MycoChase Sequence Analysis Report

Sample Details

Patient ID:	[PATIENTID]	Patient name:	[PATIENTNAME]
Sample ID:	[SAMPLEID]	Sample Received Date:	[SAMPLEDATE]
Sample Source:	[SAMPLESOURCE]	Library Prep Date:	[LABPREPDATE]
Culture Type:	[CULTURETYPE]	Sequencing Date:	[SEQDATE]
Laboratory Technician:	[LABTECH]	Report Date:	[REPORTDATE]
Contact:	[CONTACT]		

Assay Details

Sequencer:	Illumina MiSeqDx	Method:	Targeted Panel NGS
Pipeline:	MycoAnalyzer version 1.0.0	Reference:	H37Rv (NC_000962.3)
Quality Control:	[QC]		

MycoChase Species Identification

Species (%)	[SPECIES]
Lineage*	[LINEAGE]
Spoligotype*	[SPOLIGOTYPE]

Resistance (R) is reported when a reported resistance mutation is detected in loci of interest.* Except for RIF and INH, drugs-related mutations cannot be used for diagnosis because they have not been evaluated

No mutation detected

MycoChase Drug Susceptibility Test

nrough clinical tr urther verified. S r all detected m ne possibility of	No mutation detected MDR** XDR**			
Class	Drug	Gene Target# (AA change, VAF, Tier)	Result	Comments
	ISONIAZID (INH)	[0x0]	[1x0]	[2x0]
1st-line drugs	RIFAMPICIN (RIF)	[0x1]	[1x1]	[2x1]
rst-inte urugs	ETHAMBUTOL (EMB)	[0x2]	[1x2]	[2x2]
	PYRAZINAMIDE (PZA)	[0x3]	[1x3]	[2x3]
	LEVOFLOXACIN (LFX)	[0x4]	[1x4]	[2x4]
2st-line drugs (group A)	OFLOXACIN (OFX)	[0x5]	[1x5]	[2x5]
	MOXIFLOXACIN (MFX)	[0x6]	[1x6]	[2x6]
(9.0ap /1)	LINEZOLID (LZD)	[0x7]	[1x7]	[2x7]
	BEDAQUILINE (BDQ)	[0x8]	[1x8]	[2x8]
2st-line drugs (group B)	CLOFAZIMINE (CFZ)	[0x9]	[1x9]	[2x9]
	DELAMANID (DEL)	[0x10]	[1x10]	[2x10]
	AMIKACIN (AMK)	[0x11]	[1x11]	[2x11]
Out Providence	CAPREOMYCIN (CAP)	[0x12]	[1x12]	[2x12]
2st-line drugs (group C)	KANAMYCIN (KAN)	[0x13]	[1x13]	[2x13]
(group O)	STREPTOMYCIN (STM)	[0x14]	[1x14]	[2x14]
	ETHIONAMIDE (ETO)	[0x15]	[1x15]	[2x15]
	PROTHIONAMIDE (PTO)	[0x16]	[1x16]	[2x16]

^{*}The target genes for resistance mutations were derived from the Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance (2021, World Health Organization; Lancet Microbe. 2022;3(4):e265)

#AA change, amino acids change; VAF, variant allele frequency; Tier is derived from the Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance (2021, World Health Organization).

Final Result

[FINALRESULT]			

*The result for drug resistance is based on tier 1 or 2 mutations reported by the Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance (2021, World Health Organization).

Additional Comment

[ADDCOMMENT]			

The result for drug resistance is based on tier 1 or 2 mutations reported by the Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance (2021, World Health Organization).

^{*}Lineage and spoligotype are only reported for Mycobacterium tuberculosis complex. The lineage was estimated based on the 90 single nucleotide polymorphisms (SNPs) reported by Napier et al. [Genome Med. 2020;12(1):114]

^{**}MDR, multi-drug resistance; XDR: extensively drug resistance

Authorized By

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reporting Laboratory.		Signature:	
Address:	¡¡[ADDRESS]		