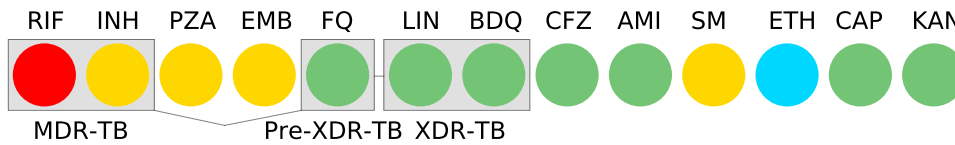
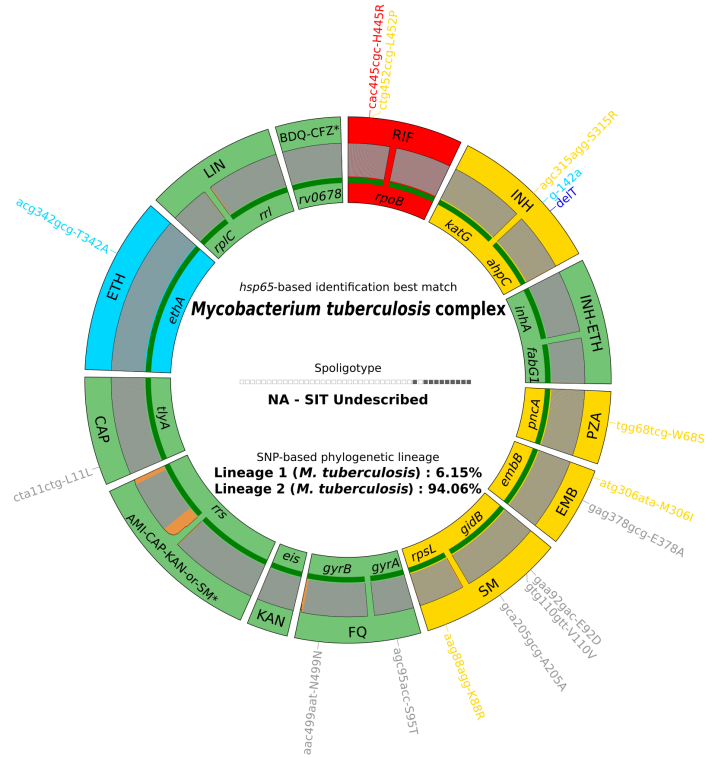


**SAMPLE ID: MIX**

Date of submission	May, 3 2022 14:31:18
Analysis mode	Deeplex Myc-TB V3.0 - Extended catalogue
Quality	+++
Experiment set	Demo
Sample source	
Validation	

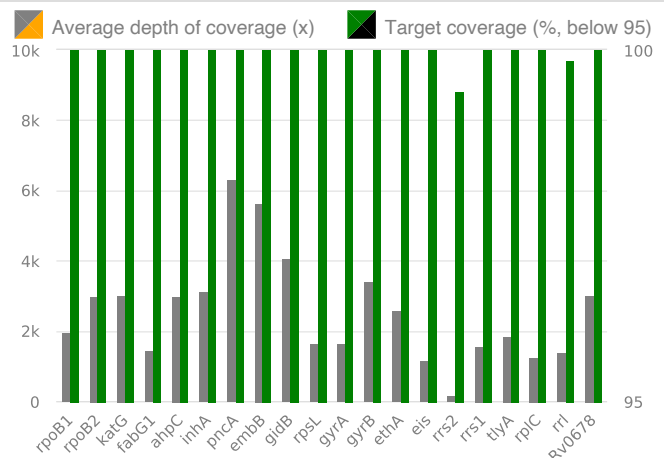


Legend <sup>1</sup>

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

<b>Sequencing Run:</b>	
Positive control*	VALID
Negative control*	VALID

<b>Sample:</b>	
Internal control*	VALID
Composite reference coverage	100.000%
Median depth of coverage*	3854x
<small>(min. rrs2: 161x; max. pncA: 6325x)</small>	



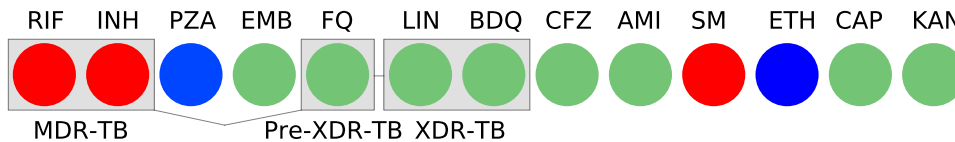
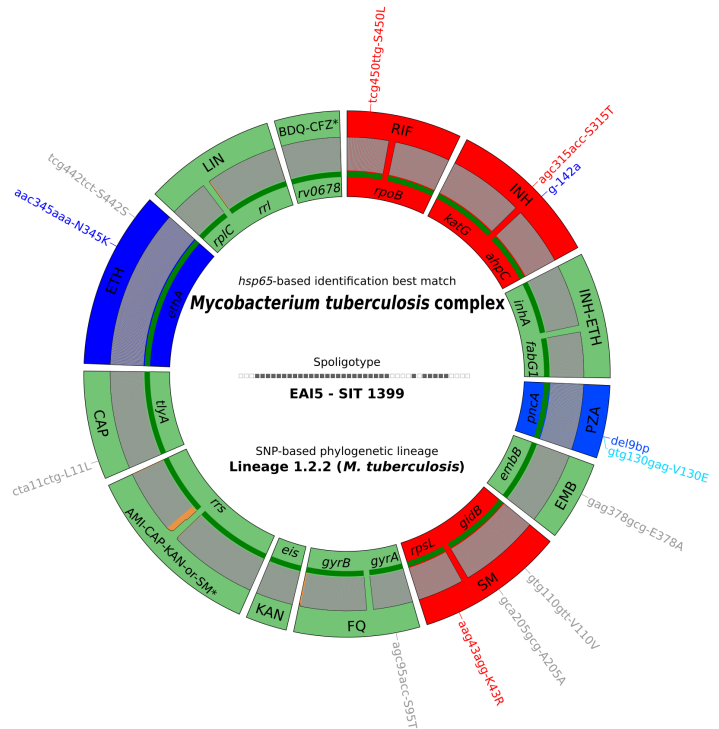
**hsp65-based species identification**

Av coverage depth (x)	Consensus length	% Identity	E-value	Best match
149.5	400.0	100.000	0.0	<i>Mycobacterium tuberculosis complex</i>



**SAMPLE ID: 3PLUS**

Date of submission	<b>May, 3 2022 14:31:18</b>
Analysis mode	<b>Deeplex Myc-TB V3.0 - Extended catalogue</b>
Quality	<b>+++</b>
Experiment set	<b>Demo</b>
Sample source	
Validation	

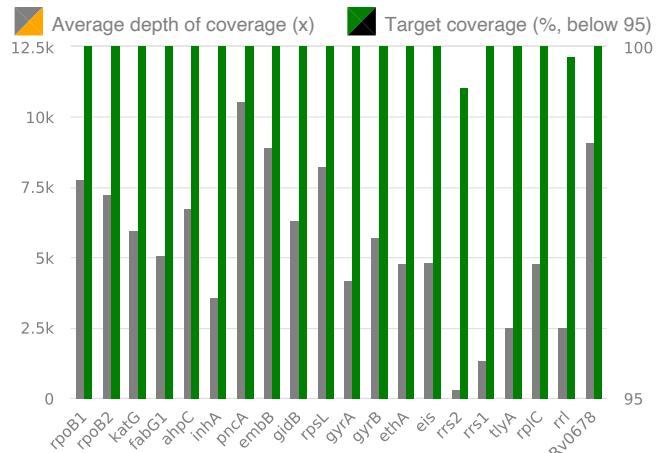


Legend <sup>1</sup>

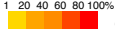
**Sample controls and metrics<sup>2</sup>**

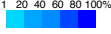



<b>Sequencing Run:</b>	
Positive control*	<b>VALID</b>
Negative control*	<b>VALID</b>






<b>Sample:</b>	
Internal control*	<b>VALID</b>
Composite reference coverage	<b>100.000%</b>
Median depth of coverage*	<b>7375x</b>
<small>(min. rrs2: 314x; max. pncA: 10581x)</small>	





<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.