SUPPLEMENTAL INFORMATION:

Multidrug-resistant tuberculosis in Panama is driven by clonal expansion of an MDR-TB strain related to the KZN XDR-TB strain from South Africa

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Table S1. Sequencing statistics, spoligotype, and resistance-related polymorphisms for each isolate in the sample (see attached spreadsheet). The isolates are presented in the same order as in the phylogenetic tree (Figure 1), and are grouped by cluster using color.

Table S2. Mutations at sites other than S315 in KatG among INH-resistant isolates.

KatG:S315T*	InhA:c-15t	num.	num. with polymorphisms in KatG other than at S315	polymorphisms in KatG other than at S315
-	-	10	8	T275I, A379V+W328R**, D94G (2), T766P+G125I, W198stop, Q722stop, W300R
-	+	9	5	T380I, W191R (2), Y304C, L617F
+	-	47	1	P136A
+	+	4	0	none

*S315G is counted as S315T; the case with the large-scale deletion of KatG is excluded.

**Note that some strains had more than one amino acid substitution in KatG.

Table S3. List of polymorphisms uniquely associated with cluster LAM9-c1.

Rv0003/recF:V54I	Rv1132:L353R	Rv1865c:G208R	3503219:G>A
Rv0045c:W45*	Rv1138c:G48R	Rv1868:T9P	3542064:C>T
130864:C>T	Rv1161/narG:D253N	2198554:A>C	3546879:A>C
Rv0138:V35V	Rv1183/mmpL10:D560D	2219567:A>C	Rv3190c:G394A
Rv0194:A302T	Rv1185c/fadD21:P548P	Rv2025c:I127T	Rv3223c/sigH:G16R
Rv0209:H313R	Rv1188:I244V	Rv2036:A209V	Rv3239c:S95F
Rv0231/fadE4:M148T	Rv1238/sugC:A385P	Rv2043c/pncA:G16G	Rv3297/nei:I111F
Rv0233/nrdB:A295E	Rv1251c:G629R	2307576:C>T	Rv3329:V21F
Rv0275c:A110V	Rv1254:V37V	Rv2124c/metH:A310V	Rv3347c/PPE55:G711G
Rv0304c/PPE5:F1845S	Rv1286/cysN:A78A	Rv2127/ansP1:A142P	Rv3391/acrA1:P615L
Rv0329c:A142T	Rv1292/argS:M91I	Rv2212:A329T	3907020:A>C
Rv0360c:S48*	Rv1308/atpA:R142R	Rv2305:L213L	Rv3527:H28H
Rv0467/icl:S142S	1475277:G>A	Rv2307c:L101L	Rv3529c:P115A
579212:T>A	1702851:G>A	2698312:G>A	4014057:G>T
Rv0538:L226L	1718720:A>G	Rv2495c/pdhC:S238S	Rv3602c/panC:G129G
Rv0586:G213G	Rv1539/lspA:P2S	Rv2510c:A14A	Rv3663c/dppD:H195H
Rv0624:S13T	Rv1547/dnaE:A1031S	Rv2515c:A81V	Rv3671c:P95Q
Rv0667/rpoB:A692T	Rv1551/plsB1:P32A	Rv2525c:G78G	4121585:G>C
Rv0691c:E4E	Rv1567c:F14F	Rv2802c:R198W	Rv3682/ponA2:P804P
812819:A>G	Rv1619:H107Y	Rv2876:L67L	Rv3746c/PE34:S87L
Rv0894:V383I	Rv1747:D841D	Rv2881c/cdsA:L125L	4196579:C>T
1108545:G>A	Rv1770:T370T	Rv2905/lppW:V137G	Rv3860:P389P
Rv0997:T58T	Rv1771:A116V	Rv2948c/fadD22:R2W	Rv3877:T11I
Rv1046c:A26V	Rv1779c:E437E	Rv3049c:V57I	Rv3881c:Q431*
Rv1052:G14S	Rv1781c/malQ:R172H	Rv3120:C71R	Rv3882c:R431R

Figure S1. Maximum parsimony phylogenetic tree of drug-susceptible isolates, based on 7,955 SNPs from a multiple-genome alignment. The locations of the four major clusters of MDR isolates within the LAM family (from Figure 1) are highlighted in red.