Supplementary Data

Detecting mixed *Mycobacterium tuberculosis* infections and differences in drug susceptibility with WGS data

BY

Arlin Keo

(4257111)

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Bioinformatics, Master of Computer Science

Faculty Electrical Engineering, Mathematics and Computer Science

Delft University of Technology, the Netherlands

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Figure S1 MTBC phylogenetic tree

SNP-based phylogenetic tree of 5992 samples and reference genome H37Rv (CP003248.2). See file *MTBC5992.pdf* to view the phylogenetic tree.

A SNP-based phylogenetic tree was constructed from a global dataset of 5992 MTBC samples. In this bifurcating tree, each branch that represents a cluster of strains splits into two new monophyletic subclusters of strains that are genetically more closely related. These 'splits' were used to define clusters and subclusters of ≥10 strains, indicated by the vertical dark and light gray bars, colored bars indicate lineage 1-6 and *M. bovis*. 496 Clusters MTBC root excluded) were defined.

Table S1 Studies included in the global dataset

Total dataset used for analysis in this study. Lineages (L) were known beforehand from *Macaw* predictions, and LB is the *M. bovis* lineage. Other contain samples for which no MTBC lineage was predicted or was predicted as a mixed lineage infection by *Macaw*.

Study	Total	L1	L2	L3	L4	L5	L6	L7	LB	Other
Perdigão *et al.*, 2014	45	0	4	1	39	0	0	0	0	1
Gardy *et al.*, 2011	36	0	0	0	36	0	0	0	0	0
Biek *et al.*, 2012	31	0	0	0	0	0	0	0	31	0
Clark *et al.*, 2013	51	1	1	14	35	0	0	0	0	0
Zhang *et al.*, 2013	161	0	122	2	37	0	0	0	0	0
Blouin *et al.*, 2014)	17	0	0	0	0	0	0	0	0	17
Walker *et al.*, 2015	2113	271	94	786	850	10	8	0	15	79
Guerra-Assuncao *et al.*, 2015	2171	303	83	222	1374	0	0	0	5	184
Bryant *et al.*, 2013	199	8	31	10	145	0	0	0	0	5
Blouin *et al.*, 2012	5	0	2	0	0	0	2	1	0	0
Cohen *et al.*, 2015	443	8	100	9	291	0	0	0	0	35
Comas *et al.*, 2013	250	42	76	33	56	16	14	4	3	6
Merker *et al.*, 2015	154	0	154	0	0	0	0	0	0	0
Winglee, Manson McGuire, *et al.*, 2016	84	1	0	0	44	1	13	0	0	25
Casali *et al.*, 2014	1319	7	772	14	377	5	2	1	11	130
TB-ARC initiative, Broad Institute *	1138	160	400	88	422	0	0	0	1	67
Total	8217	801 (9.7%)	1839 (22.4%)	1179 (14.3%)	3706 (45.1%)	32 (0.3%)	39 (0.5%)	6 (0.0007%)	66 (0.8%)	549 (6.7%)

*https://olive.broadinstitute.org/projects/tb_arc

Table S2 Prototype data set

Dataset of 421 strains used for initial SNP analysis with HierBAPS. Lineages (L) were known beforehand from *Macaw* predictions, and LB is the *M. bovis* lineage.

Study	Total	L1	L2	L3	L4	L5	L6	L7	LB
Biek *et al.*, 2012	31	0	0	0	0	0	0	0	31
Blouin *et al.*, 2012	5	0	2	0	0	0	2	1	0
Cohen et al., 2015	385	8	89	7	281	0	0	0	0
Total	421	8 (1.9%)	91 (21.6%)	7 (1.7%)	281 (66.7%)	0 (0.0%)	2 (0.5%)	1 (0.2%)	31 (7.4%)

Table S3 Training set

Dataset of 5992 strains used to construct a phylogenetic tree and find associated SNPs for hierarchical clusters. Lineages (L) were known beforehand from *Macaw* predictions, and LB is the *M. bovis* lineage.

Study	Total	L1	L2	L3	L4	L5	L6	L7	LB
Biek *et al.*, 2012	31	0	0	0	0	0	0	0	31
Walker *et al.*, 2015	2011	270	94	786	846	0	0	0	15
Guerra-Assuncao *et al.*, 2015	1958	302	83	220	1348	0	0	0	5
Blouin *et al.*, 2012	2	0	2	0	0	0	0	0	0
Cohen *et al.*, 2015	382	8	88	7	279	0	0	0	0
Comas *et al.*, 2013	185	29	64	17	44	14	14	0	3
Winglee *et al.*, 2016	59	1	0	0	44	1	13	0	0
Casali *et al.*, 2014	1143	5	748	12	371	4	2	0	1
TB-ARC initiative, Broad Institute *	221	149	28	38	6	0	0	0	0
Total	5992	764 (12.8%)	1107 (18.5%)	1080 (18.0%)	2938 (49.0%)	19 (0.3%)	29 (0.5%)	0 (0.0%)	55 (0.9%)

*https://olive.broadinstitute.org/projects/tb_arc

Table S4 SNPs associated for HierBAPS clusters

SNPs associated for HierBAPS clusters, when > 95% of the strains in a lineage (L) harbor a SNP and <5% of strains in all other clusters. LB is the *M. bovis* lineage. Subclustering of only lineage 2 and 4 was used to define sublineages. Together with the remaining lineages SNPs were obtained and filtered for group.

Sublineage	L1	L2.1	L2.2	L3	L4.1	L4.2	L4.3	L6	L7	LB	Total
Samples	8	11	80	7	107	43	132	2	1	31	422
SNPs	17683	15547	115967	10207	86528	35106	114270	4236	2109	75946	477599
Distinct SNPs	2461	2598	3765	1748	7862	1748	2081	2536	2109	2643	29551
Cluster-specific SNPs	1014	0	489	462	0	197	216	478	1128	1679	5663
SNPs not within 10 bp	915	0	436	429	0	188	207	429	1001	1576	5181
Unique markers	906	0	436	429	0	188	207	427	992	1562	5147
Para-/**M**onophyletic group	M	P	M	M	P	M	M	M	M	M	-

Sublineage	LB	L1	L2.1	L2.2	L2.3	L3	L4.1	L4.2	L4.3	L4.4	L4.5	L4.6	L4.7	L4.8	L6	L7
Samples	31	8	10	43	38	7	22	22	25	43	2	130	7	31	2	1
SNPs	75946	17683	14141	62492	54881	10207	21287	20661	12284	35106	1696	112574	5845	26451	4236	2109
Distinct SNPs	2643	2461	2331	3393	2023	1748	1784	3129	1990	1748	1032	1750	1403	2036	2536	2109
Sublineage specific SNPs	1679	1014	0	0	66	462	201	2	72	197	0	231	107	196	478	1128
SNPs not within 10 bp	1573	916	0	0	66	426	178	2	68	189	0	217	94	174	426	1001
Unique markers	1558	907	0	0	66	426	178	2	67	189	0	217	94	174	424	992
Para-/**M**onophyletic group	M	M	P	P	M	M	M	P	M	M	M	M	M	M	M	M

Table S5 Numbers of filtered SNPs and markers per cluster

Number of presence- or absence-indicating SNPs and markers per cluster. Sibling clusters that share a direct ancestor are grouped together. SNPs were removed when they occurred within 10 bp of another SNP. For each presence-indicating SNP markers were generated and each for absence-indicating SNP three complementary markers were made. Markers were then filtered for there uniqueness within the cluster.

Cluster	Strains within cluster	Presence SNPs	Absence SNPs	Filtered presence SNPs	Filtered absence SNPs	Presence markers	Absence markers	Filtered presence markers	Filtered absence markers	Total markers	Leaf cluster
L1.1	40	84	0	82	0	82	0	82	0	82	FALSE
L1.2	724	12	0	12	0	12	0	10	0	10	FALSE
L1	764	504	0	474	0	474	0	470	0	470	FALSE
L2-L3-L4	5126	0	298	0	292	876	0	864	0	864	FALSE
L1.1.1	14	208	0	208	0	208	0	208	0	208	TRUE
L1.1.2	26	212	0	204	0	204	0	204	0	204	TRUE
L1.2.1	520	39	0	39	0	39	0	39	0	39	FALSE
L1.2.2	204	89	0	87	0	87	0	87	0	87	FALSE
L1.2.1.1	302	153	0	149	0	149	0	149	0	149	TRUE
L1.2.1.2	218	0	0	0	0	0	0	0	0	0	FALSE
L1.2.1.2.1	17	55	0	55	0	55	0	55	0	55	TRUE
L1.2.1.2.2	201	63	0	63	0	63	0	63	0	63	FALSE
L1.2.1.2.2.1	32	89	0	89	0	89	0	89	0	89	TRUE
L1.2.1.2.2.2	162	312	0	306	0	306	0	306	0	306	FALSE
L1.2.1.2.2.2.1	53	4	0	4	0	4	0	4	0	4	FALSE
L1.2.1.2.2.2.2	102	11	0	11	0	11	0	11	0	11	FALSE
L1.2.1.2.2.2.1.1	37	20	0	20	0	20	0	20	0	20	FALSE
L1.2.1.2.2.2.1.2	16	14	0	14	0	14	0	14	0	14	TRUE
L1.2.1.2.2.2.1.1.1	16	4	0	2	0	2	0	2	0	2	TRUE
L1.2.1.2.2.2.1.1.2	14	0	0	0	0	0	0	0	0	0	TRUE
L1.2.1.2.2.2.2.1	74	0	0	0	0	0	0	0	0	0	FALSE
L1.2.1.2.2.2.2.2	17	22	0	22	0	22	0	22	0	22	TRUE
L1.2.1.2.2.2.2.1.1	12	64	0	64	0	64	0	64	0	64	TRUE
L1.2.1.2.2.2.2.1.2	62	0	0	0	0	0	0	0	0	0	TRUE
L1.2.2.1	63	73	0	73	0	73	0	73	0	73	FALSE
L1.2.2.2	138	116	0	116	0	116	0	116	0	116	FALSE
L1.2.2.1.1	14	175	0	175	0	175	0	175	0	175	TRUE
L1.2.2.1.2	45	78	0	78	0	78	0	78	0	78	FALSE
L1.2.2.1.2.1	12	44	0	44	0	44	0	44	0	44	TRUE
L1.2.2.1.2.2	33	46	0	46	0	46	0	46	0	46	TRUE
L1.2.2.2.1	46	0	0	0	0	0	0	0	0	0	FALSE
L1.2.2.2.2	85	14	0	14	0	14	0	14	0	14	FALSE
L1.2.2.2.1.1	19	85	0	85	0	85	0	85	0	85	TRUE
L1.2.2.2.1.2	20	18	0	18	0	18	0	18	0	18	TRUE
L1.2.2.2.2.1	10	70	0	70	0	70	0	70	0	70	TRUE
L1.2.2.2.2.2	64	31	0	31	0	31	0	31	0	31	FALSE
L1.2.2.2.2.2.1	34	6	0	6	0	6	0	6	0	6	FALSE
L1.2.2.2.2.2.2	17	1	0	1	0	1	0	1	0	1	TRUE
L1.2.2.2.2.2.1.1	10	31	0	31	0	31	0	31	0	31	TRUE
L1.2.2.2.2.2.1.2	13	2	0	2	0	2	0	2	0	2	TRUE
L2.1	14	71	0	71	0	71	0	71	0	71	TRUE
L2.2	1088	463	0	439	0	439	0	439	0	439	FALSE
L2	1107	406	0	384	0	384	0	384	0	384	FALSE
L3	1080	364	0	355	0	355	0	355	0	355	FALSE
L2-L3	2187	57	0	57	0	57	0	57	0	57	FALSE
L4	2939	0	180	0	164	492	0	492	0	492	FALSE
L2.2.1	12	28	0	28	0	28	0	28	0	28	TRUE
L2.2.2	1075	460	0	436	0	436	0	436	0	436	FALSE
L2.2.2.1	10	14	0	14	0	14	0	14	0	14	TRUE
L2.2.2.2	1053	450	0	436	0	436	0	436	0	436	FALSE
L2.2.2.2.1	23	0	0	0	0	0	0	0	0	0	TRUE
L2.2.2.2.2	1023	123	0	119	0	119	0	119	0	119	FALSE
L2.2.2.2.2.1	1004	69	0	65	0	65	0	65	0	65	TRUE
L2.2.2.2.2.2	18	0	0	0	0	0	0	0	0	0	TRUE
L3.1	1035	371	0	362	0	362	0	362	0	362	FALSE
L3.2	35	148	0	148	0	148	0	146	0	146	TRUE
L3.1.1	72	41	0	41	0	41	0	41	0	41	FALSE
L3.1.2	953	29	0	29	0	29	0	29	0	29	FALSE
L3.1.1.1	13	0	0	0	0	0	0	0	0	0	TRUE
L3.1.1.2	27	2	0	2	0	2	0	2	0	2	FALSE
L3.1.1.2.1	11	14	0	14	0	14	0	14	0	14	TRUE

L3.1.1.2.2	15	9	0	9	0	9	0	9	0	9	TRUE
L3.1.2.1	931	29	0	29	0	29	0	29	0	29	FALSE
L3.1.2.2	17	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.1	83	16	0	16	0	16	0	16	0	16	FALSE
L3.1.2.1.2	848	10	0	10	0	10	0	10	0	10	FALSE
L3.1.2.1.1.1	28	9	0	9	0	9	0	9	0	9	FALSE
L3.1.2.1.1.2	53	0	0	0	0	0	0	0	0	0	FALSE
L3.1.2.1.1.1.1	10	1	0	1	0	1	0	1	0	1	TRUE
L3.1.2.1.1.1.2	10	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.1.2.1	15	1	0	1	0	1	0	1	0	1	TRUE
L3.1.2.1.1.2.2	29	4	0	4	0	4	0	4	0	4	TRUE
L3.1.2.1.2.1	836	10	0	10	0	10	0	10	0	10	FALSE
L3.1.2.1.2.2	12	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1	809	10	0	10	0	10	0	10	0	10	FALSE
L3.1.2.1.2.1.2	27	6	0	6	0	6	0	6	0	6	TRUE
L3.1.2.1.2.1.1.1	227	0	0	0	0	0	0	0	0	0	FALSE
L3.1.2.1.2.1.1.2	582	8	0	8	0	8	0	8	0	8	FALSE
L3.1.2.1.2.1.1.1.1	22	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1.1.2	205	24	0	24	0	24	0	24	0	24	FALSE
L3.1.2.1.2.1.1.1.2.1	174	1	0	1	0	1	0	1	0	1	TRUE
L3.1.2.1.2.1.1.1.2.2	12	9	0	9	0	9	0	9	0	9	TRUE
L3.1.2.1.2.1.1.2.1	436	1	0	1	0	1	0	1	0	1	FALSE
L3.1.2.1.2.1.1.2.2	146	12	0	12	0	12	0	12	0	12	FALSE
L3.1.2.1.2.1.1.2.1.1	130	14	0	14	0	14	0	14	0	14	FALSE
L3.1.2.1.2.1.1.2.1.2	303	102	0	100	0	100	0	100	0	100	FALSE
L3.1.2.1.2.1.1.2.1.1.1	85	12	0	12	0	12	0	12	0	12	FALSE
L3.1.2.1.2.1.1.2.1.1.2	45	2	0	2	0	2	0	2	0	2	FALSE
L3.1.2.1.2.1.1.2.1.1.1.1	43	3	0	3	0	3	0	3	0	3	FALSE
L3.1.2.1.2.1.1.2.1.1.1.2	42	0	0	0	0	0	0	0	0	0	FALSE
L3.1.2.1.2.1.1.2.1.1.1.1.1	14	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1.2.1.1.1.1.2	28	43	0	43	0	43	0	43	0	43	TRUE
L3.1.2.1.2.1.1.2.1.1.1.2.1	29	5	0	5	0	5	0	5	0	5	TRUE
L3.1.2.1.2.1.1.2.1.1.1.2.2	13	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1.2.1.1.2.1	25	2	0	2	0	2	0	2	0	2	TRUE
L3.1.2.1.2.1.1.2.1.1.2.2	13	13	0	13	0	13	0	13	0	13	TRUE
L3.1.2.1.2.1.1.2.1.2.1	198	4	0	4	0	4	0	4	0	4	TRUE
L3.1.2.1.2.1.1.2.1.2.2	97	13	0	13	0	13	0	13	0	13	FALSE
L3.1.2.1.2.1.1.2.1.2.2.1	11	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1.2.1.2.2.2	80	20	0	20	0	20	0	20	0	20	FALSE
L3.1.2.1.2.1.1.2.1.2.2.2.1	19	5	0	5	0	5	0	5	0	5	TRUE
L3.1.2.1.2.1.1.2.1.2.2.2.2	61	3	0	3	0	3	0	3	0	3	FALSE
L3.1.2.1.2.1.1.2.1.2.2.2.2.1	19	28	0	28	0	28	0	28	0	28	TRUE
L3.1.2.1.2.1.1.2.1.2.2.2.2.2	30	0	0	0	0	0	0	0	0	0	FALSE
L3.1.2.1.2.1.1.2.1.2.2.2.2.2.1	12	13	0	13	0	13	0	13	0	13	TRUE
L3.1.2.1.2.1.1.2.1.2.2.2.2.2.2	15	0	0	0	0	0	0	0	0	0	TRUE
L3.1.2.1.2.1.1.2.2.1	14	13	0	13	0	13	0	13	0	13	TRUE
L3.1.2.1.2.1.1.2.2.2	130	0	0	0	0	0	0	0	0	0	FALSE
L3.1.2.1.2.1.1.2.2.2.1	90	10	0	10	0	10	0	10	0	10	FALSE
L3.1.2.1.2.1.1.2.2.2.2	40	3	0	3	0	3	0	3	0	3	FALSE
L3.1.2.1.2.1.1.2.2.2.1.1	64	17	0	17	0	17	0	17	0	17	FALSE
L3.1.2.1.2.1.1.2.2.2.1.2	25	13	0	13	0	13	0	13	0	13	TRUE
L3.1.2.1.2.1.1.2.2.2.1.1.1	14	102	0	100	0	100	0	100	0	100	TRUE
L3.1.2.1.2.1.1.2.2.2.1.1.2	46	72	0	70	0	70	0	70	0	70	TRUE
L3.1.2.1.2.1.1.2.2.2.2.1	10	25	0	25	0	25	0	25	0	25	TRUE
L3.1.2.1.2.1.1.2.2.2.2.2	30	24	0	24	0	24	0	24	0	24	TRUE
L4.1	802	0	0	0	0	0	0	0	0	0	FALSE
L4.2	2137	0	56	0	56	168	0	168	0	168	FALSE
L4.1.1	643	87	0	87	0	87	0	87	0	87	FALSE
L4.1.2	159	158	0	154	0	154	0	154	0	154	FALSE
L4.1.1.1	42	26	0	26	0	26	0	26	0	26	TRUE
L4.1.1.2	600	1	0	1	0	1	0	1	0	1	FALSE
L4.1.1.2.1	283	17	0	17	0	17	0	17	0	17	FALSE
L4.1.1.2.2	317	27	0	27	0	27	0	27	0	27	FALSE
L4.1.1.2.1.1	60	238	0	231	0	231	0	231	0	231	FALSE
L4.1.1.2.1.2	223	58	0	56	0	56	0	56	0	56	FALSE
L4.1.1.2.1.1.1	12	26	0	26	0	26	0	26	0	26	TRUE
L4.1.1.2.1.1.2	48	2	0	2	0	2	0	2	0	2	TRUE
L4.1.1.2.1.2.1	26	111	0	109	0	109	0	109	0	109	TRUE
L4.1.1.2.1.2.2	197	3	0	3	0	3	0	3	0	3	FALSE
L4.1.1.2.1.2.2.1	35	0	0	0	0	0	0	0	0	0	TRUE
L4.1.1.2.1.2.2.2	162	89	0	85	0	85	0	85	0	85	FALSE
L4.1.1.2.1.2.2.2.1	24	8	0	8	0	8	0	8	0	8	TRUE
L4.1.1.2.1.2.2.2.2	123	1	0	1	0	1	0	1	0	1	FALSE
L4.1.1.2.1.2.2.2.2.1	60	23	0	23	0	23	0	23	0	23	FALSE
L4.1.1.2.1.2.2.2.2.2	63	10	0	10	0	10	0	10	0	10	FALSE
L4.1.1.2.1.2.2.2.2.1.1	28	1	0	1	0	1	0	1	0	1	TRUE
L4.1.1.2.1.2.2.2.2.1.2	32	4	0	4	0	4	0	4	0	4	FALSE

L4.1.1.2.1.2.2.2.2.1.2.1	16	12	0	12	0	12	0	12	0	12	TRUE
L4.1.1.2.1.2.2.2.2.1.2.2	16	7	0	7	0	7	0	7	0	7	TRUE
L4.1.1.2.1.2.2.2.2.2.1	23	4	0	4	0	4	0	4	0	4	TRUE
L4.1.1.2.1.2.2.2.2.2.2	37	10	0	10	0	10	0	10	0	10	FALSE
L4.1.1.2.1.2.2.2.2.2.2.1	16	18	0	18	0	18	0	18	0	18	TRUE
L4.1.1.2.1.2.2.2.2.2.2.2	20	0	0	0	0	0	0	0	0	0	TRUE
L4.1.1.2.2.1	219	103	0	103	0	103	0	103	0	103	FALSE
L4.1.1.2.2.2	81	56	0	56	0	56	0	56	0	56	FALSE
L4.1.1.2.2.1.1	35	34	0	34	0	34	0	34	0	34	FALSE
L4.1.1.2.2.1.2	165	0	0	0	0	0	0	0	0	0	TRUE
L4.1.1.2.2.1.1.1	13	12	0	10	0	10	0	10	0	10	TRUE
L4.1.1.2.2.1.1.2	14	0	0	0	0	0	0	0	0	0	TRUE
L4.1.1.2.2.2.1	10	5	0	5	0	5	0	5	0	5	TRUE
L4.1.1.2.2.2.2	70	3	0	3	0	3	0	3	0	3	FALSE
L4.1.1.2.2.2.2.1	26	27	0	27	0	27	0	27	0	27	FALSE
L4.1.1.2.2.2.2.2	37	17	0	17	0	17	0	17	0	17	TRUE
L4.1.1.2.2.2.2.1.1	12	7	0	7	0	7	0	7	0	7	TRUE
L4.1.1.2.2.2.2.1.2	14	26	0	26	0	26	0	26	0	26	TRUE
L4.1.2.1	98	35	0	33	0	33	0	33	0	33	FALSE
L4.1.2.2	61	34	0	30	0	30	0	30	0	30	FALSE
L4.1.2.1.1	69	117	0	117	0	117	0	115	0	115	FALSE
L4.1.2.1.2	29	93	0	93	0	93	0	93	0	93	TRUE
L4.1.2.1.1.1	40	5	0	5	0	5	0	5	0	5	FALSE
L4.1.2.1.1.2	20	0	0	0	0	0	0	0	0	0	TRUE
L4.1.2.1.1.1.1	28	2	0	2	0	2	0	2	0	2	TRUE
L4.1.2.1.1.1.2	12	0	0	0	0	0	0	0	0	0	TRUE
L4.1.2.2.1	10	11	0	11	0	11	0	11	0	11	TRUE
L4.1.2.2.2	43	66	0	64	0	64	0	64	0	64	FALSE
L4.1.2.2.2.1	13	0	0	0	0	0	0	0	0	0	TRUE
L4.1.2.2.2.2	21	7	0	7	0	7	0	7	0	7	TRUE
L4.2.1	1351	125	0	119	0	119	0	117	0	117	FALSE
L4.2.2	786	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1	1281	132	0	126	0	126	0	124	0	124	FALSE
L4.2.1.2	64	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.1	286	74	0	72	0	72	0	72	0	72	FALSE
L4.2.1.1.2	995	61	0	59	0	59	0	59	0	59	FALSE
L4.2.1.1.1.1	16	41	0	39	0	39	0	39	0	39	TRUE
L4.2.1.1.1.2	262	8	0	8	0	8	0	8	0	8	FALSE
L4.2.1.1.1.2.1	17	22	0	22	0	22	0	22	0	22	TRUE
L4.2.1.1.1.2.2	245	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.1.2.2.1	91	25	0	25	0	25	0	25	0	25	FALSE
L4.2.1.1.1.2.2.2	154	100	0	100	0	100	0	100	0	100	FALSE
L4.2.1.1.1.2.2.1.1	52	1	0	1	0	1	0	1	0	1	TRUE
L4.2.1.1.1.2.2.1.2	10	4	0	4	0	4	0	4	0	4	TRUE
L4.2.1.1.1.2.2.2.1	19	1	0	1	0	1	0	1	0	1	TRUE
L4.2.1.1.1.2.2.2.2	134	3	0	3	0	3	0	3	0	3	TRUE
L4.2.1.1.2.1	86	28	0	28	0	28	0	28	0	28	FALSE
L4.2.1.1.2.2	906	76	0	72	0	72	0	72	0	72	FALSE
L4.2.1.1.2.1.1	50	7	0	7	0	7	0	7	0	7	FALSE
L4.2.1.1.2.1.2	36	6	0	6	0	6	0	6	0	6	FALSE
L4.2.1.1.2.1.1.1	14	40	0	40	0	40	0	40	0	40	TRUE
L4.2.1.1.2.1.1.2	27	68	0	66	0	66	0	66	0	66	TRUE
L4.2.1.1.2.1.2.1	11	44	0	44	0	44	0	44	0	44	TRUE
L4.2.1.1.2.1.2.2	13	0	0	0	0	0	0	0	0	0	TRUE
L4.2.1.1.2.2.1	21	9	0	9	0	9	0	9	0	9	FALSE
L4.2.1.1.2.2.2	885	82	0	78	0	78	0	78	0	78	FALSE
L4.2.1.1.2.2.1.1	10	9	0	9	0	9	0	9	0	9	TRUE
L4.2.1.1.2.2.1.2	11	43	0	43	0	43	0	43	0	43	TRUE
L4.2.1.1.2.2.2.1	21	3	0	3	0	3	0	3	0	3	TRUE
L4.2.1.1.2.2.2.2	856	44	0	44	0	44	0	44	0	44	FALSE
L4.2.1.1.2.2.2.2.1	238	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.2.2.2.2.2	614	1	0	1	0	1	0	1	0	1	FALSE
L4.2.1.1.2.2.2.2.1.1	49	26	0	26	0	26	0	26	0	26	FALSE
L4.2.1.1.2.2.2.2.1.2	189	11	0	11	0	11	0	11	0	11	FALSE
L4.2.1.1.2.2.2.2.1.1.1	25	15	0	13	0	13	0	13	0	13	TRUE
L4.2.1.1.2.2.2.2.1.1.2	13	0	0	0	0	0	0	0	0	0	TRUE
L4.2.1.1.2.2.2.2.1.2.1	159	4	0	4	0	4	0	4	0	4	FALSE
L4.2.1.1.2.2.2.2.1.2.2	22	2	0	2	0	2	0	2	0	2	TRUE
L4.2.1.1.2.2.2.2.1.2.1.1	82	2	0	2	0	2	0	2	0	2	FALSE
L4.2.1.1.2.2.2.2.1.2.1.2	77	10	0	10	0	10	0	10	0	10	FALSE
L4.2.1.1.2.2.2.2.1.2.1.1.1	46	4	0	4	0	4	0	4	0	4	TRUE
L4.2.1.1.2.2.2.2.1.2.1.1.2	36	0	0	0	0	0	0	0	0	0	TRUE
L4.2.1.1.2.2.2.2.1.2.1.2.1	24	6	0	6	0	6	0	6	0	6	TRUE
L4.2.1.1.2.2.2.2.1.2.1.2.2	43	4	0	4	0	4	0	4	0	4	TRUE
L4.2.1.1.2.2.2.2.2.1	499	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.2.2.2.2.2.2	115	2	0	2	0	2	0	2	0	2	FALSE
L4.2.1.1.2.2.2.2.2.1.1	47	3	0	3	0	3	0	3	0	3	FALSE

L4.2.1.1.2.2.2.2.2.1.2	452	1	0	1	0	1	0	1	0	1	FALSE
L4.2.1.1.2.2.2.2.2.1.1.1	16	11	0	11	0	11	0	11	0	11	TRUE
L4.2.1.1.2.2.2.2.2.1.1.2	27	3	0	3	0	3	0	3	0	3	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1	414	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.2.2.2.2.2.1.2.2	38	2	0	2	0	2	0	2	0	2	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.1	46	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2	368	1	0	1	0	1	0	1	0	1	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.1.1	14	7	0	7	0	7	0	7	0	7	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.1.2	23	23	0	23	0	23	0	23	0	23	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.1	140	8	0	8	0	8	0	8	0	8	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2	228	5	0	5	0	5	0	5	0	5	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.1.1	47	10	0	8	0	8	0	8	0	8	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.1.2	93	17	0	17	0	17	0	17	0	17	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.1.1.1	35	4	0	4	0	4	0	4	0	4	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.1.1.2	12	1	0	1	0	1	0	1	0	1	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.1	54	4	0	4	0	4	0	4	0	4	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2	174	3	0	3	0	3	0	3	0	3	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.1.1	20	5	0	5	0	5	0	5	0	5	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.1.2	24	11	0	11	0	11	0	11	0	11	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.1	43	4	0	4	0	4	0	4	0	4	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2	131	0	0	0	0	0	0	0	0	0	FALSE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.1.1	22	4	0	4	0	4	0	4	0	4	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.1.2	10	0	0	0	0	0	0	0	0	0	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.1	107	11	0	11	0	11	0	11	0	11	TRUE
L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.2	24	11	0	11	0	11	0	11	0	11	TRUE
L4.2.1.1.2.2.2.2.2.1.2.2.1	13	2	0	2	0	2	0	2	0	2	TRUE
L4.2.1.1.2.2.2.2.2.1.2.2.2	16	2	0	2	0	2	0	2	0	2	TRUE
L4.2.1.1.2.2.2.2.2.2.1	40	9	0	9	0	9	0	9	0	9	FALSE
L4.2.1.1.2.2.2.2.2.2.2	67	1	0	1	0	1	0	1	0	1	FALSE
L4.2.1.1.2.2.2.2.2.2.1.1	23	5	0	5	0	5	0	5	0	5	TRUE
L4.2.1.1.2.2.2.2.2.2.1.2	16	6	0	6	0	6	0	6	0	6	TRUE
L4.2.1.1.2.2.2.2.2.2.2.1	16	12	0	12	0	12	0	12	0	12	TRUE
L4.2.1.1.2.2.2.2.2.2.2.2	51	1	0	1	0	1	0	1	0	1	FALSE
L4.2.1.1.2.2.2.2.2.2.2.2.1	17	20	0	20	0	20	0	20	0	20	TRUE
L4.2.1.1.2.2.2.2.2.2.2.2.2	34	7	0	7	0	7	0	7	0	7	TRUE
L4.2.1.2.1	53	101	0	99	0	99	0	99	0	99	TRUE
L4.2.1.2.2	11	121	0	119	0	119	0	119	0	119	TRUE
L4.2.2.1	119	52	0	52	0	52	0	52	0	52	FALSE
L4.2.2.2	667	0	13	0	13	39	0	39	0	39	FALSE
L4.2.2.1.1	11	60	0	60	0	60	0	60	0	60	TRUE
L4.2.2.1.2	108	53	0	51	0	51	0	51	0	51	FALSE
L4.2.2.1.2.1	17	54	0	52	0	52	0	52	0	52	TRUE
L4.2.2.1.2.2	91	81	0	81	0	81	0	81	0	81	FALSE
L4.2.2.1.2.2.1	20	0	0	0	0	0	0	0	0	0	TRUE
L4.2.2.1.2.2.2	61	10	0	10	0	10	0	10	0	10	FALSE
L4.2.2.1.2.2.2.1	36	50	0	50	0	50	0	50	0	50	TRUE
L4.2.2.1.2.2.2.2	24	78	0	75	0	75	0	75	0	75	TRUE
L4.2.2.2.1	37	71	0	71	0	71	0	71	0	71	TRUE
L4.2.2.2.2	630	0	9	0	9	27	0	27	0	27	FALSE
L4.2.2.2.2.1	124	15	0	13	0	13	0	13	0	13	FALSE
L4.2.2.2.2.2	506	0	81	0	81	243	0	243	0	243	FALSE
L4.2.2.2.2.1.1	46	5	0	5	0	5	0	5	0	5	TRUE
L4.2.2.2.2.1.2	78	3	0	3	0	3	0	3	0	3	FALSE
L4.2.2.2.2.1.2.1	26	252	0	250	0	250	0	250	0	250	TRUE
L4.2.2.2.2.1.2.2	52	20	0	20	0	20	0	20	0	20	FALSE
L4.2.2.2.2.1.2.2.1	27	51	0	51	0	51	0	51	0	51	TRUE
L4.2.2.2.2.1.2.2.2	18	53	0	53	0	53	0	53	0	53	TRUE
L4.2.2.2.2.2.1	25	11	0	11	0	11	0	11	0	11	TRUE
L4.2.2.2.2.2.2	475	0	14	0	14	42	0	42	0	42	FALSE
L4.2.2.2.2.2.2.1	334	25	0	25	0	25	0	25	0	25	FALSE
L4.2.2.2.2.2.2.2	140	0	63	0	63	189	0	189	0	189	FALSE
L4.2.2.2.2.2.1.1	31	21	0	21	0	21	0	21	0	21	TRUE
L4.2.2.2.2.2.1.2	301	0	0	0	0	0	0	0	0	0	FALSE
L4.2.2.2.2.2.1.2.1	34	5	0	5	0	5	0	5	0	5	TRUE
L4.2.2.2.2.2.1.2.2	267	30	0	30	0	30	0	30	0	30	FALSE
L4.2.2.2.2.2.1.2.2.1	12	166	0	164	0	164	0	164	0	164	TRUE
L4.2.2.2.2.2.1.2.2.2	255	34	0	34	0	34	0	34	0	34	FALSE
L4.2.2.2.2.2.1.2.2.2.1	20	11	0	11	0	11	0	11	0	11	TRUE
L4.2.2.2.2.2.1.2.2.2.2	234	4	0	4	0	4	0	4	0	4	FALSE
L4.2.2.2.2.2.1.2.2.2.2.1	209	3	0	3	0	3	0	3	0	3	FALSE
L4.2.2.2.2.2.1.2.2.2.2.2	20	0	0	0	0	0	0	0	0	0	TRUE
L4.2.2.2.2.2.1.2.2.2.2.1.1	13	2	0	2	0	2	0	2	0	2	TRUE
L4.2.2.2.2.2.1.2.2.2.2.1.2	195	18	0	18	0	18	0	18	0	18	FALSE
L4.2.2.2.2.2.1.2.2.2.2.1.2.1	28	22	0	22	0	22	0	22	0	22	TRUE
L4.2.2.2.2.2.1.2.2.2.2.1.2.2	167	10	0	10	0	10	0	10	0	10	TRUE
L4.2.2.2.2.2.2.1	75	6	0	6	0	6	0	6	0	6	FALSE
L4.2.2.2.2.2.2.2	62	0	3	0	3	9	0	9	0	9	FALSE

L4.2.2.2.2.2.2.2.1.1	10	101	0	101	0	101	0	101	0	101	TRUE
L4.2.2.2.2.2.2.2.1.2	65	94	0	94	0	94	0	94	0	94	FALSE
L4.2.2.2.2.2.2.2.1.2.1	10	0	0	0	0	0	0	0	0	0	TRUE
L4.2.2.2.2.2.2.2.1.2.2	54	24	0	24	0	24	0	24	0	24	FALSE
L4.2.2.2.2.2.2.2.1.2.2.1	21	1	0	1	0	1	0	1	0	1	TRUE
L4.2.2.2.2.2.2.2.1.2.2.2	30	0	0	0	0	0	0	0	0	0	TRUE
L4.2.2.2.2.2.2.2.2.1	10	0	0	0	0	0	0	0	0	0	TRUE
L4.2.2.2.2.2.2.2.2.2	38	0	3	0	3	9	0	9	0	9	TRUE
L5	19	618	0	616	0	616	0	614	0	614	FALSE
L6-LB	84	178	0	178	0	178	0	178	0	178	FALSE
L6.1	15	60	0	58	0	58	0	58	0	58	TRUE
L6.2	14	163	0	161	0	161	0	161	0	161	TRUE
L6	29	442	0	438	0	438	0	436	0	436	FALSE
LB	55	55	0	51	0	51	0	51	0	51	TRUE
L1-L2-L3-L4	5890	0	70	0	64	192	0	186	0	186	FALSE
L5-L6-LB	103	71	0	65	0	65	0	63	0	63	FALSE

Table S6 Drug resistance in samples from Cohen *et al.*, 2015

Phenotypic DST results of 337 samples were compared to drug resistance detected by mapping sequence reads mapped against a minimized reference genome. Strains were tested by Cohen *et al.*, 2015 for being phenotypic resistant (R) or susceptible (S) against the drugs rifampicin (RIF), isoniazid (INH), kanamycin (KAN), pyrazinamide (PZA), ethambutol (EMB), streptomycin (SM), ethionamide (ETH), capreomycin (CAP), and fluiroquinolones (FQ). DST results for FQ only includes oxafloxacin. Strains for which the phenotypic and genotypic drug resistance tests differ are highlighted:

R/S	Phenotypic resistant / genotypic susceptible
S/R	Phenotypic susceptible / genotypic resistance
U/S or U/R	Missing phenotype

Strain	ID	RIF	INH	KAN	PZA	EMB	SM	ETH	CAP	FQ
TKK-01-0001	PRJNA198103	R/R	R/R	S/S	R/S	R/R	R/R	R/S	S/S	S/S
TKK-01-0002	PRJNA198104	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0003	PRJNA198105	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0004	PRJNA198106	R/R	R/R	R/R	R/S	R/R	R/R	S/R	R/R	R/R
TKK-01-0005	PRJNA198107	S/S	R/R	S/S	S/S	S/S	R/R	R/R	S/S	S/S
TKK-01-0006	PRJNA198108	R/R	R/R	S/S	S/S	S/R	S/S	S/S	S/S	S/S
TKK-01-0007	PRJNA198109	S/S	S/S	S/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0008	PRJNA183514	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0009	PRJNA198110	R/R	S/R	S/R	S/S	S/R	S/R	S/S	S/R	S/R
TKK-01-0010	PRJNA198111	S/S	R/R	S/R	S/S	S/S	R/R	S/S	S/R	S/S
TKK-01-0011	PRJNA198112	R/R	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0012	PRJNA198113	R/R	R/R	S/R	R/S	R/R	R/R	S/R	S/R	S/S
TKK-01-0013	PRJNA198114	R/R	R/R	R/S	R/S	R/R	R/R	S/S	S/S	R/S
TKK-01-0014	PRJNA198115	R/R	R/R	S/S	R/S	R/R	R/S	S/R	S/S	S/S
TKK-01-0015	PRJNA198116	R/R	R/R	R/R	S/S	S/R	R/R	S/R	R/R	S/S
TKK-01-0016	PRJNA198117	R/R	R/R	S/S	S/R	R/R	R/R	R/R	S/S	S/S
TKK-01-0017	PRJNA183515	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	S/R
TKK-01-0018	PRJNA198118	S/S	R/R	S/S	R/S	S/R	R/S	S/S	S/S	S/S
TKK-01-0019	PRJNA198119	R/R	R/R	R/R	R/S	R/R	R/R	R/S	S/R	R/S
TKK-01-0020	PRJNA183516	R/R	R/R	S/S	S/S	S/R	R/R	S/S	S/S	S/S
TKK-01-0021	PRJNA183517	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0022	PRJNA198120	R/R	R/R	S/S	R/R	S/R	S/S	S/S	S/S	R/R
TKK-01-0024	PRJNA198121	R/R	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0025	PRJNA198122	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK-01-0026	PRJNA183519	R/R	R/R	S/S	S/S	S/R	R/R	S/S	S/S	S/S
TKK-01-0027	PRJNA198123	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0028	PRJNA198124	R/R	R/R	S/R	S/R	S/R	R/R	S/R	S/R	S/S
TKK-01-0029	PRJNA198125	R/R	R/R	S/S	S/S	S/R	R/R	S/S	S/S	S/S
TKK-01-0030	PRJNA198126	R/R	R/R	S/S	S/S	S/R	S/S	S/S	S/S	S/S
TKK-01-0031	PRJNA198127	R/R	R/R	S/S	S/S	S/R	S/S	S/R	S/S	S/S
TKK-01-0032	PRJNA183520	R/R	R/R	S/S	S/S	S/R	S/S	S/R	S/S	S/S

TKK-01-0033	PRJNA198128	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK-01-0034	PRJNA198129	S/S	R/R	S/S	S/S	S/S	R/S	S/S	S/S	S/S
TKK-01-0035	PRJNA198130	R/R	R/R	S/S	R/R	R/R	R/R	S/S	S/S	S/S
TKK-01-0036	PRJNA198131	S/S	S/R	S/R	S/S	S/S	R/R	S/S	S/R	S/S
TKK-01-0037	PRJNA198132	S/S	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0038	PRJNA198133	R/R	R/R	S/S	S/R	R/R	R/R	R/R	S/S	S/S
TKK-01-0039	PRJNA198134	R/R	R/R	S/S	S/S	S/R	R/R	S/S	S/S	S/S
TKK-01-0040	PRJNA198135	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK-01-0041	PRJNA198136	R/R	R/R	S/S	S/R	R/R	R/R	R/R	R/S	S/S
TKK-01-0042	PRJNA198137	R/R	R/R	S/S	S/S	R/R	R/R	S/S	S/S	S/S
TKK-01-0043	PRJNA198138	R/R	R/R	S/S	S/S	R/R	R/R	S/S	S/S	S/S
TKK-01-0044	PRJNA198139	R/R	R/R	S/R	S/S	S/R	S/R	S/S	S/R	S/S
TKK-01-0045	PRJNA198140	R/R	R/R	S/S	S/S	S/R	R/R	S/S	S/S	S/S
TKK-01-0046	PRJNA198141	S/S	R/R	S/S	S/S	S/S	R/R	S/S	S/S	S/S
TKK-01-0047	PRJNA198142	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0048	PRJNA198143	R/R	R/R	S/S	R/S	R/R	R/S	R/R	S/S	S/S
TKK-01-0049	PRJNA198144	S/S	R/R	S/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0050	PRJNA198145	R/R	R/R	S/S	R/S	R/R	S/S	R/R	S/S	S/S
TKK-01-0052	PRJNA198147	S/R	S/R	R/R	S/S	S/R	S/R	R/R	S/R	S/S
TKK-01-0053	PRJNA198148	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0054	PRJNA198149	S/S	S/S	S/S	R/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0055	PRJNA198150	R/R	R/R	S/S	S/R	S/R	S/S	S/S	S/S	S/S
TKK-01-0056	PRJNA198151	R/R	R/R	S/S	S/R	S/R	S/S	S/S	R/S	S/S
TKK-01-0057	PRJNA198152	R/R	R/R	S/S	R/S	R/R	R/R	S/S	S/S	S/S
TKK-01-0058	PRJNA198153	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0060	PRJNA198155	S/S	R/R	S/R	S/S	S/S	S/R	S/S	R/R	S/S
TKK-01-0061	PRJNA198156	R/R	R/R	S/R	S/S	R/R	R/R	S/S	S/R	S/S
TKK-01-0062	PRJNA198157	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	S/S
TKK-01-0063	PRJNA198158	R/R	R/R	R/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0064	PRJNA198159	R/R	R/R	S/S	R/S	R/R	R/R	S/S	S/S	S/S
TKK-01-0065	PRJNA198160	S/S	R/R	S/S	R/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0066	PRJNA198161	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0067	PRJNA198162	R/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0068	PRJNA198163	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	S/S
TKK-01-0069	PRJNA183521	R/R	R/R	S/S	S/R	R/R	S/S	R/R	R/S	S/S
TKK-01-0070	PRJNA198164	R/R	R/R	S/R	S/R	R/R	R/R	R/R	S/R	S/S
TKK-01-0071	PRJNA198167	R/R	R/R	S/S	R/S	R/R	S/S	S/S	S/S	S/S
TKK-01-0073	PRJNA198168	R/R	R/R	S/S	R/R	R/R	R/S	R/R	S/S	S/S
TKK-01-0074	PRJNA198169	R/R	R/R	S/S	R/S	R/R	R/S	R/R	S/S	S/S
TKK-01-0075	PRJNA198170	R/R	R/R	S/S	R/S	R/R	R/S	R/S	S/S	S/S
TKK-01-0076	PRJNA198172	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK-01-0077	PRJNA198173	S/S	S/S	S/R	S/S	S/S	R/R	S/S	S/R	S/S
TKK-01-0078	PRJNA198174	R/R	S/S	S/S	S/S	S/R	S/S	S/S	S/S	S/S
TKK-01-0079	PRJNA198175	R/S	R/S	S/S	S/S	R/S	S/S	S/S	S/S	S/S
TKK-01-0080	PRJNA183523	R/R	S/R	S/R	S/R	R/R	R/R	S/R	S/R	S/S
TKK-01-0081	PRJNA198176	S/S	S/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S

TKK-01-0082	PRJNA198177	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0083	PRJNA198178	S/S	S/S	S/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0084	PRJNA198179	S/S	S/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0085	PRJNA198180	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0086	PRJNA198181	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0087	PRJNA198182	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0088	PRJNA198183	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0089	PRJNA198184	S/S	S/S	S/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0090	PRJNA198185	S/S	S/S	S/R	S/S	S/S	S/R	S/S	S/R	S/S
TKK-01-0091	PRJNA198186	S/S	S/R	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0092	PRJNA198187	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0093	PRJNA198188	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK-01-0094	PRJNA198189	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S	S/S
TKK_02_0001	PRJNA218225	R/R	R/R	R/R	R/S	R/R	S/R	R/R	R/R	R/R
TKK_02_0002	PRJNA218226	R/R	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R
TKK_02_0004	PRJNA190927	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0005	PRJNA190928	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0006	PRJNA218228	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0007	PRJNA190930	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0008	PRJNA190931	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0010	PRJNA190933	R/R	R/R	S/S	R/S	R/R	R/R	R/R	S/S	R/R
TKK_02_0012	PRJNA218229	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0014	PRJNA218231	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0016	PRJNA218233	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0018	PRJNA218235	R/R	R/R	S/S	R/S	R/R	R/R	R/S	S/S	R/R
TKK_02_0020	PRJNA218237	R/R	R/R	R/S	S/S	S/R	R/S	S/S	S/S	S/S
TKK_02_0021	PRJNA218238	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0023	PRJNA190947	R/R	R/R	S/S	R/S	R/R	R/S	R/R	S/S	S/S
TKK_02_0024	PRJNA190948	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0025	PRJNA218240	R/R	R/R	S/S	R/R	R/R	R/S	R/S	S/S	R/R
TKK_02_0027	PRJNA218241	R/R	R/R	R/R	R/S	R/R	R/S	R/R	S/S	R/R
TKK_02_0028	PRJNA190952	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0030	PRJNA190954	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0031	PRJNA190955	R/R	R/R	R/R	R/S	R/R	R/R	S/R	S/R	R/R
TKK_02_0035	PRJNA190959	R/R	R/R	R/R	R/S	R/R	R/S	R/R	S/S	R/R
TKK_02_0036	PRJNA218245	R/R	R/R	R/S	U/S	R/R	S/S	S/R	S/S	R/R
TKK_02_0037	PRJNA190961	R/R	R/R	S/S	R/R	R/R	R/S	R/S	R/S	R/R
TKK_02_0038	PRJNA218246	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0040	PRJNA190964	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0041	PRJNA190965	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0042	PRJNA190966	R/R	R/R	S/S	S/R	R/R	R/R	R/R	S/S	R/R
TKK_02_0043	PRJNA190967	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0044	PRJNA190968	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0046	PRJNA218249	R/R	S/R	S/R	R/S	S/R	S/R	S/R	S/R	S/R
TKK_02_0047	PRJNA190971	R/R	R/R	S/R	R/S	R/R	R/R	S/S	S/R	S/R
TKK_02_0048	PRJNA190972	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R

TKK_02_0049	PRJNA190973	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0050	PRJNA190974	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0051	PRJNA190975	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0052	PRJNA218250	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0053	PRJNA190977	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0055	PRJNA190979	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0056	PRJNA190980	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0058	PRJNA190982	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0060	PRJNA190984	R/R	R/R	R/R	R/S	R/R	R/R	R/R	R/R	R/R
TKK_02_0062	PRJNA218252	R/R	R/R	S/S	R/S	R/R	R/S	R/S	S/S	R/S
TKK_02_0065	PRJNA190989	R/R	R/R	S/S	R/S	R/R	R/S	R/R	S/S	S/S
TKK_02_0066	PRJNA190990	R/R	R/R	S/S	S/S	R/R	R/R	S/S	S/S	S/S
TKK_02_0067	PRJNA218260	R/R	R/R	R/S	S/S	R/R	S/R	R/S	S/S	S/S
TKK_02_0068	PRJNA218254	R/R	R/R	R/S	S/S	R/R	S/R	R/S	S/S	S/S
TKK_02_0071	PRJNA218257	R/R	R/R	R/R	R/S	R/R	S/R	R/S	R/R	R/R
TKK_02_0073	PRJNA218258	R/R	R/R	S/S	R/S	R/R	S/S	R/S	S/S	R/S
TKK_02_0074	PRJNA190998	R/R	R/R	S/S	R/S	R/R	R/R	S/S	S/S	S/S
TKK_02_0076	PRJNA191000	R/R	R/R	S/S	R/S	R/R	R/S	R/S	S/S	S/S
TKK_02_0079	PRJNA191003	R/R	R/R	S/S	S/S	R/R	R/S	R/S	S/S	R/R
TKK_02_0080	PRJNA191004	R/R	R/R	S/S	R/R	R/R	R/R	S/S	S/S	S/S
TKK_03_0015	PRJNA235397	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0020	PRJNA218262	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0021	PRJNA235398	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0023	PRJNA235399	S/S	S/R	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0024	PRJNA235400	S/S	R/R	S/R	U/S	S/S	R/R	U/S	U/R	S/S
TKK_03_0025	PRJNA218264	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0026	PRJNA218265	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0027	PRJNA218266	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0028	PRJNA235401	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0029	PRJNA218267	S/S	S/S	S/S	U/S	S/R	S/S	U/S	U/S	S/S
TKK_03_0030	PRJNA218268	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0031	PRJNA218269	S/S	S/R	S/S	U/S	S/S	S/S	U/R	U/S	S/S
TKK_03_0033	PRJNA218271	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0034	PRJNA218272	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0035	PRJNA235402	S/S	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0036	PRJNA218273	S/S	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0037	PRJNA235403	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0039	PRJNA235405	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0040	PRJNA235406	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0042	PRJNA235407	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0043	PRJNA218274	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0044	PRJNA235408	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0045	PRJNA218275	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0047	PRJNA235409	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0050	PRJNA235410	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0058	PRJNA235411	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S

TKK_03_0059	PRJNA235412	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0063	PRJNA235415	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0064	PRJNA235416	R/R	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0065	PRJNA235417	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0072	PRJNA235419	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0075	PRJNA235422	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0078	PRJNA218276	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0082	PRJNA218278	S/S	R/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0083	PRJNA235426	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0089	PRJNA235431	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0090	PRJNA235432	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0092	PRJNA235433	S/S	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0094	PRJNA235435	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0098	PRJNA235437	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0099	PRJNA235438	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0100	PRJNA235439	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0101	PRJNA235440	S/S	R/R	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0102	PRJNA235441	S/S	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0103	PRJNA235442	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0105	PRJNA235444	S/S	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_03_0108	PRJNA235447	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0109	PRJNA235448	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0111	PRJNA235450	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0112	PRJNA235451	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0114	PRJNA235453	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0115	PRJNA235454	S/S	S/R	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0118	PRJNA235457	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0149	PRJNA235458	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0150	PRJNA235459	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0153	PRJNA235460	S/S	S/S	S/S	U/R	S/S	S/S	U/S	U/S	S/S
TKK_03_0154	PRJNA235461	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0156	PRJNA235463	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0158	PRJNA235464	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0159	PRJNA235465	S/S	S/R	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_03_0160	PRJNA235466	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_04_0001	PRJNA218279	S/R	R/R	S/S	U/S	U/R	R/R	U/R	U/S	S/R
TKK_04_0002	PRJNA218280	S/R	R/R	S/S	U/S	U/S	R/R	U/S	U/S	S/S
TKK_04_0003	PRJNA218281	S/R	R/S	S/S	U/S	U/R	S/S	U/S	U/S	S/S
TKK_04_0005	PRJNA218295	S/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	R/R
TKK_04_0006	PRJNA218282	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0007	PRJNA218296	R/R	R/R	S/S	U/R	U/R	S/S	U/S	U/S	R/R
TKK_04_0008	PRJNA218297	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/R
TKK_04_0013	PRJNA218298	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0014	PRJNA218283	R/S	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0015	PRJNA218284	R/S	S/S	S/R	U/S	U/S	S/R	U/S	U/R	S/S
TKK_04_0017	PRJNA218285	S/R	R/R	S/S	U/S	U/S	R/R	U/S	U/S	S/S

TKK_04_0018	PRJNA218286	R/S	R/S	S/S	U/S	U/S	R/S	U/S	U/S	S/S
TKK_04_0019	PRJNA218287	R/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	S/S
TKK_04_0020	PRJNA218299	R/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	R/R
TKK_04_0021	PRJNA218288	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0022	PRJNA218289	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0023	PRJNA218290	R/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	S/S
TKK_04_0024	PRJNA218291	R/R	R/R	S/S	U/R	U/R	R/R	U/R	U/S	S/S
TKK_04_0029	PRJNA218310	S/S	S/S	S/R	U/S	U/S	S/R	U/S	U/R	S/S
TKK_04_0030	PRJNA218311	S/S	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0031	PRJNA218312	S/S	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0033	PRJNA218313	S/S	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0034	PRJNA218300	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	R/R
TKK_04_0036	PRJNA218301	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/S
TKK_04_0037	PRJNA218309	R/R	R/R	S/S	U/R	U/R	R/R	U/R	U/S	R/R
TKK_04_0038	PRJNA218302	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0039	PRJNA218303	R/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	R/R
TKK_04_0040	PRJNA218304	S/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0042	PRJNA218308	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/R
TKK_04_0043	PRJNA218292	R/R	R/R	R/R	U/S	U/R	S/R	U/R	U/R	S/S
TKK_04_0044	PRJNA218305	R/R	R/R	S/R	U/S	U/R	R/R	U/S	U/R	R/R
TKK_04_0045	PRJNA218306	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/R
TKK_04_0046	PRJNA218307	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/R
TKK_04_0047	PRJNA218293	S/R	R/R	R/R	U/S	U/R	S/R	U/R	U/R	S/S
TKK_04_0048	PRJNA218294	R/R	R/R	R/S	U/S	U/R	R/S	U/S	U/S	S/S
TKK_04_0051	PRJNA235467	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0054	PRJNA235468	R/R	R/R	S/S	U/R	U/R	R/R	U/S	U/S	R/R
TKK_04_0059	PRJNA235469	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	R/R
TKK_04_0060	PRJNA235470	R/R	R/R	S/S	U/R	U/R	S/S	U/R	U/S	R/R
TKK_04_0061	PRJNA235471	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	R/R
TKK_04_0062	PRJNA235472	R/R	R/R	S/S	U/R	U/R	S/S	U/S	U/S	R/R
TKK_04_0064	PRJNA235474	R/R	R/R	S/S	U/R	U/R	S/S	U/R	U/S	R/R
TKK_04_0066	PRJNA235475	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0067	PRJNA235476	R/R	R/R	S/S	U/R	U/R	S/S	U/S	U/S	R/R
TKK_04_0068	PRJNA235477	R/R	R/R	S/S	U/R	U/R	R/S	U/S	U/S	R/R
TKK_04_0069	PRJNA235478	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0070	PRJNA235479	R/R	R/R	S/S	U/R	U/R	S/S	U/R	U/S	R/R
TKK_04_0071	PRJNA235480	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	R/R
TKK_04_0074	PRJNA235564	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	R/R
TKK_04_0075	PRJNA235482	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	R/R
TKK_04_0078	PRJNA235483	R/R	R/R	S/S	U/R	U/R	S/S	U/R	U/S	R/R
TKK_04_0080	PRJNA235485	R/R	R/R	S/R	U/R	U/R	R/R	U/R	U/R	S/S
TKK_04_0081	PRJNA235486	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0082	PRJNA235487	S/R	R/R	S/S	U/S	U/R	S/S	U/R	U/S	S/S
TKK_04_0083	PRJNA235488	R/R	R/R	S/S	U/R	U/R	R/S	U/R	U/S	R/R
TKK_04_0084	PRJNA235489	R/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0085	PRJNA235565	R/R	R/R	S/R	U/R	U/R	R/R	U/R	U/R	S/S

TKK_04_0086	PRJNA235490	S/R	R/R	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0089	PRJNA235566	S/R	R/S	R/R	U/S	U/S	S/R	U/S	U/R	S/S
TKK_04_0090	PRJNA235567	R/R	S/R	S/S	U/S	U/R	S/S	U/R	U/S	S/R
TKK_04_0094	PRJNA235568	R/R	R/S	S/R	U/S	U/S	S/R	U/S	U/R	S/S
TKK_04_0095	PRJNA235569	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0096	PRJNA235570	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0097	PRJNA235571	R/R	R/R	S/S	U/S	U/R	S/S	U/R	U/S	S/S
TKK_04_0098	PRJNA235572	R/R	R/S	S/S	U/S	U/R	S/S	U/S	U/S	S/S
TKK_04_0099	PRJNA235573	R/R	R/R	S/S	U/R	U/R	S/S	U/R	U/S	S/S
TKK_04_0103	PRJNA235574	R/R	R/R	R/R	U/S	U/R	S/R	U/S	U/R	R/R
TKK_04_0104	PRJNA235614	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0105	PRJNA235575	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0106	PRJNA235576	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0107	PRJNA235577	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0108	PRJNA235578	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0109	PRJNA235579	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0112	PRJNA235580	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0113	PRJNA235581	R/R	R/R	R/R	U/S	U/R	S/S	U/S	U/S	R/R
TKK_04_0114	PRJNA235582	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0117	PRJNA235584	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0118	PRJNA235585	R/R	R/R	R/R	U/S	U/R	R/R	U/S	U/R	R/R
TKK_04_0120	PRJNA235587	R/R	R/R	R/R	U/R	U/R	R/R	U/R	U/R	R/R
TKK_04_0122	PRJNA235589	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0123	PRJNA235590	R/R	R/R	R/R	U/S	U/R	S/R	U/R	U/R	R/R
TKK_04_0124	PRJNA235591	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0125	PRJNA235592	R/R	R/R	R/R	U/S	U/R	R/R	U/S	U/R	S/S
TKK_04_0126	PRJNA235593	R/R	R/R	R/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0129	PRJNA235594	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0130	PRJNA235595	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0131	PRJNA235596	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	S/S
TKK_04_0132	PRJNA235597	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0134	PRJNA235598	S/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0136	PRJNA235599	S/R	R/R	S/S	U/S	U/R	R/R	U/S	U/S	S/S
TKK_04_0137	PRJNA235600	R/R	R/R	R/R	U/S	U/R	R/R	U/R	U/R	R/R
TKK_04_0139	PRJNA235601	R/R	R/R	S/S	U/S	U/R	R/S	U/S	U/S	S/S
TKK_04_0140	PRJNA235602	R/R	R/S	R/R	U/S	U/S	R/R	U/S	U/R	S/S
TKK_04_0141	PRJNA235603	R/R	R/R	S/S	U/S	U/R	S/S	U/R	U/S	S/S
TKK_04_0145	PRJNA235604	R/R	R/R	S/S	U/S	U/R	R/S	U/R	U/S	S/S
TKK_04_0148	PRJNA235605	S/R	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0149	PRJNA235606	S/R	S/S	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0150	PRJNA235607	R/R	R/R	S/S	U/S	U/R	S/S	U/S	U/S	S/S
TKK_04_0153	PRJNA235609	S/R	R/R	S/S	U/R	U/R	R/S	U/S	U/S	S/S
TKK_04_0155	PRJNA235610	R/R	R/R	S/S	U/S	U/S	S/S	U/S	U/S	S/S
TKK_04_0157	PRJNA235611	R/R	R/R	S/S	U/S	U/R	S/S	U/R	U/S	S/S
TKK_04_0158	PRJNA235612	R/S	R/R	S/S	U/R	U/R	R/S	U/R	U/S	S/S
TKK_04_0159	PRJNA235613	S/R	R/R	S/S	U/S	U/S	S/S	U/S	U/S	S/S

TKK_05MA_0004	PRJNA235493	R/R	R/R	S/S	U/S	R/R	R/R	U/S	U/S	S/S
TKK_05MA_0009	PRJNA235495	R/R	R/R	S/S	U/S	S/R	S/S	U/S	U/S	S/S
TKK_05MA_0033	PRJNA235510	R/R	R/R	S/S	U/R	R/R	R/R	U/R	U/S	S/S
TKK_05MA_0035	PRJNA235511	R/R	R/R	S/S	U/S	R/R	R/R	U/S	U/S	S/S
TKK_05MA_0037	PRJNA235513	R/R	R/R	S/S	U/S	R/R	S/R	U/S	U/S	S/S
TKK_05MA_0040	PRJNA235514	R/R	R/R	S/S	U/R	R/R	S/R	U/R	U/S	S/S
TKK_05MA_0051	PRJNA235521	R/R	R/R	S/S	U/S	R/R	S/S	U/S	U/S	S/S
TKK_05MA_2005	PRJNA235527	R/R	R/R	R/R	U/S	R/R	R/R	U/R	U/R	R/R
TKK_05MA_2008	PRJNA235528	R/R	R/R	R/R	U/S	R/R	R/R	U/R	U/R	R/R
TKK_05MA_2015	PRJNA235529	R/R	R/R	R/R	U/S	S/S	R/R	U/S	U/R	R/R
TKK_05SA_0010	PRJNA235531	R/R	R/R	S/R	U/S	S/S	R/R	U/S	U/R	S/S
TKK_05SA_0011	PRJNA235532	R/R	R/R	S/R	U/S	U/R	S/R	U/S	U/R	S/S
TKK_05SA_0014	PRJNA235534	R/R	R/R	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_05SA_0016	PRJNA235535	R/R	R/R	R/S	U/S	R/R	R/R	U/S	U/S	R/R
TKK_05SA_0018	PRJNA235537	R/R	R/R	R/R	U/S	R/R	R/S	U/R	U/S	R/R
TKK_05SA_0019	PRJNA235538	R/R	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_05SA_0020	PRJNA235539	R/R	R/R	S/S	U/S	R/R	S/R	U/R	U/S	S/S
TKK_05SA_0021	PRJNA235540	S/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_05SA_0024	PRJNA235542	S/R	S/S	S/R	U/S	S/S	S/R	U/S	U/R	S/S
TKK_05SA_0025	PRJNA235543	R/R	R/R	S/R	U/S	S/S	R/R	U/S	U/R	S/S
TKK_05SA_0041	PRJNA235549	R/R	R/R	S/S	U/S	R/R	R/R	U/S	U/S	S/S
TKK_05SA_0042	PRJNA235550	R/R	R/R	S/S	U/R	S/R	S/S	U/R	U/S	R/R
TKK_05SA_0043	PRJNA235551	R/R	R/R	R/R	U/S	R/R	R/R	U/R	U/R	R/R
TKK_05SA_0044	PRJNA235552	R/R	R/R	S/S	U/S	S/R	R/R	U/S	U/S	S/S
TKK_05SA_0046	PRJNA235553	R/S	S/S	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_05SA_0048	PRJNA235555	R/R	R/R	S/S	U/R	S/R	S/S	U/R	U/S	S/S
TKK_05SA_0050	PRJNA235556	R/R	R/R	S/S	U/S	S/R	S/S	U/S	U/S	S/S
TKK_05SA_0052	PRJNA235557	R/R	R/R	S/S	U/S	S/S	S/S	U/S	U/S	S/S
TKK_05SA_0054	PRJNA235559	R/R	R/R	S/S	U/S	R/R	R/R	U/S	U/S	S/S
TKK_05SA_0055	PRJNA235560	R/R	R/R	S/S	U/S	S/R	R/R	U/S	U/S	S/S

Table S7 118 Mixed infection samples with ambiguous drug resistance SNPs

Mixed infections found in this study are analyzed for the presence of ambiguous drug resistance SNPs. Drug resistance is detected by mapping sample reads against a minimized reference genome consisting of drug resistance genes and 1000 bp flanking regions. Detected SNPs are compared with a curated library of drug resistance mutations from Coll *et al.*, 2015.

	Sample (study)	Lineage	Mutation	Codon change	Drug	Filter	Nucleotide read count (A,C,G,T)	Nucleotide frequencies (A,C,G,T)
1	ERR025437 (Lit.Bryant2013)	L1.1.2(0.56), L4.1(0.23), L2-L3(0.21)	kasA_G312S	GGC/AGC	INH	Amb	8,0,7,0	0.53,0.0,0.47,0.0
			eis-promoter_C-12T	-	KAN	Amb	0,10,0,3	0.0,0.77,0.0,0.23
			embC_T270I	ACC/ATC	EMB	Amb	0,3,0,2	0.0,0.6,0.0,0.4
			embB_E378A	GAG/GCG	EMB	Amb	6,6,0,0	0.5,0.5,0.0,0.0
2	ERR023741 (Lit.Bryant2013)	L3.1.2.1(0.52), L4.1.1(0.48)	katG_S315T	AGC/ACC	INH	Amb	0,5,5,0	0.0,0.5,0.5,0.0
3	ERR028606 (Lit.Bryant2013)	L4.1.2(0.45), L4.1.1(0.55)	rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,9,0,3	0.0,0.75,0.0,0.25
4	ERR023753 (Lit.Bryant2013)	L4.2.1.2.1(0.5), L4.1.1(0.5)	rrs_C482T	-	AMK,CAP,KAN,SM	Amb	0,7,1,8	0.0,0.44,0.06,0.5
			kasA_G312S	GGC/AGC	INH	Amb;LowCov	1,0,2,0	0.33,0.0,0.67,0.0
5	ERR108431 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.57), L2.2.2.2.2.1(0.43)	rpoB_D435V	GAC/GTC	RIF	Amb	37,0,0,48	0.44,0.0,0.0,0.56
			rpoB_S450L	TCG/TTG	RIF	Amb	0,50,0,41	0.0,0.55,0.0,0.45
			rpsL_K43R	AAG/AGG	SM	Amb	63,0,37,0	0.63,0.0,0.37,0.0
			rrs_A504C	-	AMK,CAP,KAN,SM	Amb	33,54,0,0	0.38,0.62,0.0,0.0
			rrs_A1391G	-	AMK,CAP,KAN,SM	Amb	33,0,52,0	0.39,0.0,0.61,0.0
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,62,0,44	0.0,0.58,0.0,0.42
			katG_S315T	AGC/ACC	INH	PASS	0,87,0,0	0.0,1.0,0.0,0.0
			kasA_G269S	GGT/AGT	INH	Amb	54,0,34,0	0.61,0.0,0.39,0.0
			eis-promoter_G-10A	-	KAN	Amb	43,0,64,0	0.4,0.0,0.6,0.0
			embB_M306I	ATG/ATA	EMB	Amb	63,0,46,0	0.58,0.0,0.42,0.0
			embB_G406A	GGC/GCC	EMB	Amb	0,60,58,0	0.0,0.51,0.49,0.0
6	ERR067764 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.16), L2.2.2.2.2.1(0.84)	rpoB_S450L	TCG/TTG	RIF	PASS	0,6,0,48	0.0,0.11,0.0,0.89
			rpsL_K43R	AAG/AGG	SM	Amb	13,0,39,0	0.25,0.0,0.75,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,44,4,0	0.0,0.92,0.08,0.0
			embB_M306V	ATG/GTG	EMB	PASS	6,0,43,0	0.12,0.0,0.88,0.0
7	ERR144568 (Lit.Casali2014)	L2.2.2.2.2.1(0.54), L4.2.2(0.46)	gyrA_A90V	GCG/GTG	FQ	Amb	0,3,0,3	0.0,0.5,0.0,0.5
			rpoB_S450L	TCG/TTG	RIF	Amb	0,3,0,5	0.0,0.38,0.0,0.63
			rpoB_E761D	GAG/GAC	RIF	PASS	0,4,1,0	0.0,0.8,0.2,0.0
			katG_S315T	AGC/ACC	INH	Amb	0,5,4,0	0.0,0.56,0.44,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,0,2,4	0.0,0.0,0.33,0.67
			embB_D354A	GAC/GCC	EMB	Amb	4,3,0,0	0.57,0.43,0.0,0.0
8	ERR067642 (Lit.Casali2014)	L4.1.2.1.1.1.2(0.39), L2.2.2.2.2.1(0.61)	rpoB_S450L	TCG/TTG	RIF	Amb	0,16,0,31	0.0,0.34,0.0,0.66
			rpsL_K43R	AAG/AGG	SM	Amb	14,0,38,0	0.27,0.0,0.73,0.0
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,22,0,25	0.0,0.47,0.0,0.53
			katG_S315T	AGC/ACC	INH	PASS	0,53,0,0	0.0,1.0,0.0,0.0
			pncA_V128G	GTC/GGC	PZA	Amb	0,0,12,24	0.0,0.0,0.33,0.67
			embB_M306V	ATG/GTG	EMB	Amb	16,0,46,0	0.26,0.0,0.74,0.0
9	ERR137276 (Lit.Casali2014)	L2.2.2.2.2.1(0.27), L4.1.2.1.1.2(0.73)	rpoB_S450L	TCG/TTG	RIF	Amb	1,104,0,34	0.01,0.75,0.0,0.24
			katG_S315T	AGC/ACC	INH	Amb	0,42,118,0	0.0,0.26,0.74,0.0
10	ERR027453 (Lit.Casali2014)	L4.2.2.2.2.2.2.2.2.2(0.69), L2.2.2.2.2.1(0.31)	gyrA_A90V	GCG/GTG	FQ	Amb	0,26,0,9	0.0,0.74,0.0,0.26
			rpoB_E761D	GAG/GAC	RIF	Amb	0,14,32,0	0.0,0.3,0.7,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,0,22,10	0.0,0.0,0.69,0.31
			embB_D354A	GAC/GCC	EMB	Amb	24,9,0,0	0.73,0.27,0.0,0.0
11	ERR067738 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.29), L2.2.2.2.2.1(0.71)	rpoB_H445D	CAC/GAC	RIF	Amb	0,43,16,0	0.0,0.73,0.27,0.0
			rpoB_S450L	TCG/TTG	RIF	Amb	0,22,0,36	0.0,0.38,0.0,0.62
			rpsL_K43R	AAG/AGG	SM	PASS	8,0,32,0	0.2,0.0,0.8,0.0
			rrs_A504C	-	AMK,CAP,KAN,SM	Amb	35,15,0,0	0.7,0.3,0.0,0.0
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,47,0,19	0.0,0.71,0.0,0.29
			katG_S315T	AGC/ACC	INH	PASS	0,57,0,0	0.0,1.0,0.0,0.0
			kasA_G269S	GGT/AGT	INH	Amb	13,0,37,1	0.25,0.0,0.73,0.02
			eis-promoter_G-10A	-	KAN	Amb	39,0,22,0	0.64,0.0,0.36,0.0
			embA-promoter_C-16T	-	EMB	Amb	1,14,0,40	0.02,0.25,0.0,0.73
			embB_G406C	GGC/TGC	EMB	Amb	0,0,42,19	0.0,0.0,0.69,0.31
12	ERR234613 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.73), L2.2.2.2.2.1(0.27)	katG_S315T	AGC/ACC	INH	Amb	0,14,28,0	0.0,0.33,0.67,0.0
			kasA_G269S	GGT/AGT	INH	PASS	40,0,12,0	0.77,0.0,0.23,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,0,31,14	0.0,0.0,0.69,0.31
			embB_D354A	GAC/GCC	EMB	Amb	38,13,0,0	0.75,0.25,0.0,0.0
13	ERR403267 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.1(0.74), L2.2.2.2.2.1(0.26)	rpoB_S450L	TCG/TTG	RIF	Amb	0,60,1,19	0.0,0.75,0.01,0.24
			katG_S315T	AGC/ACC	INH	Amb	0,21,59,0	0.0,0.26,0.74,0.0
			embB_D354A	GAC/GCC	EMB	Amb	52,19,1,0	0.72,0.26,0.01,0.0
			embB_G406D	GGC/GAC	EMB	PASS	55,0,17,0	0.76,0.0,0.24,0.0
14	ERR133940 (Lit.Casali2014)	L2.2.2.2.2.1(0.32), L4.1.1.2.1.2.2.2.2.2.2.1(0.68)	rpoB_S450L	TCG/TTG	RIF	PASS	0,33,0,98	0.0,0.25,0.0,0.75
			rpsL_K43R	AAG/AGG	SM	PASS	0,0,158,0	0.0,0.0,1.0,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,167,0,0	0.0,1.0,0.0,0.0
			eis-promoter_C-12T	-	KAN	Amb	0,47,0,108	0.0,0.3,0.0,0.7
			embB_M306V	ATG/GTG	EMB	Amb	48,1,106,1	0.31,0.01,0.68,0.01
15	ERR234611 (Lit.Casali2014)	L2.2.2.2.2.1(0.61), L4.1.2.1.1.2(0.39)	rpoB_L430P	CTG/CCG	RIF	Amb	0,25,1,18	0.0,0.57,0.02,0.41
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,32,0,22	0.0,0.59,0.0,0.41
			katG_S315T	AGC/ACC	INH	Amb	0,19,35,0	0.0,0.35,0.65,0.0

16	ERR144612 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.29), L4.1.1.2.1.2.2.2(0.09), L4.1.1.2.2(0.16), L4.2.1.1.2.1.2.2(0.46)	rpoB_H445N	CAC/AAC	RIF	Amb	42,107,0,0	0.28,0.72,0.0,0.0
17	ERR144556 (Lit.Casali2014)	L2.2.2.2.2.1(0.9), L4.2.2.2.2.2.2.1.2.2.2.2.1.2.1.1(0.1)	rpoB_S450L	TCG/TTG	RIF	PASS	0,19,0,86	0.0,0.18,0.0,0.82
			rpoB_E761D	GAG/GAC	RIF	Amb	1,81,26,0	0.01,0.75,0.24,0.0
			rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,30,0,74	0.0,0.29,0.0,0.71
			katG_S315T	AGC/ACC	INH	PASS	0,127,13,0	0.0,0.91,0.09,0.0
			eis-promoter_G-37T	-	KAN	PASS	0,1,22,101	0.0,0.01,0.18,0.81
			embB_D354A	GAC/GCC	EMB	PASS	18,93,0,0	0.16,0.84,0.0,0.0
18	ERR137194 (Lit.Casali2014)	L2.2.2.2.2.1(0.37), L4.1.1.2.1.2.2.2.1(0.63)	rpsL_K43R	AAG/AGG	SM	Amb	124,0,59,0	0.68,0.0,0.32,0.0
			katG_S315T	AGC/ACC	INH	Amb	0,65,123,0	0.0,0.35,0.65,0.0
			pncA_V7G	GTC/GGC	PZA	Amb	0,0,63,94	0.0,0.0,0.4,0.6
19	ERR234566 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.51), L2.2.2.2.2.1(0.49)	rpsL_K43R	AAG/AGG	SM	PASS	2,0,50,0	0.04,0.0,0.96,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,59,2,0	0.0,0.97,0.03,0.0
			embB_N296H	AAT/CAT	EMB	Amb	52,19,0,0	0.73,0.27,0.0,0.0
20	ERR227974 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.1(0.71), L2.2.2.2.2.1(0.29)	rpoB_L452P	CTG/CCG	RIF	Amb	0,9,0,26	0.0,0.26,0.0,0.74
			katG_S315T	AGC/ACC	INH	Amb	0,18,37,0	0.0,0.33,0.67,0.0
			embB_M306V	ATG/GTG	EMB	Amb	42,0,19,0	0.69,0.0,0.31,0.0
21	ERR133821 (Lit.Casali2014)	L2.2.2.2.2.1(0.32), L4.2.2.2.2.2.2.1.1(0.02), L4.2.1.1.1.2.2.1(0.66)	rpoB_S450L	TCG/TTG	RIF	Amb	0,226,0,130	0.0,0.63,0.0,0.37
			rpsL_K43R	AAG/AGG	SM	Amb	317,0,122,0	0.72,0.0,0.28,0.0
			katG_S315T	AGC/ACC	INH	Amb	0,145,240,0	0.0,0.38,0.62,0.0
			pncA_D12A	GAC/GCC	PZA	Amb	245,106,0,0	0.7,0.3,0.0,0.0
			kasA_G269S	GGT/AGT	INH	Amb	234,0,101,1	0.7,0.0,0.3,0.0
			eis-promoter_G-10A	-	KAN	Amb	149,0,259,0	0.37,0.0,0.63,0.0
			embB_G406A	GGC/GCC	EMB	Amb	0,126,248,0	0.0,0.34,0.66,0.0
22	ERR133923 (Lit.Casali2014)	L2.2.2.2.2.1(0.43), L4.2.1.1.1.2.2.1(0.57)	rpoB_S450L	TCG/TTG	RIF	Amb	0,94,0,55	0.0,0.63,0.0,0.37
			rpsL_K43R	AAG/AGG	SM	Amb	90,0,60,0	0.6,0.0,0.4,0.0
			katG_S315T	AGC/ACC	INH	Amb	0,64,81,0	0.0,0.44,0.56,0.0
			kasA_G269S	GGT/AGT	INH	Amb	89,0,65,0	0.58,0.0,0.42,0.0
			eis-promoter_G-10A	-	KAN	Amb	63,0,90,0	0.41,0.0,0.59,0.0
			embB_G406A	GGC/GCC	EMB	Amb	0,44,82,1	0.0,0.35,0.65,0.01
23	ERR067701 (Lit.Casali2014)	L2.2.2.2.2.1(0.77), L4.1.1.2.1.2.2.2.2.2.2.1(0.23)	gyrA_A90V	GCG/GTG	FQ	Amb	0,42,0,17	0.0,0.71,0.0,0.29
			rpoB_S450L	TCG/TTG	RIF	PASS	0,0,0,54	0.0,0.0,0.0,1.0
			rpsL_K43R	AAG/AGG	SM	PASS	0,0,46,0	0.0,0.0,1.0,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,59,0,0	0.0,1.0,0.0,0.0
			eis-promoter_G-10A	-	KAN	PASS	41,0,6,0	0.87,0.0,0.13,0.0
			embB_M306V	ATG/GTG	EMB	Amb	47,0,16,0	0.75,0.0,0.25,0.0
			embB_G406A	GGC/GCC	EMB	PASS	0,50,11,0	0.0,0.82,0.18,0.0
24	ERR234604 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.62), L2.2.2.2.2.1(0.38)	rpoB_H445L	CAC/CTC	RIF	Amb	56,0,0,30	0.65,0.0,0.0,0.35
			rpsL_K43R	AAG/AGG	SM	Amb	49,0,24,0	0.67,0.0,0.33,0.0
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,55,0,32	0.0,0.63,0.0,0.37
			katG_S315T	AGC/ACC	INH	Amb	0,35,40,0	0.0,0.47,0.53,0.0
			kasA_G269S	GGT/AGT	INH	Amb	52,0,28,0	0.65,0.0,0.35,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,1,55,36	0.0,0.01,0.6,0.39
			embB_Q497R	CAG/CGG	EMB	Amb	64,0,23,0	0.74,0.0,0.26,0.0
25	ERR133972 (Lit.Casali2014)	L2.2.2.2.2.1(0.5), L4.2.2.2.2.2.2.1.2.2.2.2.1.2.1(0.5)	rpoB_S450L	TCG/TTG	RIF	PASS	0,1,1,184	0.0,0.01,0.01,0.99
			rpoB_E761D	GAG/GAC	RIF	Amb	0,104,96,0	0.0,0.52,0.48,0.0
			rpsL_K88R	AAG/AGG	SM	Amb	99,0,105,0	0.49,0.0,0.51,0.0
			rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,92,0,93	0.0,0.5,0.0,0.5
			katG_S315T	AGC/ACC	INH	Amb	0,105,102,0	0.0,0.51,0.49,0.0
			eis-promoter_G-10A	-	KAN	Amb	86,0,86,0	0.5,0.0,0.5,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,0,89,92	0.0,0.0,0.49,0.51
			embB_D354A	GAC/GCC	EMB	Amb	110,100,0,0	0.52,0.48,0.0,0.0
26	ERR027465 (Lit.Casali2014)	L4.2.2.2.2.2.2.2.2.2(0.62), L2.2.2.2.2.1(0.38)	rpoB_S450L	TCG/TTG	RIF	Amb	0,13,0,6	0.0,0.68,0.0,0.32
			rpoC_L527V	TTG/GTG	RIF	Amb	0,0,9,21	0.0,0.0,0.3,0.7
			rpsL_K43R	AAG/AGG	SM	Amb	11,0,12,0	0.48,0.0,0.52,0.0
			katG_S315T	AGC/ACC	INH	Amb	0,13,19,0	0.0,0.41,0.59,0.0
			embB_M306V	ATG/GTG	EMB	Amb	16,0,9,0	0.64,0.0,0.36,0.0
27	ERR227993 (Lit.Casali2014)	L2.2.2.2.2.1(0.71), L4.1.2.1.1.1.1(0.29)	rpoB_S450L	TCG/TTG	RIF	PASS	0,0,0,79	0.0,0.0,0.0,1.0
			rpoB_E761D	GAG/GAC	RIF	Amb	0,49,48,0	0.0,0.51,0.49,0.0
			rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,51,0,44	0.0,0.54,0.0,0.46
			katG_S315T	AGC/ACC	INH	PASS	0,90,0,0	0.0,1.0,0.0,0.0
			eis-promoter_G-10A	-	KAN	Amb	20,0,62,0	0.24,0.0,0.76,0.0
			eis-promoter_C-15G	-	KAN	Amb	0,56,21,0	0.0,0.73,0.27,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,1,34,45	0.0,0.01,0.43,0.56
			embB_D354A	GAC/GCC	EMB	Amb	36,47,0,0	0.43,0.57,0.0,0.0
			embB_G406D	GGC/GAC	EMB	Amb	26,14,45,0	0.31,0.16,0.53,0.0
28	ERR067669 (Lit.Casali2014)	L2.2.2.2.2.1(0.2), L4.1.1.2.1.2.2.2.2.2.2.2(0.8)	katG_S315T	AGC/ACC	INH	Amb	0,14,39,0	0.0,0.26,0.74,0.0
29	ERR229930 (Lit.Casali2014)	L2.2.2.2.2.1(0.86), L4.1.1.2.1.2.2.2.2.2.2.1(0.14)	rpoB_S450L	TCG/TTG	RIF	PASS	0,12,0,72	0.0,0.14,0.0,0.86
			rpoB_E761D	GAG/GAC	RIF	PASS	0,66,14,0	0.0,0.83,0.18,0.0
			rrs_C507T	-	AMK,CAP,KAN,SM	PASS	0,21,0,72	0.0,0.23,0.0,0.77
			katG_S315T	AGC/ACC	INH	PASS	0,62,17,0	0.0,0.78,0.22,0.0
			eis-promoter_G-37T	-	KAN	Amb	0,0,21,57	0.0,0.0,0.27,0.73
			embB_D354A	GAC/GCC	EMB	PASS	17,73,1,0	0.19,0.8,0.01,0.0
30	ERR047886 (Lit.Casali2014)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.93), L4.2.2.2.2.2.2.1.2.2.2.2.2(0.07)	rpoB_L452P	CTG/CCG	RIF	PASS	0,495,0,1	0.0,1.0,0.0,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,562,0,0	0.0,1.0,0.0,0.0
			pncA-promoter_T-7C	-	PZA	Amb	0,392,0,151	0.0,0.72,0.0,0.28
			embB_G406S	GGC/AGC	EMB	PASS	548,1,1,0	1.0,0.0,0.0,0.0
31	ERR403299 (Lit.Casali2014)	L2.2.2.2.2.1(0.1), L4.2.2.2.2.2.2.1.2.2.2.2.1.1(0.34), L4.1.2.1.2(0.56)	katG_S315T	AGC/ACC	INH	Amb	0,98,51,0	0.0,0.66,0.34,0.0

32	ERR403283 (Lit.Casali2014)	L4.1.1.2.2(0.44), L2.2.2.2.2.1(0.56)	gyrA_D94G rpoB_S450L rpsL_K43R katG_S315T eis-promoter_G-10A embB_G406A	GAC/GGC TCG/TTG AAG/AGG AGC/ACC - GGC/GCC	FQ RIF SM INH KAN EMB	Amb Amb Amb Amb Amb Amb	35,0,21,0 0,22,0,43 26,0,22,0 0,36,35,0 41,0,21,0 0,41,21,0	0.63,0.0,0.38,0.0 0.0,0.34,0.0,0.66 0.54,0.0,0.46,0.0 0.0,0.51,0.49,0.0 0.66,0.0,0.34,0.0 0.0,0.66,0.34,0.0
33	ERR234605 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.43), L2.2.2.2.2.1(0.57)	rpoB_S450L rpsL_K43R katG_S315T kasA_G269S eis-promoter_G-10A embB_M306L embB_D1024N	TCG/TTG AAG/AGG AGC/ACC GGT/AGT - ATG/CTG GAC/AAC	RIF SM INH INH KAN EMB EMB	Amb Amb Amb Amb Amb Amb Amb	0,35,0,48 41,0,22,0 0,57,35,0 32,0,49,0 46,0,47,0 45,44,0,0 47,0,28,0	0.0,0.42,0.0,0.58 0.65,0.0,0.35,0.0 0.0,0.62,0.38,0.0 0.4,0.0,0.6,0.0 0.49,0.0,0.51,0.0 0.51,0.49,0.0,0.0 0.63,0.0,0.37,0.0
34	ERR067732 (Lit.Casali2014)	L4.1.1.2.2(0.86), L2.2.2.2.2.1(0.14)	rrs_A1391G eis-promoter_G-37T	- -	AMK,CAP,KAN,SM KAN	Amb Amb	8,0,9,0 0,0,25,20	0.47,0.0,0.53,0.0 0.0,0.0,0.56,0.44
35	ERR234567 (Lit.Casali2014)	L2.2.2.2.2.1(0.68), L4.1.2.1.2(0.32)	rrs_C507T katG_S315T	- AGC/ACC	AMK,CAP,KAN,SM INH	Amb Amb	0,31,0,50 0,61,32,0	0.0,0.38,0.0,0.62 0.0,0.66,0.34,0.0
36	ERR108438 (Lit.Casali2014)	L2.2.2.2.2.1(0.27), L4.2.1.1.1(0.63), L4.1.2.1.1.1.1(0.1)	rpoB_D435Y rpoB_S450L rpoB_E761D fabG1-promoter_T-8A katG_S315T kasA_G269S eis-promoter_G-37T embB_M306I embB_D354A	GAC/TAC TCG/TTG GAG/GAC - AGC/ACC GGT/AGT - ATG/ATC GAC/GCC	RIF RIF RIF ETH,INH INH INH KAN EMB EMB	Amb Amb Amb Amb PASS Amb Amb Amb Amb	0,0,37,56 0,52,0,33 0,22,61,0 53,0,0,27 0,75,3,0 60,0,43,0 0,0,62,25 0,56,26,0 57,24,0,0	0.0,0.0,0.4,0.6 0.0,0.61,0.0,0.39 0.0,0.27,0.73,0.0 0.66,0.0,0.0,0.34 0.0,0.96,0.04,0.0 0.58,0.0,0.42,0.0 0.0,0.0,0.71,0.29 0.0,0.68,0.32,0.0 0.7,0.3,0.0,0.0
37	ERR403282 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.18), L2.2.2.2.2.1(0.82)	gyrA_D94G rpoB_S450L rpoC_I491T rpsL_K43R katG_S315T eis-promoter_G-10A embB_M306V	GAC/GGC TCG/TTG ATC/ACC AAG/AGG AGC/ACC - ATG/GTG	FQ RIF RIF SM INH KAN EMB	Amb PASS Amb PASS PASS Amb Amb	42,0,42,0 0,7,0,55 0,45,0,36 18,0,59,0 0,63,19,0 53,0,31,0 23,0,43,0	0.5,0.0,0.5,0.0 0.0,0.11,0.0,0.89 0.0,0.56,0.0,0.44 0.23,0.0,0.77,0.0 0.0,0.77,0.23,0.0 0.63,0.0,0.37,0.0 0.35,0.0,0.65,0.0
38	ERR234626 (Lit.Casali2014)	L2.2.2.2.2.1(0.35), L4.1.2.1.2(0.65)	rpoB_S450L rpoB_E761D rrs_C507T katG_S315T eis-promoter_G-37T embB_D354A	TCG/TTG GAG/GAC - AGC/ACC - GAC/GCC	RIF RIF AMK,CAP,KAN,SM INH KAN EMB	Amb Amb Amb PASS Amb Amb	1,86,2,43 0,53,105,0 0,110,0,51 0,157,1,0 1,0,113,55 112,43,0,0	0.01,0.65,0.02,0.33 0.0,0.34,0.66,0.0 0.0,0.68,0.0,0.32 0.0,0.99,0.01,0.0 0.01,0.0,0.67,0.33 0.72,0.28,0.0,0.0
39	ERR403285 (Lit.Casali2014)	L2.2.2.2.2.1(0.62), L4.1.2.1.1.2(0.38)	rpoB_S450L rpsL_K43R fabG1-promoter_C-15T katG_S315T pncA-promoter_A-11C eis-promoter_C-12T embB_M306V	TCG/TTG AAG/AGG - AGC/ACC - - ATG/GTG	RIF SM ETH,INH INH PZA KAN EMB	Amb Amb Amb Amb Amb Amb Amb	0,40,0,33 46,0,31,0 0,44,0,27 0,29,55,0 65,27,0,0 0,54,0,26 39,0,34,0	0.0,0.55,0.0,0.45 0.6,0.0,0.4,0.0 0.0,0.62,0.0,0.38 0.0,0.35,0.65,0.0 0.71,0.29,0.0,0.0 0.0,0.68,0.0,0.33 0.53,0.0,0.47,0.0
40	ERR144586 (Lit.Casali2014)	L4.2.1.1.1.2.2.1.1(0.76), L2.2.2.2.2.1(0.24)	gyrA_S91P rpoB_D435V rrs_A504C rrs_C507T rrs_A1391G fabG1-promoter_C-15T katG_S315T kasA_G269S eis-promoter_C-14T embB_M306I	TCG/CCG GAC/GTC - - - - AGC/ACC GGT/AGT - ATG/ATA	FQ RIF AMK,CAP,KAN,SM AMK,CAP,KAN,SM AMK,CAP,KAN,SM ETH,INH INH INH KAN EMB	PASS Amb Amb Amb Amb PASS PASS PASS Amb Amb	0,94,0,21 27,0,0,77 30,81,0,0 0,80,0,29 28,0,66,0 0,16,0,73 0,121,0,0 90,0,20,0 0,91,0,36 84,1,30,0	0.0,0.82,0.0,0.18 0.26,0.0,0.0,0.74 0.27,0.73,0.0,0.0 0.0,0.73,0.0,0.27 0.3,0.0,0.7,0.0 0.0,0.18,0.0,0.82 0.0,1.0,0.0,0.0 0.82,0.0,0.18,0.0 0.0,0.72,0.0,0.28 0.73,0.01,0.26,0.0
41	ERR040134 (Lit.Clark2013)	L4.2.1.1.2.2.2.2.1.2.1.2.1(0.98), L4.2.2.2(0.02)	rpoB_S450L katG_S315T pncA_H71R embB_G406D	TCG/TTG AGC/ACC CAT/CGT GGC/GAC	RIF INH PZA EMB	PASS PASS Amb PASS	0,0,2,271 0,342,1,0 196,0,110,1 262,1,21,0	0.0,0.0,0.01,0.99 0.0,1.0,0.0,0.0 0.64,0.0,0.36,0.0 0.92,0.0,0.07,0.0
42	ERR245795 (Lit.Guerra2014)	L3.1.2.1.2.1.1.2.1.2.2.2.2.2.2(0.36), L4.2.1.2.1(0.64)	rrs_C482T	-	AMK,CAP,KAN,SM	Amb	2,73,0,154	0.01,0.32,0.0,0.67
43	ERR036233 (Lit.Guerra2014)	L4.2.1.1.2.1.1(0.28), L1.2.1.1(0.72)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	PASS Amb	1,14,0,43 15,41,5,0	0.02,0.24,0.0,0.74 0.25,0.67,0.08,0.0
44	ERR037504 (Lit.Guerra2014)	L4.2.2.2.2.2.2.2.1.2.2.1(0.1), L4.2.2.2.2.2.2.2.1.2.2.2(0.9)	rpoB_L440L rrs_C789T rrs_C1392A rrs_G1474T pncA_L35R	CTG/CTC - - - CTG/CGG	RIF AMK,CAP,KAN,SM AMK,CAP,KAN,SM AMK,CAP,KAN,SM PZA	Amb Amb Amb Amb PASS	0,43,103,0 0,70,0,140 135,89,1,0 10,0,84,95 0,2,113,0	0.0,0.29,0.71,0.0 0.0,0.33,0.0,0.67 0.6,0.4,0.0,0.0 0.05,0.0,0.44,0.5 0.0,0.02,0.98,0.0
45	ERR036185 (Lit.Guerra2014)	L3.1.2.1.2.1.1.1.1(0.4), L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.1(0.6)	pncA_Q141P embA-promoter_C-16T	CAG/CCG -	PZA EMB	Amb Amb	17,6,0,0 0,15,0,6	0.74,0.26,0.0,0.0 0.0,0.71,0.0,0.29
46	ERR164021 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.2.1.2.1.2.2.1.2(0.7), L1.2.2.2.2.2.2(0.3)	rpoB_H445N inhA_S94A embC_T270I embB_E378A	CAC/AAC TCG/GCG ACC/ATC GAG/GCG	RIF ETH,INH EMB EMB	Amb Amb Amb Amb	40,118,0,0 0,0,48,130 0,136,0,58 121,54,3,1	0.25,0.75,0.0,0.0 0.0,0.0,0.27,0.73 0.0,0.7,0.0,0.3 0.68,0.3,0.02,0.01
47	ERR037469 (Lit.Guerra2014)	L1.2.2.1.2.2(0.37), L4.2.1.1.2.2.2.2.2.1.2.1.2.1.2(0.53), L4.2.1.1.2.2.2.2.1(0.11)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	1,188,1,90 232,115,9,0	0.0,0.67,0.0,0.32 0.65,0.32,0.03,0.0
48	ERR190379 (Lit.Guerra2014)	L1.2.1.1(0.78), L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.1(0.22)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,22,0,59 22,59,0,0	0.0,0.27,0.0,0.73 0.27,0.73,0.0,0.0
49	ERR181811 (Lit.Guerra2014)	L1.2.1.2.2.2.1.1.1(0.58), L4.1.1.2.1.2.2.2(0.42)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,14,0,18 24,27,1,0	0.0,0.44,0.0,0.56 0.46,0.52,0.02,0.0
50	ERR036211 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.1.1.2(0.59), L1.2.1.2.2.2(0.41)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,14,0,5 13,4,0,0	0.0,0.74,0.0,0.26 0.76,0.24,0.0,0.0

51	ERR176458 (Lit.Guerra2014)	L4.2.1.1.2.1.1.1(0.16), L4.2.1.1.1.2.2.2.1(0.84)	kasA_G269S	GGT/AGT	INH	Amb	31,0,11,0	0.74,0.0,0.26,0.0
52	ERR161078 (Lit.Guerra2014)	L1.2.1.2.2.2.2.2(0.42), L4.1.1.2.2.1.2(0.58)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,51,0,21 46,30,0,0	0.0,0.71,0.0,0.29 0.61,0.39,0.0,0.0
53	ERR176620 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.2.1.2.1.1.1(0.47), L4.2.1.1.1.2.2.2.1(0.53)	kasA_G269S	GGT/AGT	INH	Amb	33,0,28,0	0.54,0.0,0.46,0.0
54	ERR221561 (Lit.Guerra2014)	L4.2.1.1.2.2.1.2(0.32), L4.2.1.1.1.2.2.2.1(0.68)	kasA_G269S	GGT/AGT	INH	Amb	41,0,19,0	0.68,0.0,0.32,0.0
55	ERR190340 (Lit.Guerra2014)	L3.1.2.1.2.1.1.2.1.2.1(0.53), L4.2.2.2.2.2.2.2.1.2.2.1(0.47)	katG_S315T	AGC/ACC	INH	Amb	0,4,7,0	0.0,0.36,0.64,0.0
56	ERR216971 (Lit.Guerra2014)	L4.1.1.2.1.2.1(0.63), L4.1.2.2.2.1(0.37)	katG_S315T	AGC/ACC	INH	Amb	0,24,23,0	0.0,0.51,0.49,0.0
57	ERR176709 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.2.1(0.33), L3.1.2.1.2.1.1.2.1.2.2.2.1(0.67)	katG_S315T	AGC/ACC	INH	Amb	0,16,25,0	0.0,0.39,0.61,0.0
58	ERR473318 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.1(0.67), L1.2.1.2.2.2.2.1.1(0.33)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,39,0,27 37,15,0,0	0.0,0.59,0.0,0.41 0.71,0.29,0.0,0.0
59	ERR221663 (Lit.Guerra2014)	L1.2.1.2.2.2.1.1.1(0.65), L3.1.2.1.2.1.1.1.2.1.2.2.2.1(0.35)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,53,0,114 48,113,0,0	0.0,0.32,0.0,0.68 0.3,0.7,0.0,0.0
60	ERR181813 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.1.2.1.2.2(0.62), L1.2.1.2.2.2.2.2.1.2(0.38)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,27,0,22 39,14,0,0	0.0,0.55,0.0,0.45 0.74,0.26,0.0,0.0
61	ERR036224 (Lit.Guerra2014)	L1.2.1.2.2(0.38), L4.2.1.1.2.2.2.2.1(0.62)	rrs_G878A fabG1-promoter_C-15T embB_E378A	- - GAG/GCG	AMK,CAP,KAN,SM ETH,INH EMB	Amb Amb Amb	6,0,13,0 0,10,0,4 11,4,2,0	0.32,0.0,0.68,0.0 0.0,0.71,0.0,0.29 0.65,0.24,0.12,0.0
62	ERR163947 (Lit.Guerra2014)	L1.2.1.1(0.55), L1.2.2.2.2.2.2(0.45)	rpoB_H445N rrs_A504T inhA_S94A embC_T270I embB_E378A	CAC/AAC - TCG/GCG ACC/ATC GAG/GCG	RIF AMK,CAP,KAN,SM ETH,INH EMB EMB	Amb Amb Amb PASS PASS	23,24,0,0 37,0,0,17 0,0,28,32 0,1,0,60 4,70,0,0	0.49,0.51,0.0,0.0 0.69,0.0,0.0,0.31 0.0,0.0,0.47,0.53 0.0,0.02,0.0,0.98 0.05,0.95,0.0,0.0
63	ERR176616 (Lit.Guerra2014)	L4.2.1.1.2.2.2.2.2.1.2.1.2.2.2.2.2.1(0.63), L1.2.1.2.2.2.1.1.2(0.37)	rpoB_S450L rrs_C503T katG_S315T pncA_Q141P embC_T270I embA-promoter_C-16T embB_E378A	TCG/TTG - AGC/ACC CAG/CCG ACC/ATC - GAG/GCG	RIF AMK,CAP,KAN,SM INH PZA EMB EMB EMB	Amb Amb Amb Amb Amb Amb Amb	0,28,1,34 0,14,0,35 0,38,17,0 22,46,0,0 0,28,0,18 0,22,1,40 32,23,1,1	0.0,0.44,0.02,0.54 0.0,0.29,0.0,0.71 0.0,0.69,0.31,0.0 0.32,0.68,0.0,0.0 0.0,0.61,0.0,0.39 0.0,0.35,0.02,0.63 0.56,0.4,0.02,0.02
64	ERR278531 (Lit.Walker2012)	L3.1.2.1.2.1.1.1.2.1(0.47), L1.2.2.2.1.1(0.53)	rpsL_K88T katG_S315T embC_T270I embB_E378A	AAG/ACG AGC/ACC ACC/ATC GAG/GCG	SM INH EMB EMB	Amb Amb Amb Amb	46,59,0,0 1,44,45,0 0,49,0,55 43,42,0,0	0.44,0.56,0.0,0.0 0.01,0.49,0.5,0.0 0.0,0.47,0.0,0.53 0.51,0.49,0.0,0.0
65	ERR386890 (Lit.Walker2012)	L3.1.2.1.2.1.1.1.2.1(0.48), L1.2.2.2.1.1(0.52)	rpsL_K88T katG_S315T embC_T270I embB_E378A	AAG/ACG AGC/ACC ACC/ATC GAG/GCG	SM INH EMB EMB	Amb Amb Amb Amb	38,41,1,0 0,33,37,0 0,32,0,30 21,25,0,0	0.48,0.51,0.01,0.0 0.0,0.47,0.53,0.0 0.0,0.52,0.0,0.48 0.46,0.54,0.0,0.0
66	ERR386958 (Lit.Walker2012)	L1.1.1(0.51), L4.1.1.2.2.2.2(0.49)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,58,0,54 48,53,0,0	0.0,0.52,0.0,0.48 0.48,0.52,0.0,0.0
67	ERR230032 (Lit.Walker2012)	L3.1.2.1.2.1.1.1.1(0.13), L1.2.2.2.1.1(0.87)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	PASS Amb	0,6,0,34 10,24,0,0	0.0,0.15,0.0,0.85 0.29,0.71,0.0,0.0
68	ERR123949 (Lit.Walker2012)	L1.2.1.1(0.77), L4.1.1.2.2.1.1.2(0.23)	rpoB_D435Y embC_T270I embB_E378A	GAC/TAC ACC/ATC GAG/GCG	RIF EMB EMB	Amb PASS PASS	0,0,74,26 0,15,0,76 20,63,1,0	0.0,0.0,0.74,0.26 0.0,0.16,0.0,0.84 0.24,0.75,0.01,0.0
69	ERR123948 (Lit.Walker2012)	L5(0.16), L4.1.1.2.2.1.1.2(0.84)	rpoB_D435Y	GAC/TAC	RIF	Amb	0,0,23,39	0.0,0.0,0.37,0.63
70	ERR117660 (Lit.Walker2012)	L2.2.2.2.2.2(0.66), L3.1.2.1.2.1.1.2.2.2.1.1.1(0.34)	fabG1-promoter_C-15T	-	ETH,INH	Amb	0,32,0,56	0.0,0.36,0.0,0.64
71	ERR117639 (Lit.Walker2012)	L3.1.2.1.2.1.1.1.2.2(0.29), L1.2.2.2.2.1.1(0.71)	rpsL_K43R katG_S315T embC_T270I embB_E378A	AAG/AGG AGC/ACC ACC/ATC GAG/GCG	SM INH EMB EMB	Amb Amb PASS Amb	98,0,41,0 0,29,82,0 0,19,0,68 22,60,1,0	0.71,0.0,0.29,0.0 0.0,0.26,0.74,0.0 0.0,0.22,0.0,0.78 0.27,0.72,0.01,0.0
72	ERR117710 (Lit.Walker2012)	L1.2.2.2.1.2(0.38), L4.1.1.2.2.1.2(0.62)	katG_S315T embC_T270I embB_E378A	AGC/ACC ACC/ATC GAG/GCG	INH EMB EMB	Amb Amb Amb	0,142,78,0 0,148,0,91 114,88,0,0	0.0,0.65,0.35,0.0 0.0,0.62,0.0,0.38 0.56,0.44,0.0,0.0
73	PRJNA229653 (TBARC.Belarus)	L2.2.2.2.2.1(0.49), L4.1.1.2.1.2.2.1(0.09), L4.1.1.2.1.2.2.2.2.2.2.1(0.42)	rpoB_D435Y rpoB_S450L rpsL_K88R rrs_A1391G fabG1-promoter_C-15T katG_S315T embB_G406D embB_Q497R	GAC/TAC TCG/TTG AAG/AGG - - AGC/ACC GGC/GAC CAG/CGG	RIF RIF SM AMK,CAP,KAN,SM ETH,INH INH EMB EMB	Amb Amb Amb PASS Amb PASS Amb Amb	1,1,273,244 0,288,8,294 281,0,229,0 109,3,1266,2 0,189,2,278 2,363,1,0 136,0,241,0 212,4,228,0	0.0,0.0,0.53,0.47 0.0,0.49,0.01,0.5 0.55,0.0,0.45,0.0 0.08,0.0,0.92,0.0 0.0,0.4,0.0,0.59 0.01,0.99,0.0,0.0 0.36,0.0,0.64,0.0 0.48,0.01,0.51,0.0
74	PRJNA229703 (TBARC.Belarus)	L4.2.1.1.1.2.2.1.1(0.92), L4.2.1.2(0.08)	gyrA_A90V rpoB_H445D rrs_A504C rrs_A1391G fabG1-promoter_C-15T katG_S315T pncA_D49G kasA_G269S eis-promoter_C-12T embA-promoter_C-12T embB_Q497R	GCG/GTG CAC/GAC - - - AGC/ACC GAC/GGC GGT/AGT - - CAG/CGG	FQ RIF AMK,CAP,KAN,SM AMK,CAP,KAN,SM ETH,INH INH PZA INH KAN EMB EMB	PASS PASS PASS Amb PASS PASS PASS PASS PASS PASS PASS	0,2,4,471 2,0,486,0 2,526,0,1 407,1,462,1 0,1,1,499 1,494,3,0 1,0,463,2 349,2,0,0 0,3,2,480 0,5,3,437 0,1,442,0	0.0,0.0,0.01,0.99 0.0,0.0,1.0,0.0 0.0,0.99,0.0,0.0 0.47,0.0,0.53,0.0 0.0,0.0,0.0,1.0 0.0,0.99,0.01,0.0 0.0,0.0,0.99,0.0 0.99,0.01,0.0,0.0 0.0,0.01,0.0,0.99 0.0,0.01,0.01,0.98 0.0,0.0,1.0,0.0

75	PRJNA223585 (TBARC.CDRC)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.12), L4.2.1.1.1.2.2.1(0.88)	rpoB_S428T	AGC/ACC	RIF	Amb	0,89,147,0	0.0,0.38,0.62,0.0
			rpoB_S428R	AGC/AGG	RIF	Amb	1,148,86,0	0.0,0.63,0.37,0.0
			rpoB_S431T	AGC/ACC	RIF	Amb	0,89,147,0	0.0,0.38,0.62,0.0
			rpoB_S431R	AGC/AGG	RIF	Amb	0,148,88,0	0.0,0.63,0.37,0.0
			rpoB_D435V	GAC/GTC	RIF	Amb	182,0,1,142	0.56,0.0,0.0,0.44
			rpoB_L440L	CTG/CTC	RIF	Amb	0,113,166,0	0.0,0.41,0.59,0.0
			rpoB_H445N	CAC/AAC	RIF	Amb	108,164,0,0	0.4,0.6,0.0,0.0
			rrs_C1392A	-	AMK,CAP,KAN,SM	Amb	283,125,0,0	0.69,0.31,0.0,0.0
			rrs_G1474T	-	AMK,CAP,KAN,SM	Amb	0,2,120,220	0.0,0.01,0.35,0.64
			katG_S315T	AGC/ACC	INH	PASS	0,114,12,0	0.0,0.9,0.1,0.0
			kasA_G269S	GGT/AGT	INH	PASS	109,0,21,0	0.84,0.0,0.16,0.0
			embB_G406S	GGC/AGC	EMB	PASS	222,1,23,1	0.9,0.0,0.09,0.0
76	PRJNA219769 (TBARC.CDRC)	L2.2.2.2.2.1(0.9), L2.1(0.1)	gyrA_D94G	GAC/GGC	FQ	PASS	7,0,58,0	0.11,0.0,0.89,0.0
			rpoB_S450L	TCG/TTG	RIF	PASS	0,9,0,56	0.0,0.14,0.0,0.86
			rpsL_K43R	AAG/AGG	SM	Del;Amb	36,0,36,0	0.5,0.0,0.5,0.0
			katG_S140N	AGC/AAC	INH	Amb	52,0,37,0	0.58,0.0,0.42,0.0
			katG_Q127P	CAG/CCG	INH	Amb	48,22,0,0	0.69,0.31,0.0,0.0
			pncA-promoter_A-11G	-	PZA	PASS	8,0,41,0	0.16,0.0,0.84,0.0
			embB_M306L	ATG/TTG	EMB	PASS	8,0,1,52	0.13,0.0,0.02,0.85
			embB_G406D	GGC/GAC	EMB	PASS	35,0,6,0	0.85,0.0,0.15,0.0
77	PRJNA223557 (TBARC.CDRC)	L3.1.1.1(0.36), L2.2.2.2.2.1(0.64)	gyrA_D94A	GAC/GCC	FQ	Amb	289,256,1,0	0.53,0.47,0.0,0.0
			rpoB_S450L	TCG/TTG	RIF	Amb	2,196,0,113	0.01,0.63,0.0,0.36
			embB_H1002R	CAC/CGC	EMB	Amb	197,2,96,0	0.67,0.01,0.33,0.0
78	PRJNA223599 (TBARC.CDRC)	L4.2.1.1.1.2.2.1.1(0.22), L4.1.1.2.1.2.2.1(0.14), L4.1.1.2.1.2.2.2.2.2.1(0.64)	rpoB_H445Y	CAC/TAC	RIF	Amb	90,1,0,224	0.29,0.0,0.0,0.71
			katG_S315T	AGC/ACC	INH	Amb	0,79,214,0	0.0,0.27,0.73,0.0
79	PRJNA233338 (TBARC.CDRC)	L2.2.2.2.2.2.1(0.7), L4.2.2.2.2.1.2.2.1(0.3)	gyrA_T80A	ACC/GCC	FQ	Amb	48,0,25,0	0.66,0.0,0.34,0.0
			rpoB_S450L	TCG/TTG	RIF	PASS	0,1,0,61	0.0,0.02,0.0,0.98
			rpsL_K43R	AAG/AGG	SM	Amb	26,0,53,0	0.33,0.0,0.67,0.0
			rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,67,1,25	0.0,0.72,0.01,0.27
			katG_S315T	AGC/ACC	INH	PASS	0,80,0,0	0.0,1.0,0.0,0.0
			pncA_V139A	GTG/GCG	PZA	PASS	0,54,0,14	0.0,0.79,0.0,0.21
			embA-promoter_C-16T	-	EMB	Amb	0,40,0,16	0.0,0.71,0.0,0.29
			embB_E405D	GAG/GAC	EMB	Amb	0,16,40,0	0.0,0.29,0.71,0.0
80	PRJNA223593 (TBARC.CDRC)	L4.1.1.2.1.2.2.2.1(0.83), L4.2.2.2.1.2.2.1(0.17)	rpoB_S428T	AGC/ACC	RIF	Amb	0,33,62,0	0.0,0.35,0.65,0.0
			rpoB_S428R	AGC/AGG	RIF	Amb	0,62,33,0	0.0,0.65,0.35,0.0
			rpoB_S431T	AGC/ACC	RIF	Amb	0,33,67,0	0.0,0.33,0.67,0.0
			rpoB_S431R	AGC/AGG	RIF	Amb	0,69,33,0	0.0,0.68,0.32,0.0
			rpoB_L440L	CTG/CTC	RIF	Amb	0,93,58,0	0.0,0.62,0.38,0.0
			rpsL_K88R	AAG/AGG	SM	Amb	51,0,61,0	0.46,0.0,0.54,0.0
			rrs_C482T	-	AMK,CAP,KAN,SM	Del	2,280,1,1298	0.0,0.18,0.0,0.82
			rrs_C789T	-	AMK,CAP,KAN,SM	Del	0,421,1,1361	0.0,0.24,0.0,0.76
			rrs_C1392A	-	AMK,CAP,KAN,SM	Del	1547,380,0,0	0.8,0.2,0.0,0.0
			rrs_G1474T	-	AMK,CAP,KAN,SM	Del	0,4,390,1353	0.0,0.0,0.22,0.77
81	PRJNA233333 (TBARC.CDRC)	L3.1.2.1.2.1.1.2.1.2.1(0.67), L4.2.2.2.2.1.2.2.1(0.33)	gyrA_T80A	ACC/GCC	FQ	Amb	25,0,10,0	0.71,0.0,0.29,0.0
			rpoB_S450L	TCG/TTG	RIF	Amb	0,13,0,8	0.0,0.62,0.0,0.38
			katG_S315T	AGC/ACC	INH	Amb	0,9,21,0	0.0,0.3,0.7,0.0
82	PRJNA233331 (TBARC.CDRC)	L4.2.1.1.1.2.2.1(0.12), L4.2.2.1.2.2.1(0.88)	rpoB_S431T	AGC/ACC	RIF	Amb	0,20,38,0	0.0,0.34,0.66,0.0
			rrs_C452T	-	AMK,CAP,KAN,SM	Amb	0,70,0,37	0.0,0.65,0.0,0.35
			embC_T270I	ACC/ATC	EMB	Amb	0,28,0,20	0.0,0.58,0.0,0.42
			embB_H312R	CAC/CGC	EMB	Amb	50,0,17,0	0.75,0.0,0.25,0.0
83	PRJNA233337 (TBARC.CDRC)	L2.2.2.2.2.2.1(0.76), L4.2.2.2.2.1.2.2.1(0.24)	gyrA_T80A	ACC/GCC	FQ	Amb	27,0,13,0	0.68,0.0,0.33,0.0
			rpoB_S450L	TCG/TTG	RIF	PASS	0,0,0,68	0.0,0.0,0.0,1.0
			rpsL_K43R	AAG/AGG	SM	Amb	20,0,39,0	0.34,0.0,0.66,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,56,0,0	0.0,1.0,0.0,0.0
			pncA_V139A	GTG/GCG	PZA	PASS	0,50,0,17	0.0,0.75,0.0,0.25
			embA-promoter_C-16T	-	EMB	Amb	0,44,0,14	0.0,0.76,0.0,0.24
			embB_E405D	GAG/GAC	EMB	Amb	0,12,31,0	0.0,0.28,0.72,0.0
84	PRJNA223548 (TBARC.CDRC)	L3.1.2.1.2.1.1.2.1.1.2.1(0.6), L4.2.1.1.2.2.2.2.1(0.4)	rpoB_Q432K	CAA/AAA	RIF	Amb	79,54,0,0	0.59,0.41,0.0,0.0
			rpoB_D435V	GAC/GTC	RIF	Amb	83,0,1,56	0.59,0.0,0.01,0.4
			katG_S315T	AGC/ACC	INH	PASS	0,91,0,0	0.0,1.0,0.0,0.0
			pncA_Q10R	CAG/CGG	PZA	Amb	68,0,54,0	0.56,0.0,0.44,0.0
			embB_M306V	ATG/GTG	EMB	Amb	57,0,77,0	0.43,0.0,0.57,0.0
85	PRJNA223579 (TBARC.CDRC)	L4.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.38), L4.2.2.2.2.2.2.1.2.2.2.2.1.2.1(0.62)	rpoB_S450L	TCG/TTG	RIF	Amb	0,137,0,225	0.0,0.38,0.0,0.62
			rpsL_K43R	AAG/AGG	SM	Amb	209,0,106,0	0.66,0.0,0.34,0.0
			rpsL_K88R	AAG/AGG	SM	Amb	99,0,160,1	0.38,0.0,0.62,0.0
			eis-promoter_G-10A	-	KAN	Amb	172,0,94,0	0.65,0.0,0.35,0.0
86	PRJNA226772 (TBARC.CDRC)	L1(0.1), L2.2.1(0.9)	katG_S140N	AGC/AAC	INH	Amb	66,1,35,1	0.64,0.01,0.34,0.01
87	PRJNA233332 (TBARC.CDRC)	L3.1.2.1.2.1.1.2.1.2.1(0.67), L4.2.2.2.2.2.1.2.2.1(0.33)	rpoB_S450L	TCG/TTG	RIF	Amb	0,22,0,11	0.0,0.67,0.0,0.33
			embB_M306I	ATG/ATA	EMB	Amb	12,0,17,0	0.41,0.0,0.59,0.0
88	PRJNA223545 (TBARC.CDRC)	L4.2.2.2.2.2.1.2.2.2(0.97), L3.1(0.03)	gyrA_T80A	ACC/GCC	FQ	PASS	4,0,129,1	0.03,0.0,0.96,0.01
			rpoB_S450L	TCG/TTG	RIF	PASS	0,56,1,343	0.0,0.14,0.0,0.86
			rpoC_G332R	GGC/CGC	RIF	Amb	2,328,155,0	0.0,0.68,0.32,0.0
			rpsL_K88R	AAG/AGG	SM	Amb	539,2,233,0	0.7,0.0,0.3,0.0
			rrs_C789T	-	AMK,CAP,KAN,SM	Del	1,268,0,1186	0.0,0.18,0.0,0.82
			rrs_C1392A	-	AMK,CAP,KAN,SM	Del;Amb	1109,355,1,0	0.76,0.24,0.0,0.0
			rrs_G1474T	-	AMK,CAP,KAN,SM	Del;Amb	0,0,380,567	0.0,0.0,0.4,0.6
			katG_S315T	AGC/ACC	INH	PASS	1,212,3,0	0.0,0.98,0.01,0.0
89	PRJNA233322 (TBARC.CDRC)	L3.1.1.1(0.71), L2.2.2.2.2.1(0.29)	gyrA_D94A	GAC/GCC	FQ	Amb	6,12,0,0	0.33,0.67,0.0,0.0
			rpoB_S450L	TCG/TTG	RIF	PASS	0,0,0,23	0.0,0.0,0.0,1.0
			katG_S315T	AGC/ACC	INH	Amb	0,13,39,0	0.0,0.25,0.75,0.0
			eis-promoter_G-10A	-	KAN	Amb	22,0,35,0	0.39,0.0,0.61,0.0
			embB_H1002R	CAC/CGC	EMB	Amb	11,1,24,0	0.31,0.03,0.67,0.0

90	PRJNA223539 (TBARC.CDRC)	L4.2.2.2.2.1.2.2.2(0.75), L4.2.2.1.2.2.1(0.25)	gyrA_T80A fabG1-promoter_C-15T	ACC/GCC -	FQ ETH,INH	PASS Amb	79,1,215,0 0,77,0,175	0.27,0.0,0.73,0.0 0.0,0.31,0.0,0.69
91	PRJNA237435 (TBARC.Iran)	L1.2.2.2.1(0.1), L1.2.1.1(0.17), L4.2.1.1(0.17), L2.2.2.2.2.1(0.47), L3.1(0.08)	gyrA_A90V rpoB_S450L rrs_A1391G katG_S315T eis-promoter_C-14T embB_D354A embB_E378A	GCG/GTG TCG/TTG - AGC/ACC - GAC/GCC GAG/GCG	FQ RIF AMK,CAP,KAN,SM INH KAN EMB EMB	Amb Amb Amb Amb Amb Amb Amb	0,36,0,38 0,16,1,28 43,0,39,0 0,59,24,0 0,68,0,34 77,35,1,0 12,12,0,0	0.0,0.49,0.0,0.51 0.0,0.36,0.02,0.62 0.52,0.0,0.48,0.0 0.0,0.71,0.29,0.0 0.0,0.67,0.0,0.33 0.68,0.31,0.01,0.0 0.5,0.5,0.0,0.0
92	PRJNA183520 (Lit.Cohen2015)	L4.1(0.02), L4.2.2.1.2.2.2.1(0.92), L4.2.2.1.2.2.2.1(0.06)	rpoB_S441L fabG1-promoter_T-8A katG_S315T embB_M306I	TCG/TTG - AGC/ACC ATG/ATC	RIF ETH,INH INH EMB	PASS Amb PASS PASS	0,5,13,1161 620,2,7,422 6,1191,8,5 2,1051,8,3	0.0,0.0,0.01,0.98 0.59,0.0,0.01,0.4 0.0,0.98,0.01,0.0 0.0,0.99,0.01,0.0
93	PRJNA183518 (Lit.Cohen2015)	L2.2.2.2.2.1(0.41), L4.1.1.2.1.2.2.1(0.32), L4.1.1.2.1.2.2.2.2(0.27)	gyrA_D94G rpoB_H445Y rpoB_H445L fabG1-promoter_C-15T katG_S315T embB_E405D	GAC/GGC CAC/TAC CAC/CTC - AGC/ACC GAG/GAC	FQ RIF RIF ETH,INH INH EMB	Amb Amb Amb Amb PASS Amb	401,1,280,0 1,365,0,457 466,3,5,356 1,364,5,525 0,444,1,0 1,207,318,3	0.59,0.0,0.41,0.0 0.0,0.44,0.0,0.56 0.56,0.0,0.01,0.43 0.0,0.41,0.01,0.59 0.0,1.0,0.0,0.0 0.0,0.39,0.6,0.01
94	PRJNA198110 (Lit.Cohen2015)	L4.2.1.1.1.2.2.2.2(0.2), L4.2.2.1.2.2.2.1(0.8)	gyrA_A90V rpoB_D435G rpoB_S450L rpoB_L452P rrs_A1391G katG_S315T embB_M306I	GCG/GTG GAC/GGC TCG/TTG CTG/CCG - AGC/ACC ATG/ATC	FQ RIF RIF RIF AMK,CAP,KAN,SM INH EMB	Amb Amb Amb Amb Amb PASS PASS	0,480,1,153 522,6,176,2 2,157,2,485 1,154,2,481 570,9,374,1 1,623,2,1 4,512,98,1	0.0,0.76,0.0,0.24 0.74,0.01,0.25,0.0 0.0,0.24,0.0,0.75 0.0,0.24,0.0,0.75 0.6,0.01,0.39,0.0 0.0,0.99,0.0,0.0 0.01,0.83,0.16,0.0
95	PRJNA218261 (Lit.Cohen2015)	L1.2.1.1(0.34), L4.2.1.2.1(0.66)	rrs_C482T embC_T270I	- ACC/ATC	AMK,CAP,KAN,SM EMB	Amb Amb	1,104,1,186 1,85,1,51	0.0,0.36,0.0,0.64 0.01,0.62,0.01,0.37
96	PRJNA183522 (Lit.Cohen2015)	L4.2.2.2.2.2.2.2.1.2.2.2.2.1.2.2(0.44), L4.1.1.2.2.1.1.2(0.56)	katG_S315T	AGC/ACC	INH	Amb	1,470,562,1	0.0,0.45,0.54,0.0
97	PRJNA235418 (Lit.Cohen2015)	L2.2.2.2.2.1(0.76), L4.1.1(0.09), L4.2.1.2.1(0.06), L4.2.1.1(0.09)	rpoB_S431T embB_M482I	AGC/ACC ATG/ATC	RIF EMB	Amb Amb	0,45,107,0 0,33,85,0	0.0,0.3,0.7,0.0 0.0,0.28,0.72,0.0
98	PRJNA235404 (Lit.Cohen2015)	L4.1.1.2.1.2.1(0.52), L1.2.2.1.2.2(0.48)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	2,164,0,154 187,170,0,0	0.01,0.51,0.0,0.48 0.52,0.48,0.0,0.0
99	PRJNA235455 (Lit.Cohen2015)	L1.2.2.2.2.2.2(0.72), L2.2.2.2.2.1(0.27), L4.2.2.2.2.1.2.2.2(0.01)	embC_T270I embB_E378A	ACC/ATC GAG/GCG	EMB EMB	Amb Amb	0,120,0,274 119,293,2,0	0.0,0.3,0.0,0.7 0.29,0.71,0.0,0.0
100	PRJNA235445 (Lit.Cohen2015)	L2.2.2.2.2.1(0.28), L4.2.1.2.1(0.72)	rrs_C482T	-	AMK,CAP,KAN,SM	Amb	0,133,2,308	0.0,0.3,0.0,0.7
101	PRJNA235414 (Lit.Cohen2015)	L2.2.2.2.2.1(0.37), L4.2.1.2.1(0.63)	rrs_C482T	-	AMK,CAP,KAN,SM	Amb	1,118,3,204	0.0,0.36,0.01,0.63
102	PRJNA211645 (TBARC.Mali)	L4.1.1.1(0.07), LB(0.64), L6.2(0.28)	inhA_V78A embC_T270I embB_E378A	GTG/GCG ACC/ATC GAG/GCG	ETH,INH EMB EMB	Amb PASS PASS	0,21,0,62 0,5,0,40 7,40,0,0	0.0,0.25,0.0,0.75 0.0,0.11,0.0,0.89 0.15,0.85,0.0,0.0
103	PRJNA211666 (TBARC.Mali)	L4.1.1.1(0.14), L5(0.17), L6.2(0.69)	inhA_V78A embC_T270I embB_E378A	GTG/GCG ACC/ATC GAG/GCG	ETH,INH EMB EMB	Amb PASS PASS	0,47,1,22 0,14,0,57 14,50,1,0	0.0,0.67,0.01,0.31 0.0,0.2,0.0,0.8 0.22,0.77,0.02,0.0
104	PRJNA211649 (TBARC.Mali)	L6.2(0.85), L4.2.2.2.2.1.1(0.04), L4.1.1.1(0.06), L4.1.1.2.1.2.2.2(0.05)	inhA_V78A embC_T270I embB_E378A	GTG/GCG ACC/ATC GAG/GCG	ETH,INH EMB EMB	PASS PASS Amb	0,158,2,47 1,31,0,110 72,160,2,0	0.0,0.76,0.01,0.23 0.01,0.22,0.0,0.77 0.31,0.68,0.01,0.0
105	PRJNA234649 (TBARC.Moldova)	L4.2.1.1.1.2.2.1.1(0.54), L2.2.2.2.2.1(0.46)	kasA_G269S	GGT/AGT	INH	Amb	81,0,44,0	0.65,0.0,0.35,0.0
106	PRJNA228093 (TBARC.MRC)	L3.1.2.1.2.1.1.1.2.1.2.1(0.72), L3.1.2.1.2.1.1.1.1.1(0.28)	rpoB_D435V rrs_A896G rrs_A1391G katG_S315T embB_M306I	GAC/GTC - - AGC/ACC ATG/ATA	RIF AMK,CAP,KAN,SM AMK,CAP,KAN,SM INH EMB	PASS Amb Amb PASS PASS	1,1,2,186 201,0,76,0 204,1,111,0 1,212,1,0 123,0,0,0	0.01,0.01,0.01,0.98 0.73,0.0,0.27,0.0 0.65,0.0,0.35,0.0 0.0,0.99,0.0,0.0 1.0,0.0,0.0,0.0
107	PRJNA228132 (TBARC.MRC)	L4.1(0.09), L4.2.2.1.2.2.2.2(0.64), L4.2.2.1.2.2.1(0.26)	gyrA_D94G rpoB_S450L katG_S315T embB_M306L	GAC/GGC TCG/TTG AGC/ACC ATG/CTG	FQ RIF INH EMB	Amb PASS PASS PASS	71,0,109,0 0,6,1,227 1,244,0,0 2,231,0,0	0.39,0.0,0.61,0.0 0.0,0.03,0.0,0.97 0.0,1.0,0.0,0.0 0.01,0.99,0.0,0.0
108	PRJNA228113 (TBARC.MRC)	L2.2.2.2.2.1(0.88), L2.2.2.2.1(0.12)	rpoB_S450L katG_S315N embB_D354A embB_Q497R	TCG/TTG AGC/AAC GAC/GCC CAG/CGG	RIF INH EMB EMB	PASS PASS Amb Amb	0,1,0,215 195,2,1,0 94,43,0,0 58,0,119,0	0.0,0.0,0.0,1.0 0.98,0.01,0.01,0.0 0.69,0.31,0.0,0.0 0.33,0.0,0.67,0.0
109	PRJNA228069 (TBARC.MRC)	L4.2.1.1.1.2.2.2.2(0.51), L3.1.2.1.2.1.1.2.1.2.1(0.49)	gyrA_A90V rpoB_D435G rpoB_L452P rrs_A1391G fabG1-promoter_T-8A katG_S315T kasA_G269S embB_M306V embB_M306I	GCG/GTG GAC/GGC CTG/CCG - - AGC/ACC GGT/AGT ATG/GTG ATG/ATA	FQ RIF RIF AMK,CAP,KAN,SM ETH,INH INH INH EMB EMB	Amb Amb Amb Amb Amb PASS Amb Amb Amb	0,254,1,226 173,1,188,0 0,163,1,150 224,0,233,1 191,0,2,202 0,324,3,1 149,0,138,0 157,0,159,0 157,0,163,2	0.0,0.53,0.0,0.47 0.48,0.0,0.52,0.0 0.0,0.52,0.0,0.48 0.49,0.0,0.51,0.0 0.48,0.0,0.01,0.51 0.0,0.99,0.01,0.0 0.52,0.0,0.48,0.0 0.5,0.0,0.5,0.0 0.49,0.0,0.51,0.01
110	PRJNA228073 (TBARC.MRC)	L4.2.2.1.2.2.2.2(0.93), L4.2.2.1.2.2.1(0.07)	rrs_C507T katG_S315T embB_M306I	- AGC/ACC ATG/ATA	AMK,CAP,KAN,SM INH EMB	Amb PASS PASS	0,352,1,182 0,410,1,0 421,1,1,0	0.0,0.66,0.0,0.34 0.0,1.0,0.0,0.0 1.0,0.0,0.0,0.0
111	PRJNA228114 (TBARC.MRC)	L2.2.2.2.2.1(0.86), L2.2.2.2.1(0.14)	rpoB_S450L katG_S315N embB_M306I	TCG/TTG AGC/AAC ATG/ATA	RIF INH EMB	PASS PASS Amb	0,17,0,192 148,0,0,1 36,5,99,0	0.0,0.08,0.0,0.92 0.99,0.0,0.0,0.01 0.26,0.04,0.71,0.0

112	PRJNA228051 (TBARC.MRC)	L2.1(0.37), L4.1.1.2.2.2.2.1.2(0.63)	rpoB_D435V	GAC/GTC	RIF	Amb	301,2,0,179	0.62,0.0,0.0,0.37
			rpoB_H445D	CAC/GAC	RIF	Amb	2,169,338,1	0.0,0.33,0.66,0.0
			rrs_A504C	-	AMK,CAP,KAN,SM	Amb	308,185,1,0	0.62,0.37,0.0,0.0
			rrs_A1391G	-	AMK,CAP,KAN,SM	Amb	351,5,206,2	0.62,0.01,0.37,0.0
			fabG1-promoter_G-17T	-	ETH,INH	Amb	0,0,314,145	0.0,0.0,0.68,0.32
			katG_S315T	AGC/ACC	INH	PASS	0,480,3,0	0.0,0.99,0.01,0.0
			embB_G406D	GGC/GAC	EMB	PASS	690,6,59,2	0.91,0.01,0.08,0.0
113	PRJNA228141 (TBARC.MRC)	L4.2.1.1.2.2.2.2.1(0.13), L4.2.2.1.2.2.2.2(0.42), L4.2.2.1.2.2.1(0.24), L4.2.1.1.2.2.2.2.2.2.2.2.2(0.21)	rpoB_H445L	CAC/CTC	RIF	Amb	126,0,1,64	0.66,0.0,0.01,0.34
			rpoB_S450L	TCG/TTG	RIF	Amb	0,70,0,121	0.0,0.37,0.0,0.63
			rpsL_K43R	AAG/AGG	SM	Amb	101,1,268,0	0.27,0.0,0.72,0.0
			rrs_A1391G	-	AMK,CAP,KAN,SM	Amb	157,2,242,0	0.39,0.0,0.6,0.0
			katG_S315T	AGC/ACC	INH	PASS	0,189,2,0	0.0,0.99,0.01,0.0
			embB_M306I	ATG/ATA	EMB	Amb	95,0,55,0	0.63,0.0,0.37,0.0
			embB_G406A	GGC/GCC	EMB	Amb	0,31,51,1	0.0,0.37,0.61,0.01
			embB_D1024N	GAC/AAC	EMB	Amb	51,0,130,0	0.28,0.0,0.72,0.0
114	PRJNA228070 (TBARC.MRC)	L3.1.2.1.2.1.1.2.1.2.1(0.89), L3.1.2.1.2.1.1.1.1(0.11)	rpoB_H445Y	CAC/TAC	RIF	Amb	0,466,0,158	0.0,0.75,0.0,0.25
			rpoB_S450L	TCG/TTG	RIF	Amb	1,417,6,181	0.0,0.69,0.01,0.3
			katG_S315T	AGC/ACC	INH	PASS	1,551,2,1	0.0,0.99,0.0,0.0
			embB_M306I	ATG/ATA	EMB	PASS	564,2,0,0	1.0,0.0,0.0,0.0
115	PRJNA228074 (TBARC.MRC)	L4.2.2.1.2.2.2.2(0.9), L4.2.2.1.2.2.1(0.1)	rrs_C507T	-	AMK,CAP,KAN,SM	Amb	0,167,1,259	0.0,0.39,0.0,0.61
			katG_S315T	AGC/ACC	INH	PASS	0,333,3,0	0.0,0.99,0.01,0.0
			embB_M306I	ATG/ATA	EMB	PASS	349,1,3,0	0.99,0.0,0.01,0.0
116	PRJNA228083 (TBARC.MRC)	L4.1.1.2.2.1.1.1(0.38), L4.2.2.2.2.2.2.1.2.1(0.62)	rpoB_S450L	TCG/TTG	RIF	PASS	0,2,1,341	0.0,0.01,0.0,0.99
			rpsL_K43R	AAG/AGG	SM	Amb	140,0,232,0	0.38,0.0,0.62,0.0
			fabG1-promoter_C-15T	-	ETH,INH	Amb	0,203,1,93	0.0,0.68,0.0,0.31
			katG_S315T	AGC/ACC	INH	PASS	1,358,1,1	0.0,0.99,0.0,0.0
			embB_M306V	ATG/GTG	EMB	Amb	141,0,211,0	0.4,0.0,0.6,0.0
			embB_M306I	ATG/ATA	EMB	Amb	139,1,215,0	0.39,0.0,0.61,0.0
117	PRJNA228142 (TBARC.MRC)	L4.2.1.1.2.2.2.2.1(0.32), L4.2.2.1.2.2.2.2(0.21), L4.2.2.1.2.2.1(0.16), L4.2.1.1.2.2.2.2.2.2.2.2.2(0.31)	rpoB_H445L	CAC/CTC	RIF	Amb	64,0,0,102	0.39,0.0,0.0,0.61
			rpoB_S450L	TCG/TTG	RIF	Amb	0,87,2,56	0.0,0.6,0.01,0.39
			rpsL_K43R	AAG/AGG	SM	Amb	226,0,149,0	0.6,0.0,0.4,0.0
			rrs_A1391G	-	AMK,CAP,KAN,SM	Amb	372,3,183,0	0.67,0.01,0.33,0.0
			katG_S315T	AGC/ACC	INH	PASS	1,177,1,0	0.01,0.99,0.01,0.0
			embB_G406A	GGC/GCC	EMB	PASS	0,54,15,0	0.0,0.78,0.22,0.0
			embB_D1024N	GAC/AAC	EMB	Amb	138,0,59,1	0.7,0.0,0.3,0.01
118	PRJNA229272 (TBARC.Sweden)	L1(0.04), L2.2.2.2.2.1(0.75), L3.1(0.21)	rpoB_S450L	TCG/TTG	RIF	PASS	0,23,0,128	0.0,0.15,0.0,0.85
			rpsL_K88R	AAG/AGG	SM	PASS	21,0,84,12	0.18,0.0,0.72,0.1
			fabG1-promoter_C-15T	-	ETH,INH	PASS	0,13,0,57	0.0,0.19,0.0,0.81
			katG_S315T	AGC/ACC	INH	Amb	0,42,21,0	0.0,0.67,0.33,0.0
			pncA-promoter_T-7C	-	PZA	PASS	0,168,1,24	0.0,0.87,0.01,0.12
			embA-promoter_C-12T	-	EMB	PASS	0,23,0,127	0.0,0.15,0.0,0.85
			embB_Y334H	TAC/CAC	EMB	Amb	0,78,0,37	0.0,0.68,0.0,0.32

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