

# Fatal Nosocomial MDR-TB Identified through Routine Genetic Analysis and Whole-Genome Sequencing

## Technical Appendix

Technical Appendix Table. Characteristics of 4 clinical isolates from patients with multidrug-resistant tuberculosis\*

Patient	MIRU-VNTR	RIF	rpoB	rpoB	INH	katG	mabA†	PZA	pncA	EMB	embB	STR	gidB‡	gidB‡
1	224331432615324 33241328	R	L452P§	H1028R	R	S315T	-8(t>a)	R	ins¶	R	M306V	S	130 bp del	R
2	224331432615324	R	L452P§	H1028R	R	S315T	-8(t>a)	R	ins¶	R	M306V	-	130 bp del	R
3	22433143261532- 3324132-	S	-	-	R	S315T	-	S	-	S	-	R	-	L26S
4	22433143261532- 33241328	S	-	-	R	S315T	-	S	-	S	-	R	-	L26S

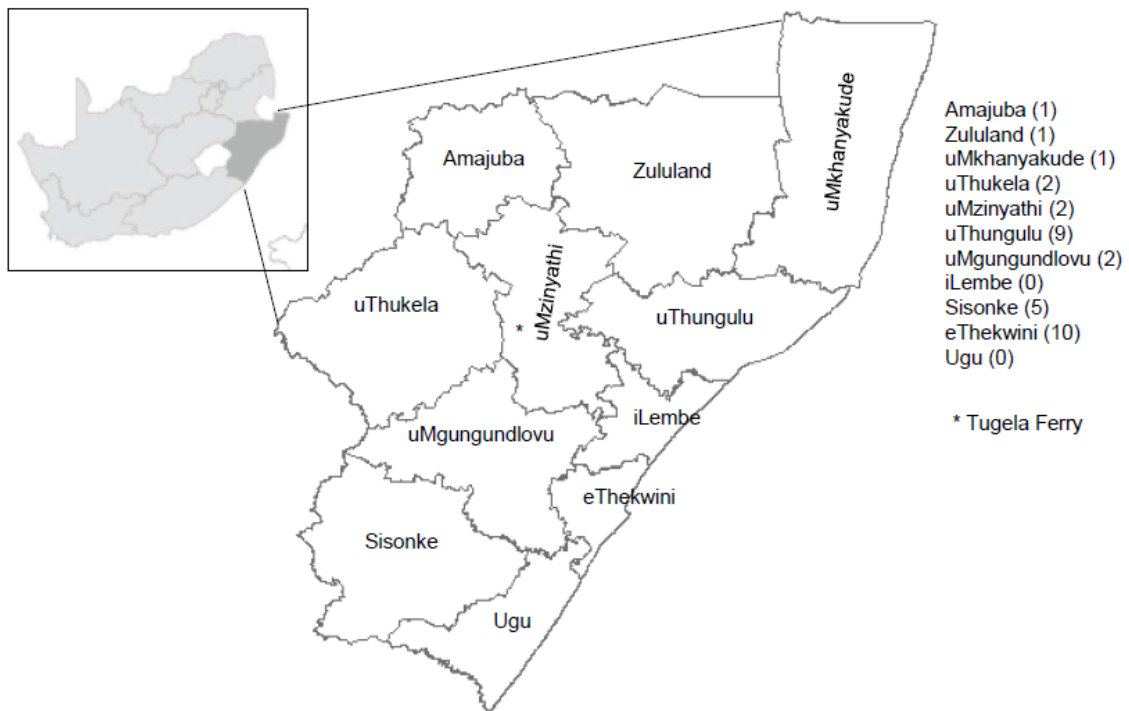
\*EMB, ethambutol; INH, isoniazid; MIRU-VNTR, mycobacterial interspersed repetitive units-variable-number tandem-repeat; PZA, pyrazinamide; R, resistant; RIF, rifampin; S, sensitive; STR, streptomycin.

†Promoter mutation, cross-resistance to thioamides.

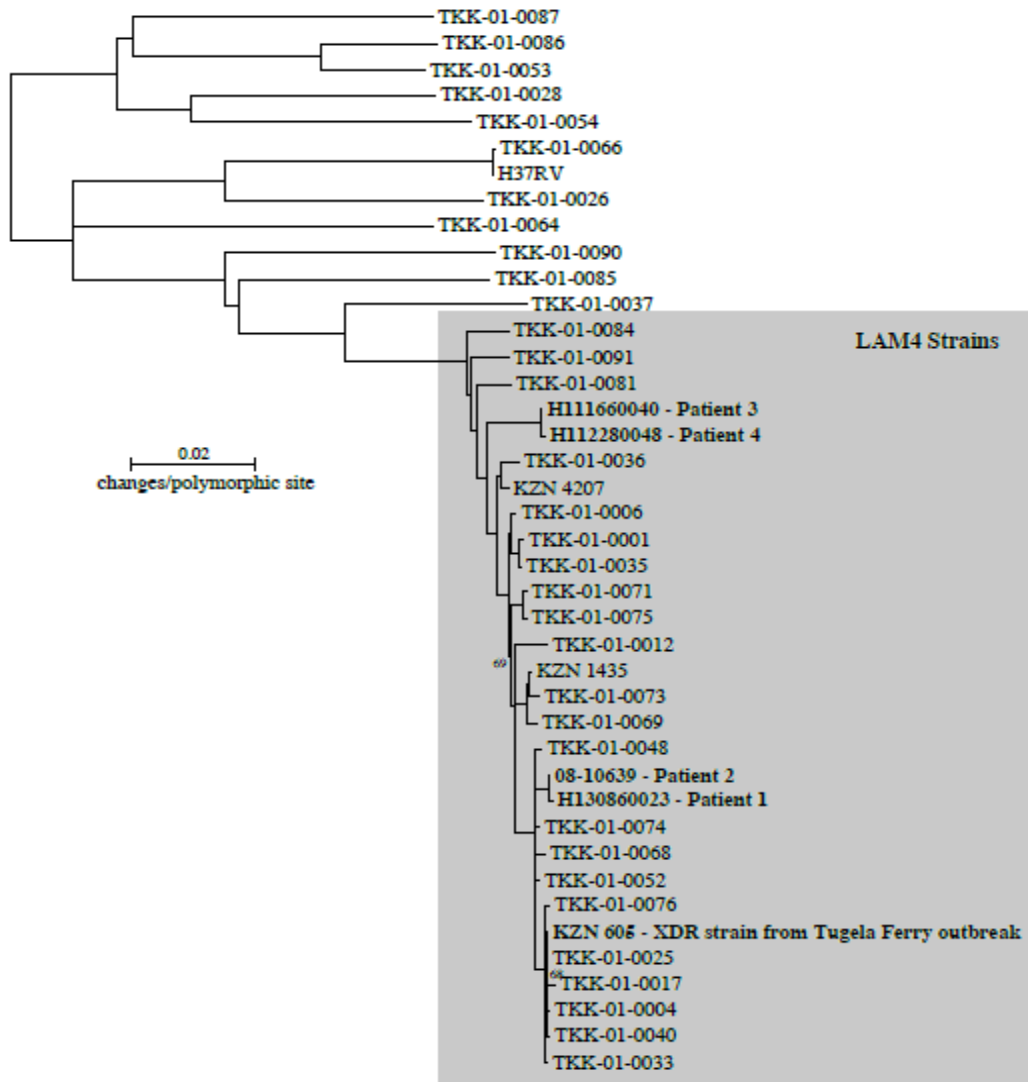
§*Escherichia coli* L533P

‡No resistance single-nucleotide polymorphisms in rpsL or rrs.

¶1 bp insertion in codon 153.



Technical Appendix Figure 1. Isolates sequenced from KwaZulu-Natal (KZN), South Africa, with number from each district sampled as part of KZNSUR project. Inset: Map of South Africa with KZN shaded



Technical Appendix Figure 2. Phylogenetic representation of isolates collected from the United Kingdom (patients 1–4) and KZN (33) Nodes with bootstrap values <80 are indicated. Sequencing data were submitted to the Sequence Read Archive with identifiers: PRJNA198182, PRJNA198181, PRJNA198148, PRJNA198149, PRJNA198124, PRJNA198185, PRJNA198180, PRJNA198186, PRJNA198176, PRJNA198108, PRJNA198103, PRJNA198130, PRJNA183521, PRJNA198168, PRJNA227150, PRJNA198163, PRJNA198172, PRJNA198106, PRJNA183515, PRJNA198122, PRJNA227148, PRJNA198135, PRJNA198128, PRJNA198147, PRJNA198169, PRJNA198143, PRJNA198113, PRJNA198167, PRJNA198170, PRJNA198131, PRJNA227149, PRJNA198179, PRJNA198132, PRJNA183519, PRJNA198161, PRJNA198159 ERS568284, ERS568285, ERS568286, ERS 568287