

MTBC ERR2041727

MTBC functional genotyping report - RUO

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Date: 05/18/20 13:07:02
Name: MTBC ERR2041727

Run_accession: ERR2041727

Predicted lineage:	4	Euro-American
	4.4	Euro-American
	4.4.1	Euro-American
	4.4.1.1	Euro-American
		(S-type)

- Predicted resistance :

Rifampicin (RMP)
Ethambutol (EMB)
Isoniazid (INH)
Pyrazinamide (PZA)
- Predicted susceptibility:

Para-aminosalicylic acid (PAS)
Bedaquiline (BED)
Clofazimine (CLO)
Ethionamide (ETH)
Linezolid (LZD)
- Unknown:

Fluoroquinolone (FQ)
Ofloxacin (OFX)
Capreomycin (CAP)
Moxifloxacin (MFL)
Amikacin (AMK)
Kanamycin (KAN)
Levofloxacin (LFX)
Streptomycin (SM)

Multidrug-resistant: True
Extensively drug-resistant: False

Details

Resistance

Mutations

Antibiotic	Locus	Codon position	Genomic position	WT	Call	Conclusion	Coverage	Relative coverage	Notes
Ethambutol	embA_promoter		4243222	C	T	Unknown	106	99.07%	atypical
Ethambutol	embB	1000		M	R	Resistant	39	100.00%	
Isoniazid	katG	315		S	T	Resistant	99	97.06%	
Pyrazinamide	pncA	19		L	P	Resistant	147	98.00%	
Rifampicin	rpoB	445		H	R	Resistant	88	96.70%	

Premature stop codons

No matches found.

Insertions/deletions

No matches found.

Quality metrics I

Antibiotic	Locus	Gene	QC Passed	Size	Number of bases covered	Average coverage	Start	Stop
INH	(Rv0565c_promoter)	Rv0565c_promoter	V	77	77	97.17	1	77
	(Rv1979c_promoter)	Rv1979c_promoter	V	178	178	100.88	1	178
	(Rv2671_promoter)	Rv2671_promoter	V	1108	1108	117.55	1	1108
	(ahpC_promoter)	ahpC_promoter	V	105	105	152.13	1	105
	(ald_promoter)	ald_promoter	V	65	65	128.86	1	65
	(alr_promoter)	alr_promoter	V	293	293	246.10	1	293
AMK, KAN	(atpE_promoter)	atpE_promoter	V	48	48	132.42	1	48
	(ddn_promoter)	ddn_promoter	V	111	111	91.86	1	111
EMB	(eis_promoter)	eis_promoter	V	139	139	105.72	1	139
EMB	(embA_promoter)	embA_promoter	V	85	85	97.87	1	85
	(ethA_promoter)	ethA_promoter	V	75	75	81.55	1	75
ETH, INH	(fabG1_promoter)	fabG1_promoter	V	140	140	134.96	1	140
	(fbiA_promoter)	fbiA_promoter	V	401	401	141.52	1	401
	(fbiC_promoter)	fbiC_promoter	V	249	249	119.05	1	249
	(fgd1_promoter)	fgd1_promoter	V	77	77	103.39	1	77
	(gidB_promoter)	gidB_promoter	V	131	131	84.78	1	131
	(gyrA_promoter)	gyrA_promoter	V	34	34	123.47	1	34
	(gyrB_promoter)	gyrB_promoter	V	242	242	209.76	1	242
	(inhA_promoter)	inhA_promoter	V	855	855	113.28	1	855
	(katG_promoter)	katG_promoter	V	37	37	139.49	1	37
	(mmpR_promoter)	mmpR_promoter	V	84	84	105.40	1	84
	(mshA_promoter)	mshA_promoter	V	47	47	129.36	1	47
	(nat_promoter)	nat_promoter	V	251	251	177.77	1	251
	(ndh_promoter)	ndh_promoter	V	141	141	150.34	1	141
	(pepQ_promoter)	pepQ_promoter	V	33	33	104.09	1	33
PZA	(pncA_promoter)	pncA_promoter	V	40	40	124.68	1	40
	(rplC_promoter)	rplC_promoter	V	16	16	144.00	1	16
	(rpoB_promoter)	rpoB_promoter	V	497	497	129.46	1	497
	(rpsA_promoter)	rpsA_promoter	V	162	162	85.26	1	162
	(rpsL_promoter)	rpsL_promoter	V	248	248	164.97	1	248
LZD	(rrl)	rrl	V	3138	3138	106.92	1	3138
	(rrl_promoter)	rrl_promoter	V	275	275	75.05	1	275
AMK, CAP, KAN, SM	(rrs)	rrs	V	1537	1537	110.37	1	1537
	(rrs_promoter)	rrs_promoter	V	103	103	131.38	1	103
	(thyX_promoter)	thyX_promoter	V	243	243	128.86	1	243
CAP	(tlyA_promoter)	tlyA_promoter	V	101	101	87.64	1	101
	(ubiA_promoter)	ubiA_promoter	V	6	6	103.67	1	6
	(whiB7_promoter)	whiB7_promoter	V	429	429	118.17	1	429

Antibiotic	Locus	Gene	QC Passed	Size	Number of bases covered	Average coverage	Start	Stop
FQ, LFX, OFX	Rv0005	gyrB	V	2028	2028	165.19	1	2028
FQ, LFX, MFL, OFX	Rv0006	gyrA	V	2517	2517	126.51	1	2517
	Rv0341	iniB	V	1440	1440	60.45	1	1440
EMB, INH	Rv0342	iniA	V	1923	1923	79.16	1	1923
EMB, INH	Rv0343	iniC	V	1482	1482	86.71	1	1482
	Rv0407	fgd1	V	1011	1011	92.69	1	1011
ETH	Rv0486	mshA	V	1443	1443	95.49	1	1443
	Rv0565c	Rv0565c	V	1461	1461	124.77	1	1461
RMP	Rv0667	rpoB	V	3519	3519	116.76	1	3519
RMP	Rv0668	rpoC	V	3951	3951	111.65	1	3951
	Rv0676c	mmpL5	V	2895	2895	113.15	1	2895
	Rv0677c	mmpS5	V	429	429	114.27	1	429
BED, CLO	Rv0678	mmpR	V	498	498	92.82	1	498
SM	Rv0682	rpsL	V	375	375	199.13	1	375
LZD	Rv0701	rpIC	V	654	654	102.91	1	654
	Rv1173	fbiC	V	2571	2571	112.33	1	2571
EMB	Rv1267c	embR	V	1167	1167	111.12	1	1167
	Rv1305	atpE	V	246	246	143.74	1	246
	Rv1483	fabG1	V	744	744	111.53	1	744
ETH, INH	Rv1484	inhA	V	810	810	89.02	1	810
PZA	Rv1630	rpsA	V	1446	1446	118.56	1	1446
CAP	Rv1694	tlyA	V	807	807	94.23	1	807
INH	Rv1854c	ndh	V	1392	1392	109.93	1	1392
INH	Rv1908c	katG	V	2223	2223	108.24	1	2223
	Rv1979c	Rv1979c	V	1446	1446	144.32	1	1446
PZA	Rv2043c	pncA	V	561	561	151.22	1	561
INH	Rv2245	kasA	V	1251	1251	69.44	1	1251
	Rv2416c	eis	V	1209	1209	126.74	1	1209
INH	Rv2428	ahpC	V	588	588	169.21	1	588
PAS	Rv2447c	folC	V	1464	1464	68.46	1	1464
	Rv2535c	pepQ	V	1119	1119	102.18	1	1119
PAS	Rv2671	ribD	V	777	777	103.92	1	777
	Rv2763c	dfrA	V	480	480	78.51	1	480
PAS	Rv2764c	thyA	V	792	792	135.45	1	792
	Rv2780	ald	V	1116	1116	114.30	1	1116
	Rv3262	fbiB	V	1347	1347	80.17	1	1347
	Rv3423c	alr	V	1227	1227	127.53	1	1227
	Rv3457c	rpoA	V	1044	1044	133.74	1	1044
	Rv3547	ddn	V	456	456	106.09	1	456
	Rv3566c	nat	V	852	852	152.49	1	852
PZA	Rv3601c	panD	V	420	420	104.67	1	420
	Rv3608c	folP1	V	843	843	94.98	1	843
	Rv3609c	folE	V	609	609	119.51	1	609
	Rv3696c	glpK	V	1554	1554	150.07	1	1554
	Rv3792	aftA	V	1932	1932	100.75	1	1932
EMB	Rv3793	embC	V	3285	3285	104.19	1	3285
EMB	Rv3794	embA	V	3285	3285	89.35	1	3285
EMB	Rv3795	embB	V	3297	3297	102.68	1	3297
	Rv3806c	ubiA	V	909	909	118.62	1	909
ETH	Rv3854c	ethA	V	1470	1470	150.50	1	1470
	Rv3855	ethR	V	651	651	115.69	1	651
CAP, SM	Rv3919c	gid	V	675	675	112.00	1	675

Quality metrics II

Antibiotic	Locus	QC Passed	Unresolved bases	Start Codon	Stop Codon	Internal stop codon
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Antibiotic	Locus	QC Passed	Unresolved bases	Start Codon	Stop Codon	Internal stop codon
INH	(Rv0565c_promoter)	V	0			
	(Rv1979c_promoter)	V	0			
	(Rv2671_promoter)	V	0			
	(ahpC_promoter)	V	0			
	(ald_promoter)	V	0			
	(alr_promoter)	V	2			
	(atpE_promoter)	V	0			
AMK, KAN	(ddn_promoter)	V	0			
	(eis_promoter)	V	0			
EMB	(embA_promoter)	V	0			
ETH, INH	(ethA_promoter)	V	0			
	(fabG1_promoter)	V	0			
	(fbiA_promoter)	V	0			
INH	(fbiC_promoter)	V	0			
	(fgd1_promoter)	V	0			
	(gidB_promoter)	V	0			
	(gyrA_promoter)	V	0			
	(gyrB_promoter)	V	0			
	(inhA_promoter)	V	0			
	(katG_promoter)	V	0			
	(mmpR_promoter)	V	0			
	(mshA_promoter)	V	0			
	(nat_promoter)	V	0			
	(ndh_promoter)	V	0			
	(pepQ_promoter)	V	0			
	(pncA_promoter)	V	0			
	(rplC_promoter)	V	0			
PZA	(rpoB_promoter)	V	0			
	(rpsA_promoter)	V	0			
	(rpsL_promoter)	V	0			
	(rrl)	V	0			
LZD	(rrl_promoter)	V	0			
AMK, CAP, KAN, SM	(rrs)	V	0			
CAP	(rrs_promoter)	V	0			
	(thyX_promoter)	V	0			
	(tlyA_promoter)	V	0			
	(ubiA_promoter)	V	0			
	(whiB7_promoter)	V	0			
FQ, LFX, OFX	Rv0005	V	0	Yes	Yes	No
FQ, LFX, MFL, OFX	Rv0006	V	0	Yes	Yes	No
EMB, INH	Rv0341	V	0	Yes	Yes	No
	Rv0342	V	0	Yes	Yes	No
EMB, INH	Rv0343	V	0	Yes	Yes	No
ETH	Rv0407	V	0	Yes	Yes	No
	Rv0486	V	0	Yes	Yes	No
	Rv0565c	V	0	Yes	Yes	No
RMP	Rv0667	V	0	Yes	Yes	No
RMP	Rv0668	V	0	Yes	Yes	No
BED, CLO SM	Rv0676c	V	0	Yes	Yes	No
	Rv0677c	V	0	Yes	Yes	No
	Rv0678	V	0	Yes	Yes	No
	Rv0682	V	0	Yes	Yes	No
	Rv0701	V	0	Yes	Yes	No
LZD	Rv1173	V	0	Yes	Yes	No
	Rv1267c	V	0	Yes	Yes	No
	Rv1305	V	0	Yes	Yes	No

Antibiotic	Locus	QC Passed	Unresolved bases	Start Codon	Stop Codon	Internal stop codon
	Rv1483	V	0	Yes	Yes	No
ETH, INH	Rv1484	V	0	Yes	Yes	No
PZA	Rv1630	V	0	Yes	Yes	No
CAP	Rv1694	V	0	Yes	Yes	No
INH	Rv1854c	V	0	Yes	Yes	No
INH	Rv1908c	V	0	Yes	Yes	No
	Rv1979c	V	0	Yes	Yes	No
PZA	Rv2043c	V	0	Yes	Yes	No
INH	Rv2245	V	0	Yes	Yes	No
	Rv2416c	V	0	Yes	Yes	No
INH	Rv2428	V	0	Yes	Yes	No
PAS	Rv2447c	V	0	Yes	Yes	No
	Rv2535c	V	0	Yes	Yes	No
PAS	Rv2671	V	0	Yes	Yes	No
	Rv2763c	V	0	Yes	Yes	No
PAS	Rv2764c	V	0	Yes	Yes	No
	Rv2780	V	0	Yes	Yes	No
	Rv3262	V	0	Yes	Yes	No
	Rv3423c	V	0	Yes	Yes	No
	Rv3457c	V	0	Yes	Yes	No
	Rv3547	V	0	Yes	Yes	No
	Rv3566c	V	0	Yes	Yes	No
PZA	Rv3601c	V	0	Yes	Yes	No
	Rv3608c	V	0	Yes	Yes	No
	Rv3609c	V	0	Yes	Yes	No
	Rv3696c	V	0	Yes	Yes	No
	Rv3792	V	0	Yes	Yes	No
EMB	Rv3793	V	0	Yes	Yes	No
EMB	Rv3794	V	0	Yes	Yes	No
EMB	Rv3795	V	0	Yes	Yes	No
	Rv3806c	V	0	Yes	Yes	No
ETH	Rv3854c	V	0	Yes	Yes	No
	Rv3855	V	0	Yes	Yes	No
CAP, SM	Rv3919c	V	0	Yes	Yes	No

Quality metrics III

Antibiotic	Locus	QC Passed	NA mutations	AA mutations	Unknown mutations	Number of deletions	Unknown deletions	Number of insertions	Unknown insertions
	(Rv0565c_promoter)	V	0		0	0	0	0	0
	(Rv1979c_promoter)	V	1		1	0	0	0	0
	(Rv2671_promoter)	V	0		0	0	0	0	0
INH	(ahpC_promoter)	V	0		0	0	0	0	0
	(ald_promoter)	V	1		1	0	0	0	0
	(alr_promoter)	V	0		0	0	0	0	0
	(atpE_promoter)	V	0		0	0	0	0	0
	(ddn_promoter)	V	0		0	0	0	0	0
AMK, KAN	(eis_promoter)	V	0		0	0	0	0	0
EMB	(embA_promoter)	V	1		1	0	0	0	0
	(ethA_promoter)	V	0		0	0	0	0	0
ETH, INH	(fabG1_promoter)	V	0		0	0	0	0	0
	(fbiA_promoter)	V	1		1	0	0	0	0
	(fbiC_promoter)	V	0		0	0	0	0	0
	(fgd1_promoter)	V	0		0	0	0	0	0
	(gidB_promoter)	V	0		0	0	0	0	0
	(gyrA_promoter)	V	0		0	0	0	0	0
	(gyrB_promoter)	V	0		0	0	0	0	0
	(inhA_promoter)	V	0		0	0	0	0	0
INH	(katG_promoter)	V	0		0	0	0	0	0

Antibiotic	Locus	QC Passed	NA mutations	AA mutations	Unknown mutations	Number of deletions	Unknown deletions	Number of insertions	Unknown insertions
PZA	(mmpR_promoter)	V	0		0	0	0	0	0
	(mshA_promoter)	V	0		0	0	0	0	0
	(nat_promoter)	V	0		0	0	0	0	0
	(ndh_promoter)	V	0		0	0	0	0	0
	(pepQ_promoter)	V	0		0	0	0	0	0
	(pncA_promoter)	V	0		0	0	0	0	0
	(rplC_promoter)	V	0		0	0	0	0	0
	(rpoB_promoter)	V	0		0	0	0	0	0
	(rpsA_promoter)	V	0		0	0	0	0	0
	(rpsL_promoter)	V	1		1	0	0	0	0
LZD	(rrl)	V	0		0	0	0	0	0
	(rrl_promoter)	V	0		0	0	0	0	0
AMK, CAP, KAN, SM	(rrs)	V	1		1	0	0	0	0
CAP	(rrs_promoter)	V	0		0	0	0	0	0
	(thyX_promoter)	V	0		0	0	0	0	0
	(tlyA_promoter)	V	0		0	0	0	0	0
	(ubiA_promoter)	V	0		0	0	0	0	0
	(whiB7_promoter)	V	0		0	0	0	0	0
FQ, LFX, OFX	Rv0005	V	0	0	0	0	0	0	0
FQ, LFX, MFL, OFX	Rv0006	V	3	3	3	0	0	0	0
EMB, INH	Rv0341	V	0	0	0	0	0	0	0
	Rv0342	V	1	0	0	0	0	0	0
EMB, INH	Rv0343	V	0	0	0	0	0	0	0
	Rv0407	V	0	0	0	0	0	0	0
ETH	Rv0486	V	0	0	0	0	0	0	0
	Rv0565c	V	0	0	0	0	0	0	0
RMP	Rv0667	V	1	1	0	0	0	0	0
RMP	Rv0668	V	0	0	0	0	0	0	0
	Rv0676c	V	1	1	1	0	0	0	0
	Rv0677c	V	0	0	0	0	0	0	0
BED, CLO	Rv0678	V	0	0	0	0	0	0	0
SM	Rv0682	V	0	0	0	0	0	0	0
LZD	Rv0701	V	0	0	0	0	0	0	0
EMB	Rv1173	V	0	0	0	0	0	0	0
	Rv1267c	V	0	0	0	0	0	0	0
	Rv1305	V	0	0	0	0	0	0	0
	Rv1483	V	0	0	0	0	0	0	0
ETH, INH	Rv1484	V	0	0	0	0	0	0	0
PZA	Rv1630	V	0	0	0	0	0	0	0
CAP	Rv1694	V	1	0	0	0	0	0	0
INH	Rv1854c	V	1	1	1	0	0	0	0
INH	Rv1908c	V	1	1	0	0	0	0	0
	Rv1979c	V	0	0	0	0	0	0	0
	Rv2043c	V	1	1	0	0	0	0	0
INH	Rv2245	V	0	0	0	0	0	0	0
	Rv2416c	V	0	0	0	0	0	0	0
	Rv2428	V	0	0	0	0	0	0	0
PAS	Rv2447c	V	0	0	0	0	0	0	0
	Rv2535c	V	0	0	0	0	0	0	0
	Rv2671	V	0	0	0	0	0	0	0
PAS	Rv2763c	V	0	0	0	0	0	0	0
	Rv2764c	V	0	0	0	0	0	0	0
	Rv2780	V	0	0	0	0	0	0	0
	Rv3262	V	0	0	0	0	0	0	0
	Rv3423c	V	0	0	0	0	0	0	0
	Rv3457c	V	0	0	0	0	0	0	0

Antibiotic	Locus	QC Passed	NA mutations	AA mutations	Unknown mutations	Number of deletions	Unknown deletions	Number of insertions	Unknown insertions
PZA	Rv3547	V	0	0	0	0	0	0	0
	Rv3566c	V	1	1	1	0	0	0	0
	Rv3601c	V	0	0	0	0	0	0	0
	Rv3608c	V	0	0	0	0	0	0	0
	Rv3609c	V	0	0	0	0	0	0	0
	Rv3696c	V	0	0	0	0	0	0	0
	Rv3792	V	1	0	0	0	0	0	0
EMB	Rv3793	V	1	0	0	0	0	0	0
EMB	Rv3794	V	0	0	0	0	0	0	0
EMB	Rv3795	V	1	1	0	0	0	0	0
ETH	Rv3806c	V	0	0	0	0	0	0	0
	Rv3854c	V	0	0	0	0	0	0	0
	Rv3855	V	0	0	0	0	0	0	0
CAP, SM	Rv3919c	V	0	0	0	1	1	0	0

Genomic variants

Antibiotic	Locus	Gene	Size	Position	Genomic position	Type	WT	Call	Relative coverage	Strand
EMB	(Rv1979c_promoter)	Rv1979c_promoter	178	50	2223293	Mutation	A	G	100.00%	neg
	Rv3792	aftA	1932	1032	4238963	Mutation	C (H)	T (H)	96.77%	pos
	(ald_promoter)	ald_promoter	65	34	3086788	Mutation	T	C	100.00%	pos
	(alr_promoter)	alr_promoter	293	51	3841663	Mutation	G	A	11.45%	neg
	(alr_promoter)	alr_promoter	293	52	3841662	Mutation	A	G	38.25%	neg
	(alr_promoter)	alr_promoter	293	89	3841625	Mutation	T	C	22.30%	neg
	(alr_promoter)	alr_promoter	293	124	3841590	Deletion	G		18.03%	neg
	(alr_promoter)	alr_promoter	293	130	3841584	Mutation	C	A	18.67%	neg
	(alr_promoter)	alr_promoter	293	132	3841582	Mutation	A	G	17.96%	neg
	(alr_promoter)	alr_promoter	293	136	3841578	Mutation	G	T	18.22%	neg
	(alr_promoter)	alr_promoter	293	140	3841574	Mutation	T	G	17.62%	neg
	(alr_promoter)	alr_promoter	293	143	3841571	Deletion	A		14.69%	neg
	(alr_promoter)	alr_promoter	293	146	3841568	Mutation	G	A	15.45%	neg
	(alr_promoter)	alr_promoter	293	168	3841546	Mutation	C	A	10.00%	neg
	(embA_promoter)	embA_promoter	85	75	4243222	Mutation	C	T	99.07%	pos
EMB	Rv3795	embB	3297	2999	4249512	Mutation	T (M)	G (R)	100.00%	pos
EMB	Rv3793	embC	3285	2781	4242643	Mutation	C (R)	T (R)	97.06%	pos
PAS	(fbiA_promoter)	fbiA_promoter	401	180	3640321	Mutation	T	A	97.90%	pos
	Rv3262	fbiB	1347	513	3642047	Mutation	G (A)	C (A)	10.53%	pos
	Rv1173	fbiC	2571	235	1303165	Mutation	A (S)	C (R)	10.08%	pos
	Rv2447c	folC	1464	276	2747323	Mutation	C (R)	A (R)	11.32%	neg
CAP, SM	Rv3919c	gid	675	115	4408088	Deletion	C		96.00%	neg
FQ, LFX, MFL, OFX	Rv0006	gyrA	2517	61	7362	Mutation	G (E)	C (Q)	97.06%	pos
FQ, LFX, MFL, OFX	Rv0006	gyrA	2517	284	7585	Mutation	G (S)	C (T)	98.67%	pos
FQ, LFX, MFL, OFX	Rv0006	gyrA	2517	2003	9304	Mutation	G (G)	A (D)	97.83%	pos
EMB, INH	Rv0342	iniA	1923	534	411371	Mutation	T (G)	C (G)	94.83%	pos
	Rv0341	iniB	1440	919	410280	Mutation	T (L)	C (L)	13.89%	pos
	Rv1908c	katG	2223	944	2155168	Mutation	G (S)	C (T)	97.06%	neg
INH	Rv0676c	mmpL5	2895	2842	775639	Mutation	A (I)	G (V)	99.15%	neg
	Rv3566c	nat	852	619	4007564	Mutation	G (G)	A (R)	95.89%	neg
	Rv1854c	ndh	1392	53	2102990	Mutation	T (V)	C (A)	98.64%	neg
PZA	Rv2043c	pncA	561	56	2289186	Mutation	T (L)	C (P)	98.67%	neg
RMP	Rv0667	rpoB	3519	1334	761140	Mutation	A (H)	G (R)	96.70%	pos
	(rpsL_promoter)	rpsL_promoter	248	84	781395	Mutation	T	C	98.76%	pos
AMK, CAP, KAN, SM	(rrs)	rrs	1537	1112	1472957	Mutation	C	A	96.59%	pos
CAP	Rv1694	tlyA	807	33	1917972	Mutation	A (L)	G (L)	100.00%	pos

Algorithm settings	Value
Resistance database	Curated database (version 6.0)

Lineage

Mutations:

Lineage	Locus	Position	WT	Call	Coverage	Relative coverage	Notes
4 Euro-American	Rv0835	171	C	T	108	97.30%	
4.4 Euro-American	Rv3834c	1029	C	T	73	98.65%	
4.4.1 Euro-American	Rv3708c	660	C	T	92	96.84%	
4.4.1.1 Euro-American (S-type)	Rv0291	684	G	A	70	98.59%	

Quality metrics I

Locus	QC Passed	Size	Number of bases covered	Average coverage	Start	Stop
Rv0058	V	2625	2625	137.97	1	2625
Rv0098	V	552	552	194.34	1	552
Rv0284	V	3993	3993	102.25	1	3993
Rv0291	V	1386	1386	70.14	1	1386
Rv0338c	V	2649	2649	114.33	1	2649
Rv0411c	V	987	987	57.41	1	987
Rv0425c	V	4620	4620	82.02	1	4620
Rv0450c	V	2904	2904	103.09	1	2904
Rv0524	V	1389	1389	89.95	1	1389
Rv0668	V	3951	3951	111.65	1	3951
Rv0684	V	2106	2106	119.67	1	2106
Rv0697	V	1440	1440	214.93	1	1440
Rv0781	V	711	711	221.53	1	711
Rv0798c	V	798	798	122.30	1	798
Rv0835	V	645	645	128.95	1	645
Rv0973c	V	2004	2004	109.90	1	2004
Rv1013	V	1635	1635	90.41	1	1635
Rv1018c	V	1488	1488	103.16	1	1488
Rv1111c	V	984	984	80.09	1	984
Rv1299	V	1074	1074	126.73	1	1074
Rv1324	V	915	915	80.68	1	915
Rv1326c	V	2196	2196	162.44	1	2196
Rv1332	V	657	657	87.27	1	657
Rv1333	V	1035	1035	66.35	1	1035
Rv1524	V	1245	1245	103.01	1	1245
Rv1552	V	1752	1752	137.56	1	1752
Rv1599	V	1317	1317	87.48	1	1317
Rv1617	V	1419	1419	92.88	1	1419
Rv1640c	V	3519	3519	108.90	1	3519
Rv1661	X	6381	6200	72.75	1	6381
Rv1662	V	4809	4809	123.07	1	4809
Rv2152c	V	1485	1485	75.34	1	1485
Rv2231c	V	1095	1095	85.04	1	1095
Rv2343c	V	1920	1920	74.15	1	1920
Rv2397c	V	1056	1056	100.64	1	1056
Rv2515c	V	1248	1248	88.42	1	1248
Rv2555c	V	2715	2715	107.16	1	2715
Rv2707	V	975	975	101.53	1	975
Rv2907c	V	531	531	121.77	1	531
Rv2936	V	996	996	123.13	1	996
Rv3029c	V	801	801	108.87	1	801
Rv3097c	V	1314	1314	125.45	1	1314

Locus	QC Passed	Size	Number of bases covered	Average coverage	Start	Stop
Rv3101c	V	894	894	100.83	1	894
Rv3111	V	513	513	118.81	1	513
Rv3198c	V	2103	2103	96.73	1	2103
Rv3336c	V	1011	1011	90.56	1	1011
Rv3417c	V	1620	1620	79.68	1	1620
Rv3538	V	861	861	141.90	1	861
Rv3683	V	960	960	108.92	1	960
Rv3708c	V	1038	1038	89.63	1	1038
Rv3782	V	915	915	139.78	1	915
Rv3794	V	3285	3285	89.35	1	3285
Rv3795	V	3297	3297	102.68	1	3297
Rv3800c	V	5202	5202	80.39	1	5202
Rv3834c	V	1260	1260	81.35	1	1260
Rv3843c	V	1029	1029	119.76	1	1029
Rv3910	V	3555	3555	98.41	1	3555
Rv3915	V	1221	1221	156.54	1	1221

Quality metrics II

Locus	QC Passed	Unresolved bases	Start Codon	Stop Codon	Internal stop codon
Rv0058	V	0	Yes	Yes	No
Rv0098	V	0	Yes	Yes	No
Rv0284	V	0	Yes	Yes	No
Rv0291	V	0	Yes	Yes	No
Rv0338c	V	0	Yes	Yes	No
Rv0411c	V	0	Yes	Yes	No
Rv0425c	V	0	Yes	Yes	No
Rv0450c	V	0	Yes	Yes	No
Rv0524	V	0	Yes	Yes	No
Rv0668	V	0	Yes	Yes	No
Rv0684	V	0	Yes	Yes	No
Rv0697	V	0	Yes	Yes	No
Rv0781	V	0	Yes	Yes	No
Rv0798c	V	0	Yes	Yes	No
Rv0835	V	0	Yes	Yes	No
Rv0973c	V	0	Yes	Yes	No
Rv1013	V	0	Yes	Yes	No
Rv1018c	V	0	Yes	Yes	No
Rv1111c	V	0	Yes	Yes	No
Rv1299	V	0	Yes	Yes	No
Rv1324	V	0	Yes	Yes	No
Rv1326c	V	0	Yes	Yes	No
Rv1332	V	0	Yes	Yes	No
Rv1333	V	0	Yes	Yes	No
Rv1524	V	0	Yes	Yes	No
Rv1552	V	0	Yes	Yes	No
Rv1599	V	0	Yes	Yes	No
Rv1617	V	0	Yes	Yes	No
Rv1640c	V	0	Yes	Yes	No
Rv1661	X	11	Yes	Yes	No
Rv1662	V	0	Yes	Yes	No
Rv2152c	V	0	Yes	Yes	No
Rv2231c	V	0	Yes	Yes	No
Rv2343c	V	0	Yes	Yes	No
Rv2397c	V	0	Yes	Yes	No
Rv2515c	V	0	Yes	Yes	No
Rv2555c	V	0	Yes	Yes	No
Rv2707	V	0	Yes	Yes	No

Locus	QC Passed	Unresolved bases	Start Codon	Stop Codon	Internal stop codon
Rv2907c	V	0	Yes	Yes	No
Rv2936	V	0	Yes	Yes	No
Rv3029c	V	0	Yes	Yes	No
Rv3097c	V	0	Yes	Yes	No
Rv3101c	V	0	Yes	Yes	No
Rv3111	V	0	Yes	Yes	No
Rv3198c	V	0	Yes	Yes	No
Rv3336c	V	0	Yes	Yes	No
Rv3417c	V	0	Yes	Yes	No
Rv3538	V	0	Yes	Yes	No
Rv3683	V	0	Yes	Yes	No
Rv3708c	V	0	Yes	Yes	No
Rv3782	V	0	Yes	Yes	No
Rv3794	V	0	Yes	Yes	No
Rv3795	V	0	Yes	Yes	No
Rv3800c	V	0	Yes	Yes	No
Rv3834c	V	0	Yes	Yes	No
Rv3843c	V	0	Yes	Yes	No
Rv3910	V	0	Yes	Yes	No
Rv3915	V	0	Yes	Yes	No

Quality metrics III

Locus	QC Passed	NA mutations	AA mutations	Number of deletions	Number of insertions
Rv0058	V	1	1	0	0
Rv0098	V	0	0	0	0
Rv0284	V	1	1	0	0
Rv0291	V	1	0	0	0
Rv0338c	V	3	3	0	0
Rv0411c	V	0	0	0	0
Rv0425c	V	1	1	0	0
Rv0450c	V	2	1	0	0
Rv0524	V	0	0	0	0
Rv0668	V	0	0	0	0
Rv0684	V	0	0	0	0
Rv0697	V	0	0	0	0
Rv0781	V	1	0	0	1
Rv0798c	V	0	0	0	0
Rv0835	V	0	0	0	0
Rv0973c	V	0	0	0	0
Rv1013	V	0	0	0	0
Rv1018c	V	0	0	0	0
Rv1111c	V	0	0	0	0
Rv1299	V	0	0	0	0
Rv1324	V	0	0	0	0
Rv1326c	V	0	0	0	0
Rv1332	V	0	0	0	0
Rv1333	V	0	0	0	0
Rv1524	V	0	0	0	0
Rv1552	V	1	0	0	0
Rv1599	V	0	0	0	0
Rv1617	V	0	0	0	0
Rv1640c	V	0	0	0	0
Rv1661	X	0	0	1	0
Rv1662	V	1	1	0	0
Rv2152c	V	0	0	0	0
Rv2231c	V	0	0	0	0
Rv2343c	V	0	0	0	0

Locus	QC Passed	NA mutations	AA mutations	Number of deletions	Number of insertions
Rv2397c	V	0	0	0	0
Rv2515c	V	0	0	0	0
Rv2555c	V	0	0	0	0
Rv2707	V	0	0	0	0
Rv2907c	V	0	0	0	0
Rv2936	V	0	0	0	0
Rv3029c	V	0	0	0	0
Rv3097c	V	0	0	0	0
Rv3101c	V	0	0	0	0
Rv3111	V	0	0	0	0
Rv3198c	V	0	0	0	0
Rv3336c	V	0	0	0	0
Rv3417c	V	0	0	0	0
Rv3538	V	0	0	0	0
Rv3683	V	0	0	0	0
Rv3708c	V	2	0	0	0
Rv3782	V	0	0	0	0
Rv3794	V	0	0	0	0
Rv3795	V	1	1	0	0
Rv3800c	V	1	0	0	0
Rv3834c	V	2	0	0	0
Rv3843c	V	0	0	0	0
Rv3910	V	0	0	0	0
Rv3915	V	0	0	0	0

Run on 05/18/20 13:06:51 with plugin version 2.0.

Disclaimer

The resistance markers listed in this report were chosen based on an extensive body of research into genes associated with resistance or reduced susceptibility in MTBC, with additional refinement possible. None of the above has been clinically validated at this time. Therefore, the predictions provided in this report should not replace the current guidelines for phenotypical antimicrobial susceptibility testing.