MYCOBACTERIUM TUBERCULOSIS GENOME SEQUENCING REPORT

NOT FOR DIAGNOSTIC USE

Patient Name	DIANE EVANS	Barcode	BARCODE
Birth Date	1887-04-04	Patient ID	34567890
Location	LONDON	Sample Type	SPUTUM
Sample Source	PULMONARY	Sample Date	1916-12-30; 18:45
Sample ID	917BAHDYB1	SequencedFrom	MGIT CULTURED ISOLATE
Reporting Lab	OXFORD	Report Date/Time	1917-01-09
Requested By	DR. REQUESTOR NAME	Requester Contact	CONTACT@GENOME.COM

Summary

The specimen was positive for **Mycobacterium tuberculosis**. It is predicted to be **resistant to Ethambutol, Pyrazinimide, Isoniazid, Rifampin, and Streptomycin**. It belongs to a cluster, suggesting **recent transmission**

Organism

The specimen was positive for ***Mycobacterium tuberculosis***, lineage 2.2.1 (**East-Asian Beijing**)

Drug Susceptibility

Resistance is reported when a high-confidence resistance-conferring mutation is detected. **"No mutation detected" does not exclude the possibility of resistance**

☐ No drug resistance predicted
☐ Mono-resistance predicted
☐ Multi-drug resistance predicted
☑ Extensive drug resistance predicted

Drug class	Interpretation	Drug	Resistance Gene (Amino Acid Mutation)
First-line	Resistant	Ethambutol	emb (M306I)
		Pyrazinimide	pncA (T47A)
		Isoniazid	katG (S315T)
		Rifampin	rpoB (S531L)
Second-line	Susceptible	Ciprofloxacin	No resistance mutation detected
		Moxifloacin	No resistance mutation detected
		Amikacin	No resistance mutation detected
		Kanamycin	No resistance mutation detected
		Capreomycin	No resistance mutation detected
	Resistant	Streptomycin	rpsL (K43R)

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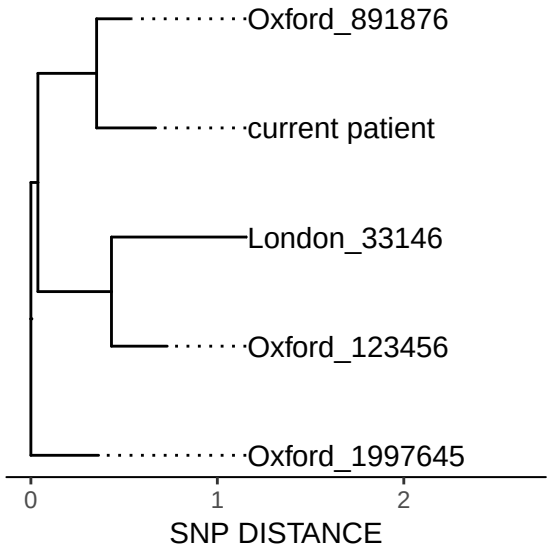
Cluster Detection

Current specimen was found to be closely clustered with previous specimens suggesting **recent transmission**

Relatedness	Number of prior matching isolates
Likely Related (< 5 SNPS apart)	**2** isolates
Possibly Related (6 to 30 SNPS apart)	**2** isolates



Assay Details

Sample ID	A12345678	Barcode	
Sequencer	ILLUMINA HISEQ 2500	Method	WGS
Pipeline	RESEQTB V.3.2C	Reference	H37RV

Comments

No additional comments

Standard Disclaimer: *Low frequency hetero-resistance below the limit of detection by sequencing may affect typing results. The interpretation provided is based on the current understanding of genotype-phenotype relationships.*

Authorised

Signature	Name
Position	Date