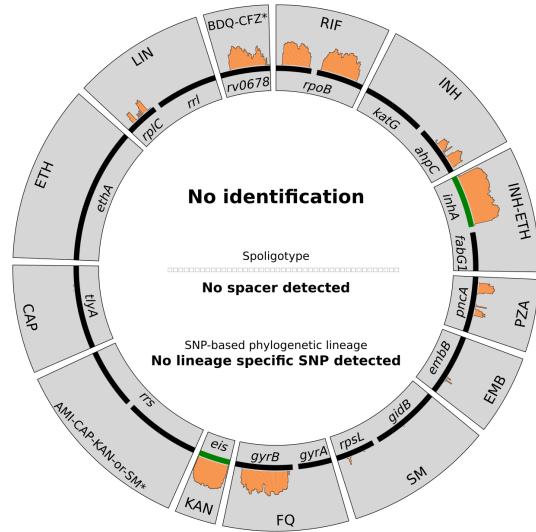
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

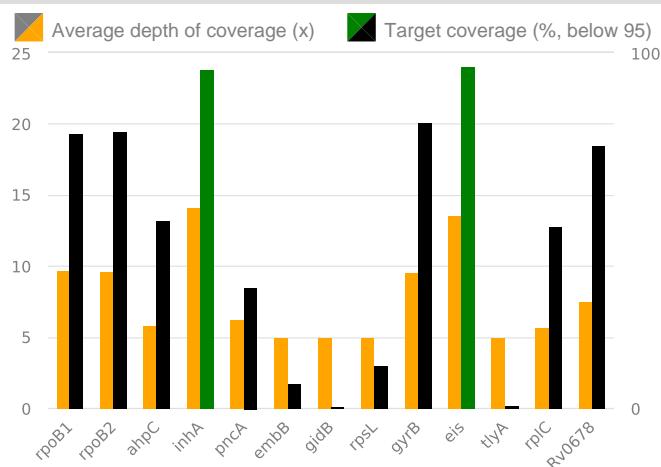
**Not detected.**

**SAMPLE ID: IC**

Date of submission	Sep, 4 2024 21:48:23
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	ND
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>74.665%</b>
Median depth of coverage*	<b>1x</b>
(min. 0x; max. inhA: 14x)	



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
3.0	334.0	N/A	N/A	



**Internal control** Coverage: 99.802% Average depth: 4028x

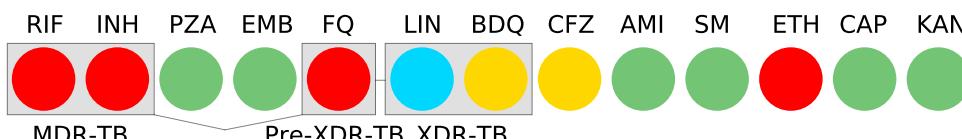
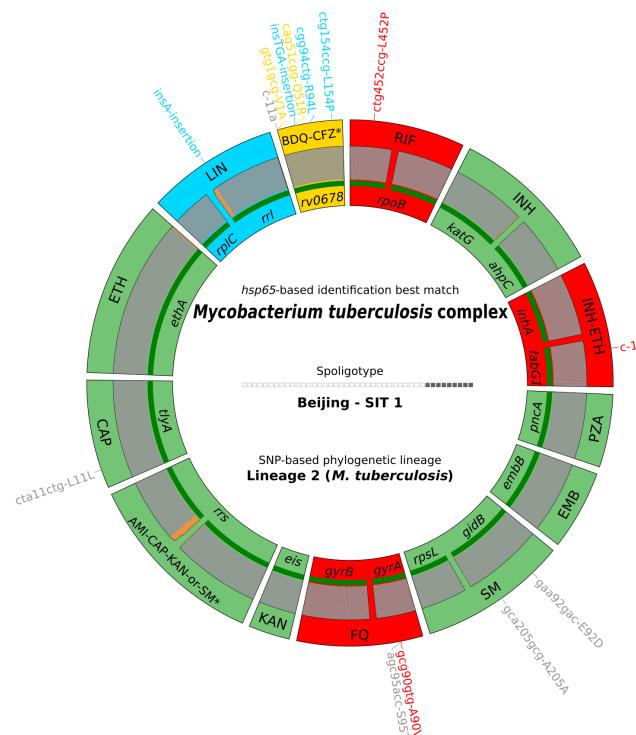
No interpretable result or Negative control



## DEEPLEX® Myc-TB Report

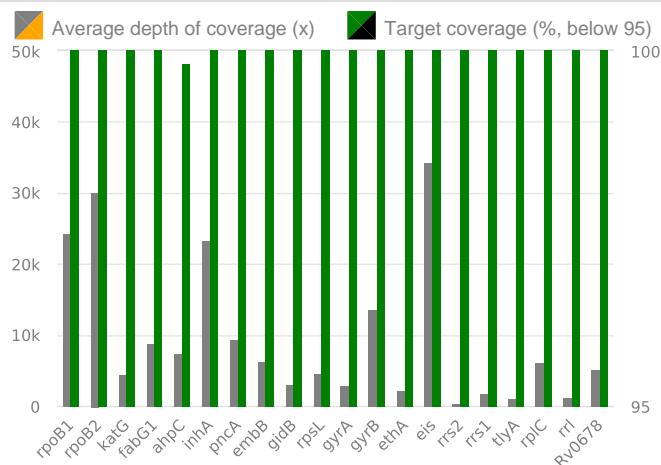
### SAMPLE ID: R36431

Date of submission	Sep, 4 2024 21:48:23
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	

Legend <sup>1</sup>

### Sample controls and metrics<sup>2</sup>

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>99.992%</b>
Median depth of coverage*	<b>5417x</b>
(min. rss2: 313x; max. eis: 34202x)	



**hsp65-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
3944.7	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
gyrA	7570	gcg90gtg	99.790	718.00	A90V	LEV,MXF	Associated with resistance	intermediate	<a href="#">WHO 2021</a>
fabG1	1673425	c-15t	99.890	3062.75	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
rpoB	7611161	ctg452ccg	99.930	6220.00	L452P	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
rv0678	778991	gtg1gcf	4.320	15.00	V1A	BDQ,CFZ	High	Resistant	<a href="#">PUBMED</a>
rv0678	778991	gtg1gcf	4.320	15.00	V1A	BDQ,CFZ	High	Resistant	<a href="#">PUBMED</a>
rv0678	778991	gtg1gcf	4.320	15.00	V1A	BDQ,CFZ	High	Resistant	<a href="#">PUBMED</a>
rv0678	778991	gtg1gcf	4.320	15.00	V1A	BDQ,CFZ	High	Resistant	<a href="#">PUBMED</a>
rv0678	779141	cag51ccg	4.220	63.25	Q51R	CFZ	Minimal	Resistant	<a href="#">PUBMED</a>
rv0678	779131	delC	9.190	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779182	delG	5.070	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779130	insC	3.600	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779181	insG	5.930	0.00	frameshift	n/a	n/a	Resistant	n/a

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
rv0678	779270	cgg94ctg	3.380	46.25	R94L	n/a	Uncharacterised	n/a
rv0678	779450	ctg154ccg	17.990	247.25	L154P	n/a	Uncharacterised	n/a
rrl	1476009	insA	3.430	0.00	insertion	n/a	Uncharacterised	n/a
rv0678	779126	insTGA	3.720	0.00	insertion	n/a	Uncharacterised	n/a

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
000000000003771	23193.8	1	5800	Beijing
0000000000000000000000000000000011111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

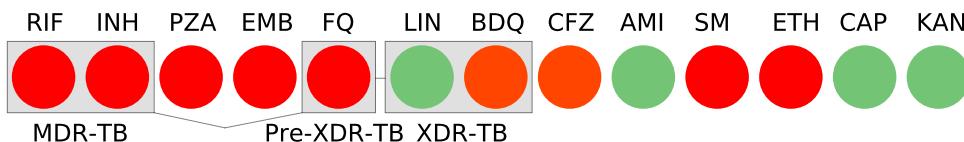
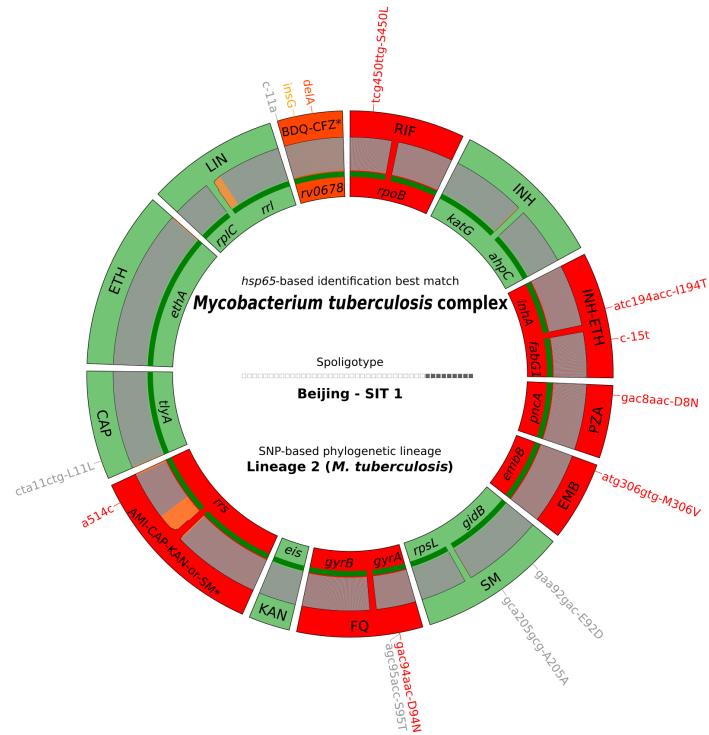
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

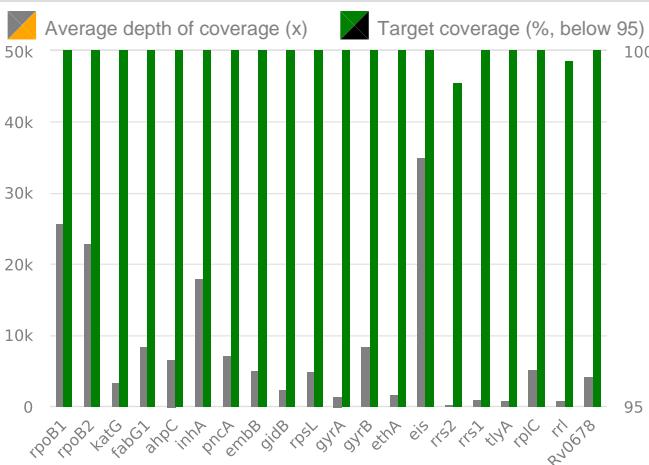
Not detected.

**SAMPLE ID: R31095**

Date of submission	Sep, 4 2024 21:48:23
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

<b>Sequencing Run:</b>	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
<b>Sample:</b>	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>99.992%</b>
Median depth of coverage*	<b>3888x</b>
(min. rrs2: 172x; max. eis: 34944x)	



***hsp65-based species identification***

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
5776.5	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
embB	4247429	atg306gtg	99.950	515.75	M306V	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
gyrA	7581	gac94aac	99.860	353.00	D94N	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
inhA	1674782	atc194acc	99.940	4498.75	I194T	INH,ETH	n/a	Resistant	<a href="#">PUBMED</a>
fabG1	1673425	c-15t	99.950	2878.25	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
pncA	2289220	gac8aac	99.880	2142.00	D8N	PZA	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
rpoB	761155	tgc450ttg	99.900	6559.75	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
rrs	1472359	a514c	100.000	51.25	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
rv0678	779281	delA	68.600	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779127	insG	25.550	0.00	frameshift	n/a	n/a	Resistant	n/a

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

No uncharacterized variants detected in any gene target.

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
0000000000003771	20983.1	1	5800	Beijing
000111111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

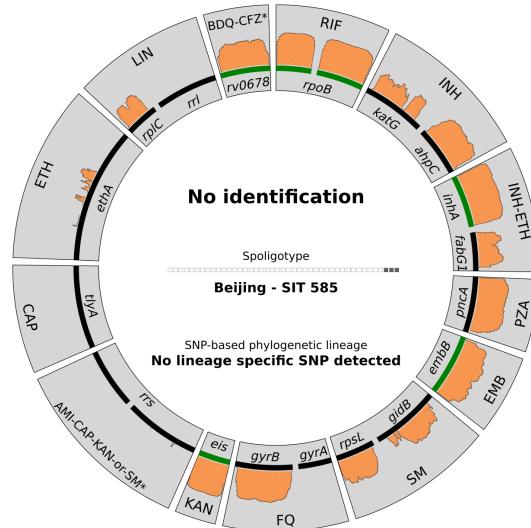
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

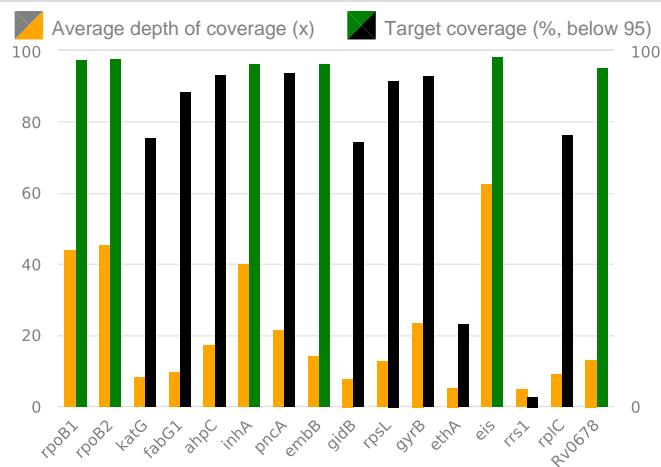
**Not detected.**

**SAMPLE ID: Neg-Ctrl**

Date of submission	<b>Sep, 4 2024 21:48:23</b>
Analysis mode	<b>Deeplex Myc-TB V3_0_1 - Extended catalogue</b>
Quality	<b>ND</b>
Experiment set	
No or low coverage in some critical drug resistance-associated targets. No mutations or identification results reported.	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>89.498%</b>
Median depth of coverage*	<b>3x</b>
(min. 0x; max. eis: 63x)	



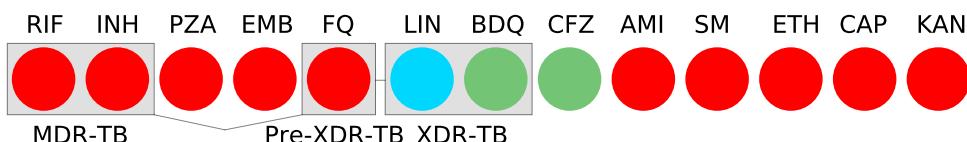
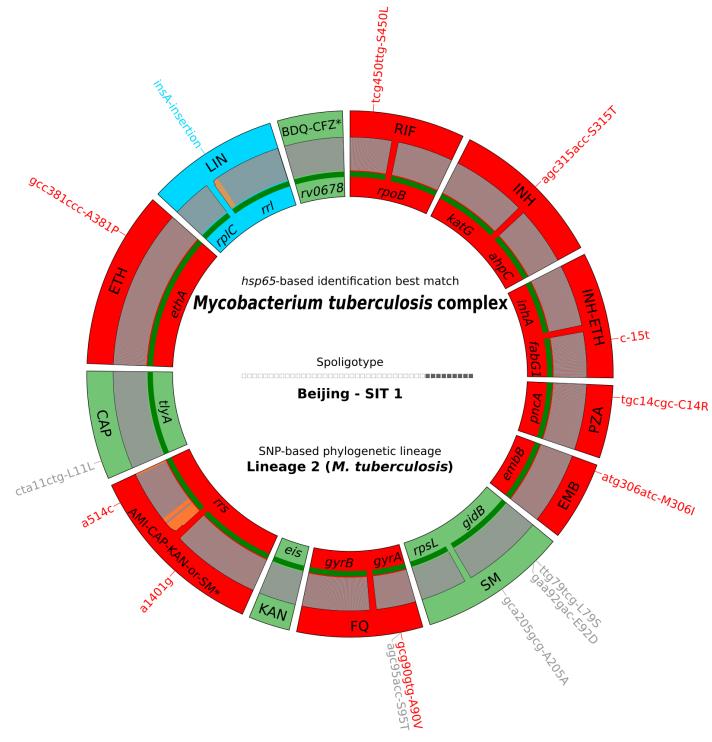
***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
12.1	396.0	N/A	N/A	N/A

**No interpretable result or Negative control**

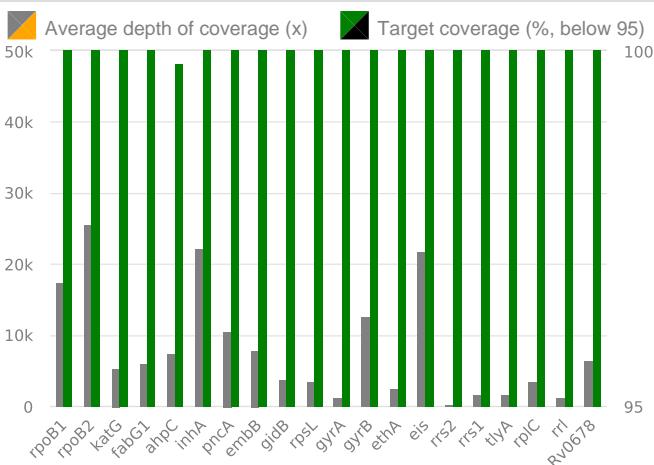
**SAMPLE ID: R26791**

Date of submission	Sep, 4 2024 21:48:23
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>6409x</b>

(min. rrs2: 201x; max. rpoB2: 25527x)



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
3506.2	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247431	atg306atc	99.830	891.00	M306I	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>ethA</i>	4326333	gcc381ccc	99.960	634.00	A381P	ETH	n/a	Resistant	<a href="#">PUBMED</a>
<i>gyrA</i>	7570	gcg90gtg	100.000	324.25	A90V	LEV,MXF	Associated with resistance	Intermediate	<a href="#">WHO 2021</a>
<i>fabG1</i>	1673425	c-15t	99.930	2054.75	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>katG</i>	2155168	agc315acc	99.920	300.75	S315T	INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>pncA</i>	2289202	tgc14cgc	99.920	3564.00	C14R	PZA	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761155	tcg450ttg	99.900	4505.25	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1472359	a514c	100.000	58.25	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1473246	a1401g	100.000	329.00	n/a	AMI,CAP,KAN	Associated with resistance	Resistant	<a href="#">WHO 2021</a>

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rrs</i>	1473246	a1401g	100.000	329.00	n/a	STM	Uncertain significance	<a href="#">WHO 2021</a>
<i>rrl</i>	1476009	insA	6.510	0.00	insertion	n/a	Uncharacterised	n/a

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
000000000003771	18589.8	1	5800	Beijing
00011111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

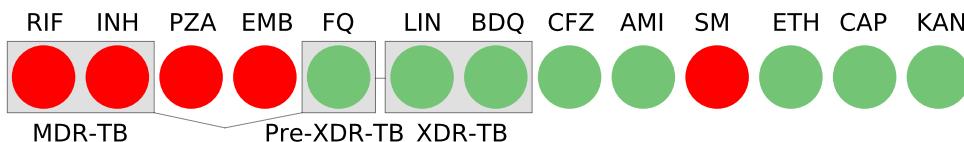
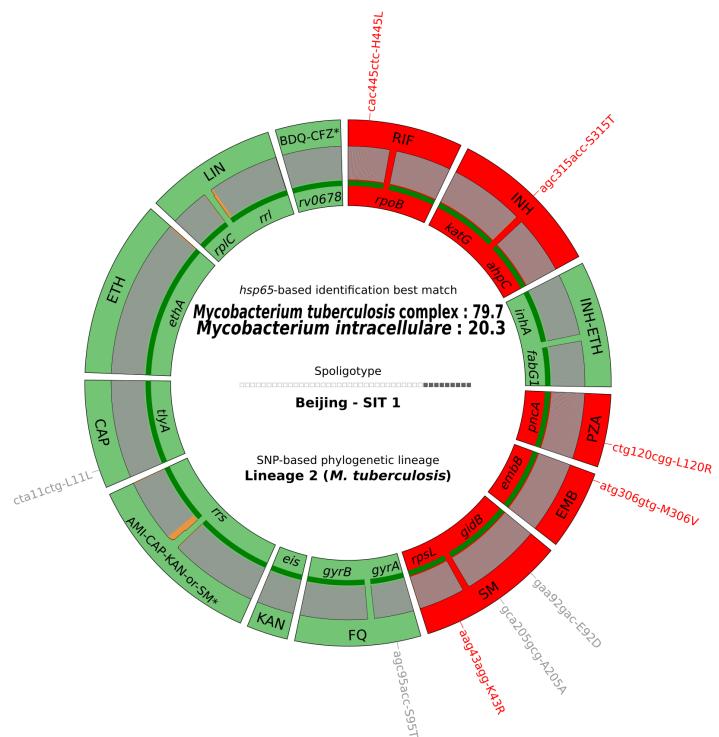
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

**Not detected.**

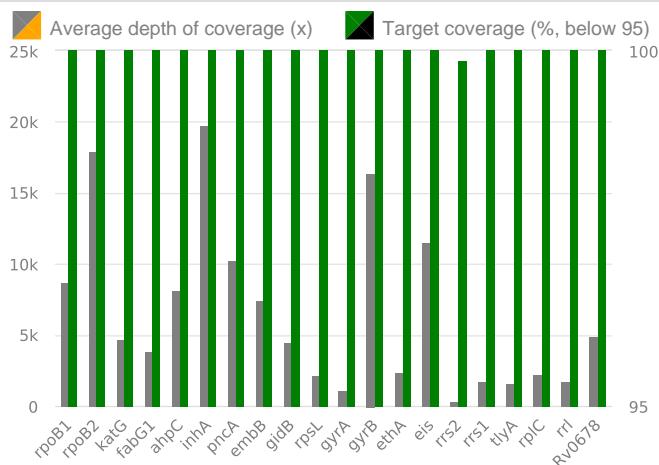
**SAMPLE ID: R25048**

Date of submission	Sep, 4 2024 21:48:23
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	+++
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>5540x</b>

(min. rrs2: 299x; max. inhA: 19723x)



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E- value	Best match
2822.3	400.0	100.0 / 100.0	0.0 / 0.0	<i>Mycobacterium tuberculosis</i> complex : 79.7 / <i>Mycobacterium intracellulare</i> : 20.3

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug *	Confidence	Resistance level	Reference
<i>embB</i>	4247429	atg306gtg	99.970	727.75	M306V	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>katG</i>	2155168	agc315acc	100.000	258.25	S315T	INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>pncA</i>	2288883	ctg120cg	99.880	3205.50	L120R	PZA	Associated with resistance - Interim	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761140	cac445ctc	99.730	2551.75	H445L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpsL</i>	781687	aag43agg	99.960	662.50	K43R	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

No uncharacterized variants detected in any gene target.

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
000000000003771	21833.4	1	5800	Beijing
0011111111				

**SNP-based phylogenetic lineage**

Lineage 2 (*M. tuberculosis*)

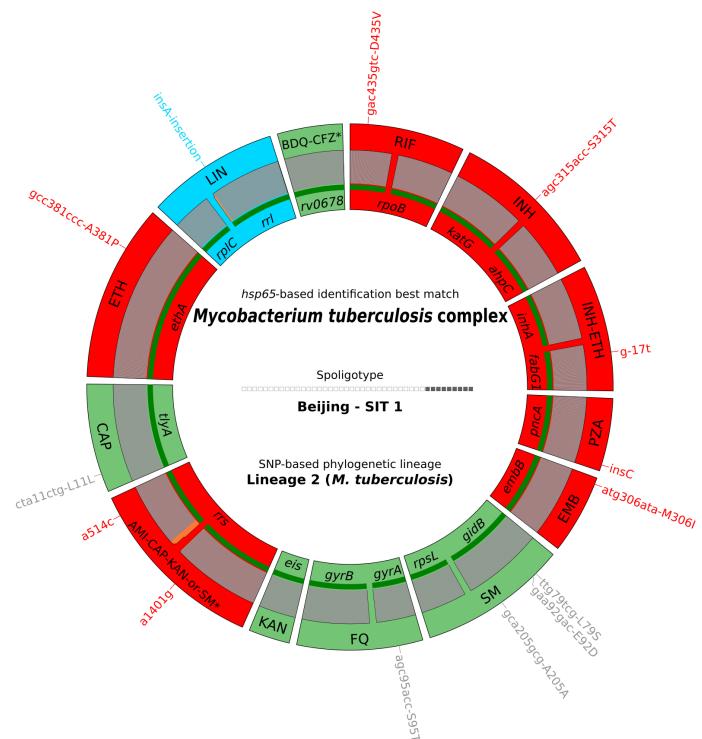
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

**Not detected.**

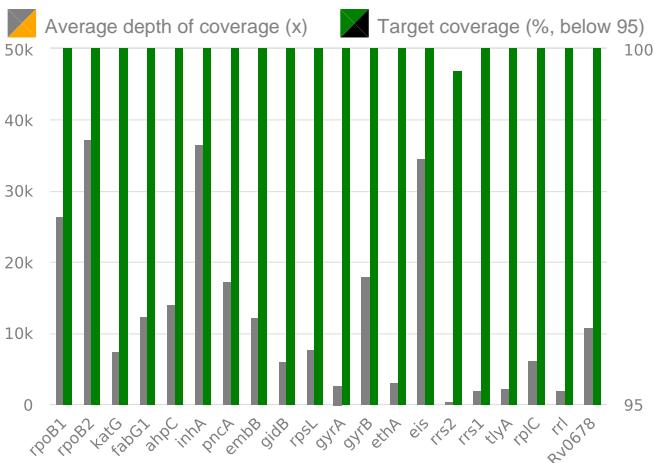
**SAMPLE ID: R28980**

Date of submission	Sep, 4 2024 21:48:01
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	+++
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>8836x</b>

(min. rrs2: 340x; max. rpoB2: 37194x)



***hsp65-based species identification***

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
8378.6	400.0	100.000	0.0	<i>Mycobacterium tuberculosis complex</i>

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247431	atg306ata	99.920	1269.25	M306I	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>ethA</i>	4326333	gcc381ccc	99.860	872.25	A381P	ETH	n/a	Resistant	<a href="#">PUBMED</a>
<i>fabG1</i>	1673423	g-17t	99.920	4214.50	n/a	INH,ETH,PTH	n/a	Resistant	<a href="#">PUBMED</a>
<i>katG</i>	2155168	agc315acc	100.000	383.50	S315T	INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761110	gac435gtc	99.850	8313.75	D435V	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1472359	a514c	99.770	108.25	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1473246	a1401g	99.930	370.25	n/a	AMI,CAP,KAN	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>pncA</i>	2288726	insC	89.540	0.00	frameshift	n/a	n/a	Resistant	n/a

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rrs</i>	1473246	a1401g	99.930	370.25	n/a	STM	Uncertain significance	<a href="#">WHO 2021</a>
<i>rrl</i>	1476009	insA	4.120	0.00	insertion	n/a	Uncharacterised	n/a

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
00000000003771	16419.8	1	5800	Beijing
0000000000000000000000000000000011111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

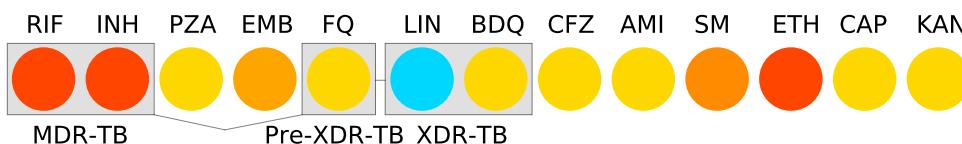
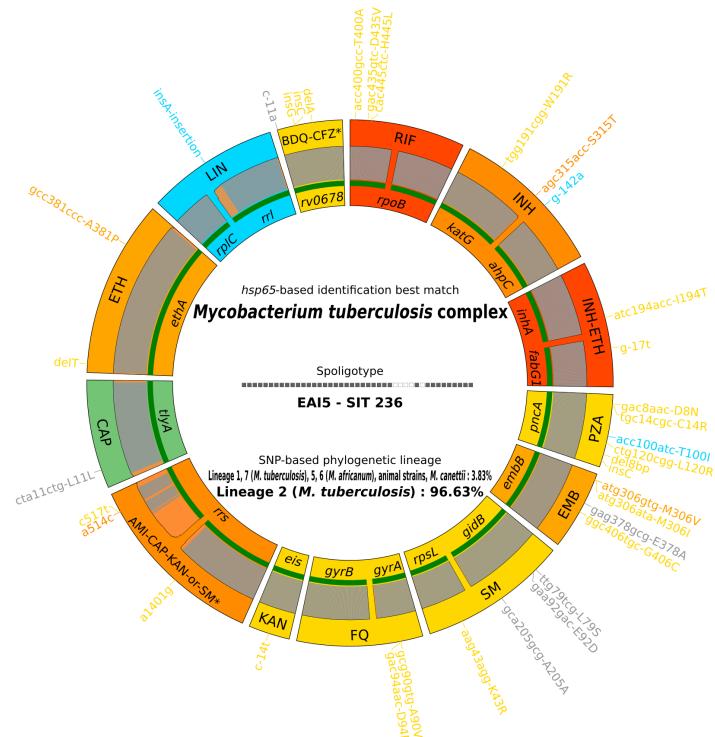
**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

**Not detected.**

**SAMPLE ID: Undetermined**

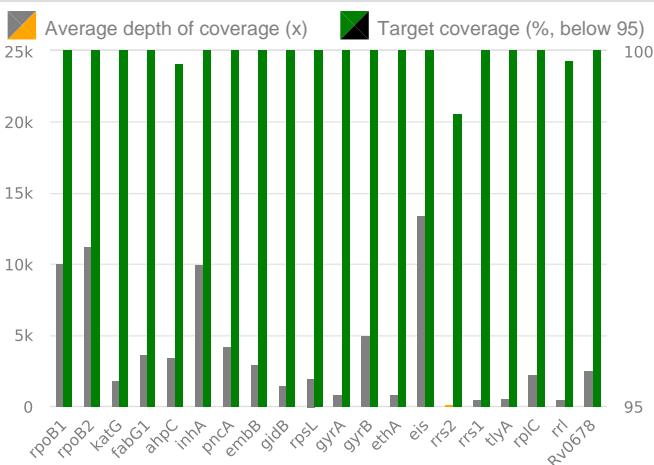
Date of submission	Sep, 4 2024 21:47:59
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>

Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>99.992%</b>
Median depth of coverage*	<b>2225x</b>

(min. rrs2: 108x; max. eis: 13395x)



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
2430.5	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

### Drug resistance associated variants<sup>3</sup>

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug *	Confidence	Resistance level	Reference
eis	2715346	c-14t	5.320	172.50	n/a	AMI,KAN	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
embB	4247429	atg306gtg	31.190	88.50	M306V	EMB	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
embB	4247431	atg306ata	17.550	62.75	M306I	EMB	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
embB	4247431	atg306atc	11.680	41.75	M306I	EMB	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
embB	4247729	ggc406tgc	5.180	49.75	G406C	EMB	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
ethA	4326333	gcc381ccc	35.800	84.75	A381P	ETH	n/a	Resistant	<a href="#">PUBMED</a>
gyrA	7570	gcg90gtg	7.440	16.75	A90V	LEV,MXF	Associated with resistance	intermediate	<a href="#">WHO_2021</a>
gyrA	7581	gac94aac	6.020	13.25	D94N	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
gyrA	7582	gac94ggc	20.000	43.75	D94G	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
gyrA	7582	gac94gcc	3.540	7.75	D94A	LEV,MXF	Associated with resistance	intermediate	<a href="#">WHO_2021</a>
inhA	1674782	atc194acc	11.910	303.25	I194T	INH,ETH INH,ETH, PTH	n/a	Resistant	<a href="#">PUBMED</a>
fabG1	1673423	g-17t	19.780	244.50	n/a	ETH,INH	n/a	Resistant	<a href="#">PUBMED</a>
fabG1	1673425	c-15t	61.670	749.00	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
katG	2155541	tgg191cgg	5.410	28.25	W191R	INH	n/a	Resistant	<a href="#">PUBMED</a>
katG	2155168	agc315acc	51.860	48.75	S315T	INH	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
pncA	2289202	tgc14cgc	12.210	165.00	C14R	PZA	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rpoB	761004	acc400gcc	5.780	94.25	T400A	RIF	n/a	Resistant	<a href="#">PUBMED</a>
rpoB	761110	gac435gtc	18.530	588.25	D435V	RIF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rpoB	761155	tcg450ttg	62.380	1623.00	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rpoB	761161	ctg452ccg	11.630	288.50	L452P	RIF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rpsL	781687	aag43agg	4.170	25.00	K43R	STM	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rrs	1472359	a514c	59.420	20.50	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rrs	1472362	c517t	9.150	3.25	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
rrs	1473246	a1401g	20.850	17.25	n/a	AMI,CAP, KAN	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
pncA	2289220	gac8aac	7.760	4.25	D8N	PZA	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
pncA	2288883	ctg120cgg	6.940	6.00	L120R	PZA	Associated with resistance - Interim	Resistant	<a href="#">WHO_2021</a>
rpoB	761140	cac445ctc	2.110	15.00	H445L	RIF	Associated with resistance	Resistant	<a href="#">WHO_2021</a>
ethA	4327409	delT	20.280	0.00	frameshift	n/a	n/a	Resistant	n/a
pncA	2288777-84	del8bp	11.960	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779281	delA	3.480	0.00	frameshift	n/a	n/a	Resistant	n/a
pncA	2288726	insC	19.760	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779127	insG	11.220	0.00	frameshift	n/a	n/a	Resistant	n/a
rv0678	779130	insC	8.050	0.00	frameshift	n/a	n/a	Resistant	n/a

### Uncharacterized and uncertain significance variants<sup>3</sup>

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rrs</i>	1473246	a1401g	20.850	17.25	n/a	STM	Uncertain significance	<a href="#">WHO 2021</a>
<i>ahpC</i>	2726051	g-142a	3.190	6.75	n/a	n/a	Uncharacterised	n/a
<i>pncA</i>	2288943	acc100atc	8.820	6.00	T100I	PZA	Uncertain significance	<a href="#">WHO 2021</a>
<i>rrl</i>	1476009	insA	7.140	0.00	insertion	n/a	Uncharacterised	n/a

### Spoligotype

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
77777777413771	2521.7	236	130	EA15
11111111111111111111111111000010111111111				

### SNP-based phylogenetic lineage

Lineage 1, 7 ( *M. tuberculosis* ), 5, 6 ( *M. africanum* ), animal strains, *M. canettii* : 3.83% Lineage 2 ( *M. tuberculosis* ) : 96.63%

### Potential mixed infection

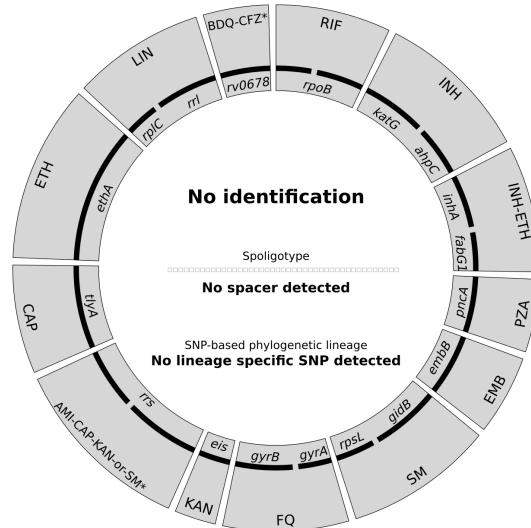
Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

Gene	Genomic position	Codon change	% Variant	AA change	Lineage	Reference
<i>embB</i>	4247646	gag378gcg	3.830	E378A	1, 5, 6, 7, <i>M. bovis</i> , <i>M. canettii</i> , <i>M. caprae</i> , <i>M. microti</i> , <i>M. pinipedii</i>	<a href="#">PUBMED</a>
<i>gidB</i>	4407927	gaa92gac	96.630	E92D	2	<a href="#">PUBMED</a>

Comment: the spoligotype should be inspected for potential biphasic distribution of coverage depth across spacers, also suggestive of mixed profile.

**SAMPLE ID: PC**

Date of submission	Sep, 4 2024 21:47:59
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	ND
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>1.991%</b>
Median depth of coverage*	<b>1x</b>



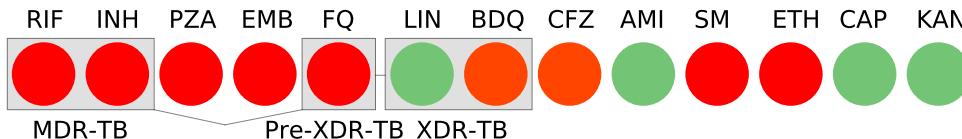
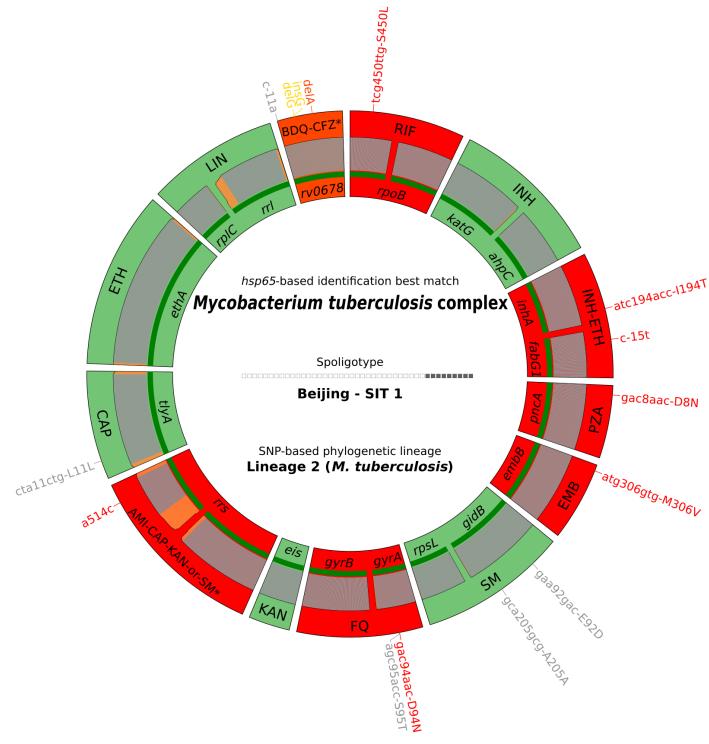
***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
0.0	0.0	N/A	N/A	

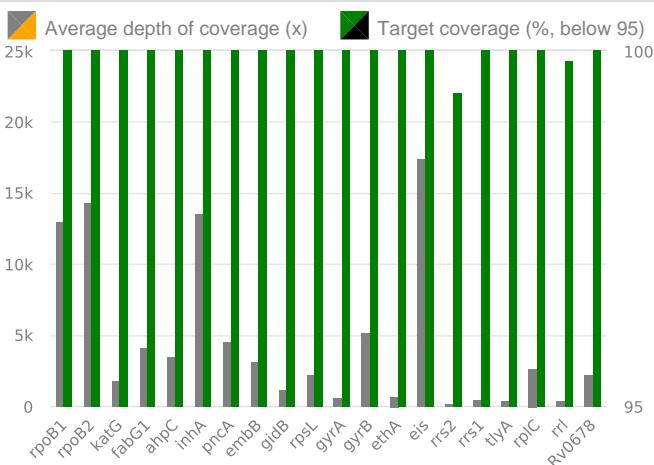
**No interpretable result or Negative control**

**SAMPLE ID: R30234**

Date of submission	Sep, 4 2024 21:47:58
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	+
Experiment set	

Legend <sup>1</sup>**Sample controls and metrics<sup>2</sup>**

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>99.992%</b>
Median depth of coverage*	<b>2226x</b>
(min. rrs2: 137x; max. eis: 17446x)	



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
2589.8	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247429	atg306gtg	100.000	308.00	M306V	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>gyrA</i>	7581	gac94aac	99.860	176.00	D94N	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>inhA</i>	1674782	atc194acc	99.940	3597.25	I194T	INH,ETH	n/a	Resistant	<a href="#">PUBMED</a>
<i>fabG1</i>	1673425	c-15t	99.940	1332.00	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>pncA</i>	2289220	gac8aac	99.950	1424.25	D8N	PZA	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761155	tcg450ttg	99.900	3851.75	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rrs</i>	1472359	a514c	100.000	41.75	n/a	STM	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rv0678</i>	779126	delG	6.780	0.00	frameshift	n/a	n/a	Resistant	n/a
<i>rv0678</i>	779281	delA	67.010	0.00	frameshift	n/a	n/a	Resistant	n/a
<i>rv0678</i>	779127	insG	11.160	0.00	frameshift	n/a	n/a	Resistant	n/a

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

No uncharacterized variants detected in any gene target.

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
00000000003771	41596.0	1	5800	Beijing
00111111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

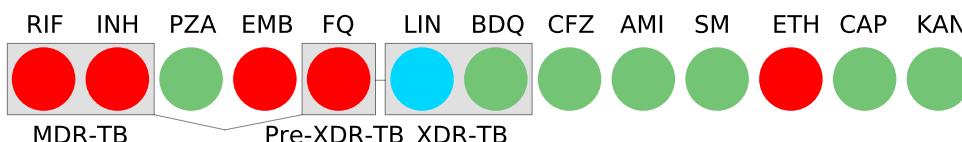
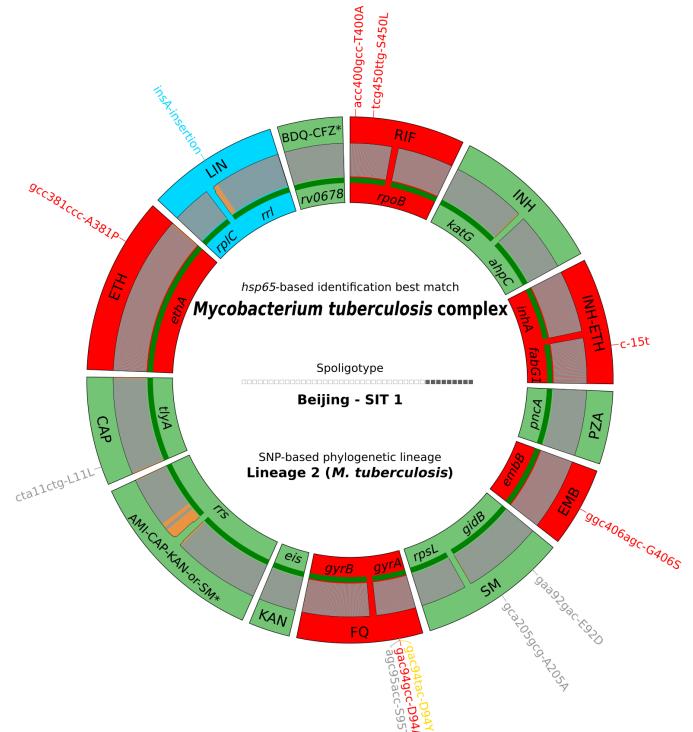
Not detected.



## DEEPLEX® Myc-TB Report

### SAMPLE ID: R21893

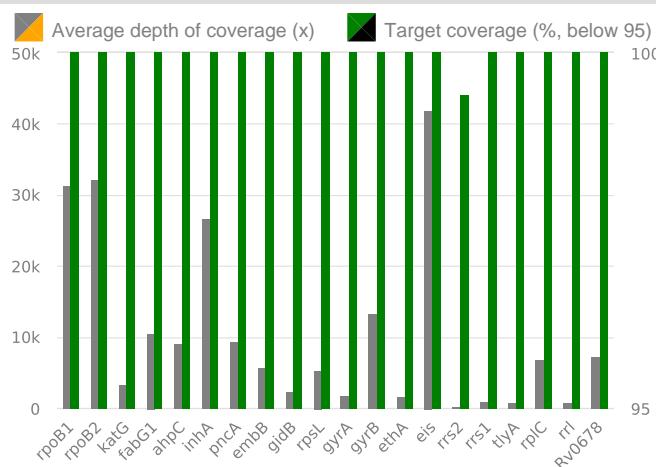
Date of submission	Sep, 4 2024 21:47:58
Analysis mode	Deeplex Myc-TB V3_0_1 - Extended catalogue
Quality	++
Experiment set	



Legend <sup>1</sup>

### Sample controls and metrics<sup>2</sup>

Sequencing Run:	
Positive control*	<b>Positive control not included</b>
Negative control*	<b>Negative control not included</b>
Sample:	
Internal control*	<b>Internal control not included</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>3854x</b>
(min. rrs2: 228x; max. eis: 41994x)	



***hsp65*-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
6904.3	400.0	100.000	0.0	<i>Mycobacterium tuberculosis</i> complex

**Drug resistance associated variants<sup>3</sup>**

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Confidence	Resistance level	Reference
<i>embB</i>	4247729	ggc406agc	99.860	1723.25	G406S	EMB	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>ethA</i>	4326333	gcc381ccc	100.000	461.50	A381P	ETH	n/a	Resistant	<a href="#">PUBMED</a>
<i>gyrA</i>	7581	gac94tac	3.290	12.50	D94Y	LEV,MXF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>gyrA</i>	7582	gac94gcc	99.940	438.50	D94A	LEV,MXF	Associated with resistance	intermediate	<a href="#">WHO 2021</a>
<i>fabG1</i>	1673425	c-15t	99.920	3567.00	n/a	ETH,INH	Associated with resistance	Resistant	<a href="#">WHO 2021</a>
<i>rpoB</i>	761004	acc400gcc	99.900	6132.00	T400A	RIF	n/a	Resistant	<a href="#">PUBMED</a>
<i>rpoB</i>	761155	tcg450ttg	99.920	8474.50	S450L	RIF	Associated with resistance	Resistant	<a href="#">WHO 2021</a>

**Uncharacterized and uncertain significance variants<sup>3</sup>**

Uncharacterized variants designate sequence variants of as yet unknown association with drug resistance or drug susceptibility. Uncertain significance variants designate variants that could not be characterized yet as either drug resistant or drug susceptible according to the current WHO confidence grading classification.

Gene	Genomic position	Codon change	% Variant	Dx-score	AA change	Drug*	Category	Reference
<i>rrl</i>	1476009	insA	5.810	0.00	insertion	n/a	Uncharacterised	n/a

**Spoligotype**

Octal code/ Binary code	Av. coverage depth (x)	SIT	SITVIT occurrence	Clade
000000000003771	25859.9	1	5800	Beijing
0011111111				

**SNP-based phylogenetic lineage**

Lineage 2 ( *M. tuberculosis* )

**Potential mixed infection**

Mixed infection is signaled by a phylogenetic variant detected at less than 97%, indicating the simultaneous presence of 1 strain harboring this variant present at this percentage and another strain sharing the same sequence as the reference at this position, present at approx. 100% minus this percentage.

**Not detected.**

<sup>1</sup> Deeplex map: the circular map is divided in 13 “sectors” associated with 13 drugs or drug classes. Sectors are colour-coded as follows: drug resistance-associated variants (or indels) detected in gene target with percent subpopulation according to colouring; uncharacterized variants (or indels) detected in gene target with percent subpopulation according to colouring; no variant or indel detected in gene target or only variants or indels unrelated to drug resistance; suboptimal gene target coverage; nontuberculous *Mycobacterium* (NTM) identified. Detected variants or indels are specified by codon, amino acid or nucleotide changes (deletions shown as \*) on the outermost part, using the same colour codes as above for drug resistance-associated and uncharacterized categories, or in grey () for variants or indels unrelated to drug resistance. Target reference sequences are coloured according to gene target coverage as follows: coverage >95%, coverage <95%. Limit of detection histogram for each target is colour-coded as follows: 1% ≤ limit of detection ≤ 3%, 3% < limit of detection ≤ 80%.

**Resistotype:** First-line drugs: rifampicin (RIF), isoniazid (INH), pyrazinamide (PZA), ethambutol (EMB). Second-line injectables: Streptomycin (SM), kanamycin (KAN), amikacin (AMI), capreomycin (CAP); fluoroquinolone class (FQ) includes levofloxacin (LEV), ofloxacin (OFX) and moxifloxacin (MOX); ethionamide (ETH); linezolid (LIN); bedaquiline (BDQ); clofazimine (CFZ). MDR-TB, multidrug-resistant TB defined as resistance to at least rifampicin and isoniazid. XDR-TB, extensively drug-resistant TB defined as MDR-TB plus resistance to at least one fluoroquinolone and a second-line injectable.

<sup>2</sup> Positive control: valid if identified as *Mycobacterium tuberculosis* complex with spoligotype SIT 482, lineage *Mycobacterium bovis* BCG and 9 expected mutations detected at >99% and no other mutations detected at >5%; Negative control: composite reference coverage breadth <40% (far below minimal coverage considered for identification and resistance prediction); Internal control: valid if average coverage depth >100x and coverage breadth >95% on internal control, and average coverage depth <100x over the other targets; Composite reference coverage: coverage breadth over the concatenated reference sequences associated with drug resistance; Median depth of coverage: median of average read depths among reference sequences associated with drug resistance; (min x, max x): minimal/maximal average coverage depth among the targets

<sup>3</sup> **Dx-score** designates the excess of coverage depth at the variant position, relative to the minimal coverage depth required to detect the observed percent of variant. Minimal value is 1. \* Antibiotics highlighted in graded colours according to percent of drug resistance associated or uncharacterized variant detected (see colour grades above).

<sup>4</sup>OFX is not used for the treatment of *Mycobacterium tuberculosis* although potential resistance to OFX is tested, as part of the Fluoroquinolones

## Disclaimer

Resistance is reported when a documented resistance-conferring mutation is detected in targets of interest\*. **The absence of detected mutations does not exclude the possibility of resistance.** Low-frequency hereteroresistance below the limit of detection by sequencing may affect typing results. The interpretation provided is based on the current understanding of genotype-phenotype relationships. All results reference the *M. tuberculosis* mutation numbering system, which differs from *Escherichia coli* numbering system. \*Resistance-conferring mutations as documented in the "Catalogue of mutations in *Mycobacterium tuberculosis* complex and their association with drug resistance" (WHO, 2021), the ReSeqTB Data Platform, Miotto P. et al. Eur Resp J 2017, Miotto P. et al. mBio 2014, PhyResSE (Feurriegel et al. J. Clin. Microbiol. 2015), Walker et al. Lancet. Infect. Dis. 2015. Additional expert rules, (as yet) not endorsed by WHO, are used for *tlyA* and *rv0678*, where all premature stop codon and frameshift-causing indels, or complete gene deletion are assumed to result in a loss of function phenotype and are consequently associated with drug resistance.