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Strain Classification of *Mycobacterium tuberculosis* Isolates in Brazil Based on Genotypes Obtained by Spoligotyping, Mycobacterial Interspersed Repetitive Unit Typing and the Presence of Large Sequence and Single Nucleotide Polymorphism

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Abstract

Rio de Janeiro is endemic for tuberculosis (TB) and presents the second largest prevalence of the disease in Brazil. Here, we present the bacterial population structure of 218 isolates of *Mycobacterium tuberculosis*, derived from 186 patients that were diagnosed between January 2008 and December 2009. Genotypes were generated by means of spoligotyping, 24 MIRU-VNTR typing and presence of fbpC^{103}, RD^{Rio} and RD174. The results confirmed earlier data that predominant genotypes in Rio de Janeiro are those of the Euro American Lineages (99%). However, we observed differences between the classification by spoligotyping when comparing to that of 24 MIRU-VNTR typing, being respectively 43.6% vs. 62.4% of LAM, 34.9% vs. 9.6% of T and 18.3% vs. 21.5% of Haarlem. Among isolates classified as LAM by MIRU typing, 28.0% did not present the characteristic spoligotype profile with absence of spacers 21 to 24 and 32 to 36 and we designated these conveniently as ''LAM-like'', 79.3% of these presenting the LAM-specific SNP *fbpC*^{103}. The frequency of RD^{Rio} and RD174 in the LAM strains, as defined both by spoligotyping and 24 MIRU-VNTR loci, were respectively 11% and 15.4%, demonstrating that RD174 is not always a marker for LAM/RD^{Rio} strains. We conclude that, although spoligotyping alone is a tool for classification of strains of the Euro-American lineage, when combined with MIRU-VNTRs, SNPs and RD typing, it leads to a much better understanding of the bacterial population structure and phylogenetic relationships among strains of *M. tuberculosis* in regions with high incidence of TB.

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Introduction

Tuberculosis (TB) is an infectious disease with an effective treatment but remains an important cause of morbidity and mortality in many countries. In Brazil, 73.000 new TB cases and 4.600 cases that deceased were registered in 2011. The southeast region has 44.8% of all cases reported in the country and the state of Rio de Janeiro has the highest disease incidence (72.3/100,000) and mortality rate (5.7/100,000) in the country [1].

A couple of years ago, *Mycobacterium tuberculosis* (Mtb) strains designated as RD^{Rio} were reported as being a predominant genotype in Rio de Janeiro [2]. These strains have a deletion of 26.3 kb and seem to be restricted to the Latin American-Mediterranean (LAM) family. The RD^{Rio} strains have been associated with higher levels of recent transmission and of Multi-Drug Resistance (MDR) but there are contradictory data about their relation with disease severity [3], [4], [5], [6]. Another Region of Difference called RD174 has been described as a co-

marker of RD^{Rio} and as a marker for the LAM type [7], [8], [9], [10] and strains with the RD174 deletion were found to have an increased secondary case rate ratio in San Francisco [10].

The most commonly used genotyping methods to characterize *M. tuberculosis* Complex (MTBC) isolates are IS*6110*-RFLP, 24-locus MIRU-VNTR, spoligotyping, detection of Single Nucleotide Polymorphisms (SNPs) and Large Sequence Polymorphisms (LSP). Typing of MTBC by IS*6110*-RFLP was considered the gold-standard during more than a decade [11], but is labor intensive. Currently, the two most commonly used methods are spoligotyping and Mycobacterium Interspersed Repetitive Units – Variable Number of Tandem Repeats (MIRU-VNTR) typing, based on the variability of the direct repeat (DR) locus [12] and of minisatellites [13], [14], respectively. However, for epidemiologic studies, spoligotyping overestimates the proportion of clustered strains and should be used in combination with MIRU-VNTR typing [15]. Spoligotyping alone is also unable to reveal exact phylogenetic relationships between MTBC strains, particularly for the classification of Euro-American strains, part of the PGG2/PGG3 group [9], [16], [17], [18]. These phylogenetic subtypes include the genotype families LAM, H, T, S and X, frequently observed in Brazil, in South America and elsewhere [2], [4]. [8], [18], [19], [20], [21], [22], [23].

The generalized use of spoligotyping and MIRU-VNTR resulted in the construction of large international databases of genotypes, allowing the study of global distribution and phylogenetic analysis of the distribution of *M. tuberculosis* worldwide [23], [24], [25], [26], [27], [28], [29]. Combined MIRU-VNTR typing and spoligotyping also helps in revealing epidemiologically meaningful clonal diversity of *M. tuberculosis* strain lineages and is useful to explore internal phylogenetic ramifications [8]. In addition, SNPs and LSPs represent robust markers for inferring phylogenies and for strain classification [30], [31], [32], [33], [34], [35]. Besides the presence of RDs, that of determinate SNPs is also a characteristic of LAM strains, [8], [9], [10] such as $fbpC^{103}$ in codon 103 (G to A) of the gene encoding antigen 85 Complex $Ag85^{c}$ (Rv0129c) resulting in a Glu103Asp amino acid replacement in a protein that is involved in biosynthesis of cell wall components of *M. tuberculosis* [7], [36]. Other LAM-specific SNPs are (i) the silent C to G *ligB* mutation at genome position 3426795 [37], validated by the Abadia *et al.* [17] and (ii) the SNP at 240 codon of *mgtC* (C to T) that was discovered by Homolka *et al.* [38].

The objective of this study was to evaluate 24 MIRU-VNTR typing for alternative classification of strain families/lineages by means of phylogenetic tree building and comparison with MIRU databases (MIRU-VNTRPlus), as compared with spoligotypes-based classification (SITVITWEB and SITVIT2), and increase the consistency of the analysis by including a SNP and two LSPs. In addition, the differentiating power of both techniques in a population that is almost exclusively of the Euro-American lineages.

Materials and Methods

Study setting

The study was based on a convenience sampling of TB patients diagnosed between January 2008 and December 2009 at the "Hospital Municipal Raphael de Paula e Sousa", Curicica, Rio de Janeiro, Brazil. Two hundred eighteen clinical isolates were obtained from 188 patients and 28 cases had more than one isolate, including 25 patients with two and three patients with three isolates. Multiple isolates from the same patient were included to evaluate the consistency of the results of genotyping and to verify eventual multiple infections.

Ethics statement

This study was approved by the Research Ethics Committee of the Municipal Health and Civil Defense of the city of Rio de Janeiro Number 160/09 CAAE: 0182.0.314.000-9. Isolates of this study were obtained through bacteriological culture from clinical specimens of patients diagnosed at the Hospital Raphael and Paula Souza as part of routine diagnosis and drug susceptibility testing. The ethical committee stated that, as genotyping of *M. tuberculosis* isolates is complementary to routine diagnosis, there was no need for a written or verbal consent. No information other than that provided for the diagnosis was used.

Culture, DNA extraction and identification of Mycobacterium tuberculosis complex

Sputum samples were cultured on Löwenstein-Jensen (LJ) medium following standard microbiological laboratory procedures as a routine of the Clinical Analysis Laboratory of "Hospital Raphael de Paula e Souza". After cultivation, bacterial mass was re-suspended in 400 µl of sterile distilled water and heat inactivated at 90°C for one hour, followed by DNA extraction and purification using the CTAB method [39].

Spoligotyping

Spoligotyping was performed either as described by Kamerbeek *et al.* (1997) [12], using commercially available kit from Ocimum Biosolutions (Hyderabad, India) according to the manufacturer's instructions or using microbead-based hybridization assay as described by Zhang *et al.* (2009) [40].

MIRU-VNTR typing

Amplification of 24 MIRU-VNTR *loci* was performed by using a commercial typing kit (Genoscreen, Lille, France) and automated MIRU-VNTR analysis performed as previously described [14]. Fragment size of the amplicons was analyzed on a ABI 3730 DNA sequence analyzer (Applied Biosystems, California, USA) and number of copies of each locus was determined by automated assignment using the Genemapper 4.0 software (Applied Biosystems, California, USA). In the case of doubtful results, the size of the repeats was double checked by size estimation as compared to a DNA ladder (50 and 100 bp) and the positive control (H37Rv) on agarose gels and by comparing to a reference table as described [13].

PCR-RFLP of $fbpC^{103}$

For characterization of SNP $fbpC^{103}$, we adapted the procedure described by Gibson *et al.* in 2008 [7]. Amplifications were performed in 50 µl reactions containing 40 pmol each of the primers Ag85C103F (5-CTG GCT GTT GCC CTG ATA CTG CGA GGG CCA-3) and Ag85C103R (5-CGA GCA GCT TCT GCG GCC ACA ACG TT-3), 2 mM MgCl2, 0.2 mM dNTPs, 1 U Taq DNA polymerase (Invitrogen, Brazil), buffer (10 mM Tris-HCl, 1, 5 mM MgCl2, 50 mM KCl, pH 8.3), 5% DMSO (v/v) and 10 ng of target DNA. Amplification was performed in a Vieriti Thermal Cycler (Applied Biosystems, Foster City, CA), starting with denaturation at 95°C for 5 min, followed by 45 cycles of 1 min at 95°C, 1 min at 60°C, 4 min at 72°C and final extension for 10 min at 72°C. The amplified products of 519 bp were analyzed on 2% agarose gels after staining with ethidium bromide. Fifteen microliters of the amplified products were subjected to enzymatic digestion with 1 U of *Mnl*I (New England

BioLabs Inc. USA) at 37°C for four hours, generating three fragments of 365 bp, 96 bp and 48 bp for the wild type allele and two bands of 461 bp and 48 bp when the SNP G103A is present. Bands were detected in 3% agarose gel and their size estimated by comparison with a 100 bp DNA ladder (Invitrogen).

RD174 deletion

For detection of RD174, we used the protocol described earlier [7], performing multiplex-PCR using two primers that anneal to the RD174 flanking regions and one to the internal sequence. For amplification, we used 40 pmol of each of the primers RD174F (5′-AGC TGC TCC GGC CGG TCG TCG TCC TTG TC-′3), RD174Fi (5′-TAT GCC GCA GCC CGG GCA TCC GTG ATT A-′3) and RD174R (5′-ATC GTG AAC GCA GCG GTT TCG ACG GCA TCT-′3) in a 50 µl reaction containing 2 mM MgCl2, 0.2 mM dNTP, 1 U Taq DNA polymerase, 1× buffer, 1M of betaine and 10 ng of bacterial DNA. Amplification was performed starting with 5 min incubation at 95°C, followed by 45 cycles of 1 min at 95°C, 1 min at 60°C, 4 min at 72°C and final extension for 10 min at 72°C. To determine the size of the amplicons, 10 µl of PCR product was applied in 2% agarose gel and after electrophoresis, bands of either 300 bp (intact RD174) or 500 bp (deleted) are observed.

RD^{Rio} deletion

Detection of RD^{Rio} was performed using the multiplex PCR-protocol described by Lazzarini *et al.* (2007) [2]. For amplification, we used 20 pmol of each of the primers BridgeF (5′-CAC TCC GGC TGC CAA TCT CGT C′3), BridgeR (5′-CAC GAG GCT CGC GAA TGA GAC C-′3), IS1561F (5′-GAC CTG ACG GCC ACA CTG C′-3) and IS1561R (5′-CAC CTA CAC CGC TTC CTG CC′-3) in 50 µl reactions containing 2 mM $MgCl_2$, 0.2 mM dNTP, 1 U Taq DNA polymerase), 1× buffer, 5% DMSO (v/v) and 10 ng of target DNA. Amplifications were performed starting with incubation for 5 min at 95°C, followed by 45 cycles of 1 min at 95°C, 1 min at 60°C, 4 min at 72°C and final extension of 10 min at 72°C. The amplified products of 1175 bp or 530 bp in the presence or absence of the deletion, respectively were analyzed in 1.5% agarose.

Classification and definition of genotype-based lineages and families

Spoligotype and MIRU patterns were defined according to the definitions in the SITVITWEB database [23], (http://www.pasteurguadeloupe.fr:8081/SITVIT_ONLINE/) in the format of November 20, 2012. In addition, spoligotypes were compared with those in SITVIT2 (proprietary database of the "Institut Pasteur de la Guadeloupe", which is an updated in-house version of the publicly released SpolDB4 and SITVITWEB [23], [24] to be released in 2014. This comparison led to the characterization of families and lineages by spoligotyping and Spoligotype International Types (SIT), MIRU International Types (12-MIT, 15-MIT AND 24-MIT) and 5 *loci* VNTR International Types (VIT). The SIT, MIT and VIT were designated identical patterns when shared by two or more patient isolates, whereas "orphan" patterns were those observed in a single isolate that did not correspond to any of the patterns present in the SITVIT2 database. In order to classify "orphan" patterns, we used SpotClust (http://tbinsight.cs.rpi.edu/run_spotclust.html).

The 24 MIRU-VNTR profiles and spoligotypes were also compared with the MIRU-VNTR*plus* database [28] available at (http://www.miru-vntrplus.org/MIRU/index.faces). The definition of lineages was done on 24 MIRU-VNTR loci by Best-match analysis and Tree-based identification using the categorical index. The Multi-locus Variable Number Tandem Repeat analysis (MLVA) MtbC 15 and MtbC 12 were determined.

Data analysis

The number and size of genotype clusters were defined initially by introducing numerical values into an Excel table and different criteria for definition of clusters were used, being either individual identical spoligotypes or 15–24 MIRU-based genotypes, or by combining with Spoligotyping both. Excel tables were introduced into BioNumerics software (version 6.1, Applied Maths, Belgium) for construction of similarity matrices and phylogenetic trees, using the Jaccard Index (spoligotypes) and Categorical value (MIRU-VNTR) for construction of the Neighbor Joining (NJ) and Minimal Spanning Tree (MST).

The MIRU-VNTR allelic diversity (*h*) at each of the 24 loci was calculated by the equation described by Graur and Li [41] and the Diversity index was calculated as the Hunter Gaston diversity index (HGDI) [42]. Statistical analysis were performed using chi-square analysis with a confidence interval of 95% using Epi Info.Version 3.51 (Centers for Disease Control and Prevention, Atlanta, GA,USA), by using $\chi 2$ test or Fisher exact test for the comparison of proportions. A p value<0.05 was considered significant.

To visualize the classification difference observed between Spoligotyping and 24 loci MIRU-VNTRs, we constructed a Confusion Matrix for the frequency of correct and incorrect predictions. From the confusion matrix, the Positive Predictive Value or precision (PPV = TP/TP+FN), Accuracy rate (AAC = TP+TN/TP+FP+TN+FN), True Positive Rate or Sensitivity (TPR = TP/TP+TN), True Negative Rate or Specify (TNR = TN/TP+TN), Negative Predictive Value (NPV = TN/FN+TN) and Error Rate (ER = FP+FN/TP+FP+TN+FN) were calculated. (TP = True Positive, FP = False Positive, TN = True Negative, FN = False Negative).

Results

Classification by spoligotyping

The identification of spoligotype profiles as well as their definition to the family and lineage level was realized by comparison with profiles deposited in the SITVITWEB database and in SITVIT2 and compared with the classification obtained with previous version of the spoligotype database (Table S1).

Based on comparison with SITVIT2, 83 SITs were encountered in 195 isolates (89.4%), while 10 SIT (n = 15) had Unknown profiles and 23 isolates showed to have Orphan patterns. For classification of the latter two pattern types, we used Spotclust (Table S1). Ninety five isolates (43.6%) were classified as belonging to the LAM clade, 76 (34.9%) as belonging to the T clade, 40 (18.3%) as belonging to the Haarlem clade, five to the EAI5 clade (2.29%) and one each to the X clade (0.45%) and to Beijing. Overall, T1 (n = 52/23.8%), LAM9 (n = 32/14.7%) and H3 (n = 24/11%) were the most frequent subclades, while SIT53 (n = 26/50%), SIT42 (n = 18/56.25%) and SIT50 (n = 16/72,7%) were the most frequent SITs.

Table 1 illustrates the difference in frequency of SIT clusters containing three or more isolates (at least 3%) in this study, versus their worldwide distribution (macro-regions and countries), as defined in the SITVIT2 database. We observed a significantly higher frequency of genotypes T1 SIT53 (11.9% vs 5.5%; p = 0,027, $X^2 = 3,49$) and a lower frequency of LAM9 SIT42 (8.2% vs 12.5%; p = 0,0001; $X^2 = 15.82$). In addition, SIT 3907 (T1), SIT 2498 (H3) and SIT 3908 (LAM2) have so-far only been

observed in Brazil. Presently, we also observed five SITs, 136 (LAM5), 189 (T1), 268 (H3), 2107 (unknown) and 2322 (T2), that had not been reported before in Brazil. When comparing our results with the previous and the present version of the SITVIT database, we noticed some differences in classification (Table S1). Thirty-six isolates could be classified using the new version and among these nine new SITs were observed: 3125 (LAM6), 3504 (LAM6), 3904 (LAM6) 3905 (T1) 3906 (T3), 3907 (T1), 3908 (LAM2; originally designated as SIT2560 Unknown in SITVITWEB), 3909 (LAM8) and 3910 (T1). In addition, nineteen orphan profiles were classified and SIT268, SIT1241 and SIT2539, without classification in SITVITWEB, were now classified respectively as H3, LAM9 and LAM1. In addition, some SIT showed changes in clade and/or subclade classification (SITs 73, 102, 159, 451, 742 and 777). Further information is detailed in Table S1.

Classification based on MIRU-VNTR analysis

The 218 isolates were also submitted to 24 loci MIRU-VNTR typing with the objective to confirm or not spoligotype-based classification of existing and new sublineages and to correct eventual miss classification that could have occurred using the latter technique. We observed 208 different patterns and seven clusters with two to four strains (clustering rate = 1.37%) (Figure S1). The allelic diversity of each MIRU-VNTR locus for 218 isolates was evaluated and classified as either highly (HGDI$>$0.6), moderately (0.6$\leq$0.3) and poorly discriminative (HGDI$<$0.3), according to Sola *et al*. [15], as summarized in Table 2. Eight loci were highly discriminatory (QUB4156, QUB11, MTUB04, MIRU10, MIRU40, MIRU 23, MIRU26 and MIRU21) ten were moderate (MTUB30, MTUB39, MIRU16, ETR-C, ETR-A, QUB26, MTUB34, MIRU31, MIRU29 AND ETR-B) and six were poorly discriminative (MIRU24, MIRU29, MIRU04, MIRU27, MIRU20 and MIRU2). In the Table 2, we can observe a difference in discriminatory power of some loci according to lineage by Spoligotyping.

The patterns were classified based on the database tool that allows construction of a Neighbor-Joining based phylogenetic tree, visualizing proximity of a particular genotype with that of a set of reference strains to the genotype family level. One hundred thirty-six isolates (62.4%) were classified as LAM (127 patterns), 47 (21.5%) as Haarlem (45 patterns), 21 (9.6%) as T (21 patterns), 11 (5%) as S (11 patterns), and one isolate (0.45%) each as Beijing and EAI. Considerable differences were observed between Spoligotyping and 24 MIRU-VNTR loci-based classifications, even after excluding eventual small typing errors by repeating the assays. The differences observed between the two classifications are presented in the table 3 and in the Confusion Matrix (Figure 1). The precision, accuracy, sensitivity and error rate were respectively 0.74, 0.64, 0.82 and 0.36. The T lineage showed the highest incongruence rate related to classification (sensitivity = 0.26).

Combined analysis of 24 MIRU-VNTR and spoligotyping

The LAM family. For better understanding of the population structure of the Mtb strains, dendrograms of spoligotyping and 24 MIRU-VNTRs, either separately or as combined patterns were constructed using BioNumerics. Among the 136 (62.4%) isolates that were classified as LAM based on MIRU-VNTR analysis, 99 (72.8%) exhibited the characteristic LAM spoligotype profile with absence of spacers 21 to 24 and 33–36. Among these however, four spoligotype isolates were designated to the T clade by SITVIT2 (SITs: 306/n = 3, 1688/n = 1, 3905/n = 1) and one as T2/orphan. Another thirty-seven strains (27.2%) defined as LAM by MIRU-VNTRs did not present the lack of spacers 21–24 and were therefore designated as "LAM-like". Among isolates initially classified as LAM by spoligotyping (n = 95), 91 were confirmed as LAM (95.8%/TPR = 0.96) by 24 loci MIRU-VNTR (Figure 1). Six spoligotypes referred to as "Unknown" in SITVIT2 (SITs 132/n = 1; 1952/n = 1; 2107/n = 2; 2511/n = 2; 2535/n = 1 and 2548/n = 1) were also classified as LAM. Using SpotClust, SIT132 and SIT2511 were classified as EAI and SIT1952 as Haarlem. All Orphans patterns classified as LAM by SITVIT2 (n = 10) were also classified as LAM according to the MIRU-VNTR based phylogenetic tree.

Signatures based on MIRU copy number for "real" LAM (n = 99) types showed that the majority had two copies of MIRU04 (94; 95%) and two MIRU20 (n = 96; (97%), one copy of MIRU24 (n = 91; 92%), two copies of MIRU39 and ETR-A (n = 93; 94%) and 86 (87%) one copy of MTUB30. This indicates that the 221221 combination of these six alleles is representative for LAM strains, except for LAM3, presenting two copies of MTUB30 (221222).

The "LAM-like" isolates. The thirty-seven isolates that did not present the typical LAM spoligotype signature (absence of spacers 21 to 24 and 33–36) were positioned within the LAM branch in the neighbor-joining tree using MIRU-VNTR*Plus* and were conveniently designated as "LAM-like". These had been classified by spoligotyping earlier as T (n = 24), H (n = 10) and three "Unknown" patterns (SIT2511/n = 2 and SIT1952/n = 1; classified by SpotClust as EAI and H1 respectively). Ninety-one percent of these strains showed one copy of MIRU24 and two copies of MIRU04. Intriguingly, when including both 24 MIRU-VNTRs and spoligotypes for tree building, these isolates are localized among those classified as T and H.

The T family. Among the isolates initially classified as T by spoligotyping, only 26.3% (20/76) was confirmed by MIRU-VNTR 24 loci (TPR: 0.2631) (Table 3 and figure 1). By a Neighbor-Joining based phylogenetic tree, 31 of these isolates (40.9%) were positioned in LAM branch, 16 (21%) in the Haarlem branch and 9 (11.8%) in the S branch. The MIRU-VNTR characteristic signature for the T lineage confirmed by both techniques, was one copy of MIRU24 (95.8%), two copies each of MIRU02 (95.8%), MIRU04 (87.5%), MIRU20 (95.8%), MIRU39 (100%) and three copies each of MIRU27 (87.5%) and MTUB34 (87.5%). Unlike LAM isolates that present a single copy of MTUB30, isolates of the T family presented two or four copies of this allele.

The Haarlem family. Forty-seven isolates were classified as belonging to the H family representing 21.5% of all isolate, 85% of the these isolates initially classified as Haarlem by Spoligotyping were confirmed by MIRU-VNTRs 24 *loci* (TPR = 0.65, TNR = 0,88) (Table 3 and figure 1). Among these isolated 16 (34%) presented spoliotype profile compatible with T family, 3 (6.4%) with LAM family and 2 (2% each) isolates, respectively compatible with X and EAI. The MIRU-VNTRs characteristic for Haarlem are two copies of MIRU02 (100%) and MIRU39 (89.1%) and three copies of MTUB34 (100%), MIRU16 (91.3%), MIRU27 (97.8%), ETR-A (95.6%) and ETR-C (91.3%). Different from LAM isolates having a single copy of MTUB30, H isolates present either three or four copies of this MIRU. Combined analysis of the MIRU-24 and spoligotyping showed that isolates of genotype H1 (absences of spacers 26–31) have two copies of MIRU04, ETR-B and MTUB29 and three copies of MIRU16, MIRU31, ETR-A and ETR-C. Isolates of genotype H3 (absences of spacer 31) share two copies of MIRU02, ETR-C, MIRU4 and MTUB29 and three copies of MIRU27, ETR-A, ETR-B and MTUB34.

Table 1. Description of clusters containing 3 or more isolates in this study and their worldwide distribution in the SITVIT2 database (interrogation made on September 25th 2013).

SIT (Lineage) Octal Number; Spoligotype Description	Number (%) in study	% in study vs. database	Distribution in Regions with ≥3% of a given SITs *	Distribution in countries with ≥3% of a given SITs **
53 (T1) 777777777760771	26 (11.93)	0.41	EURO-W 15.65, AMER-N 13.48, AMER-S 12.45, EURO-S 9.41, EURO-N 7.48, ASIA-W 7.31, AFRI-S 4.97, AFRI-E 4.65, ASIA-E 4.23, AFRI-N 3.52, EURO-E 3.26, AMER-C 3.23	USA 13.2, FXX 7.88, BRA 5.54, ITA 5.33, ZAF 4.86, TUR 3.47, AUT 3.42, CHN 3.09
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42 (LAM9) 777777607760771	18 (8.26)	0.54	AMER-S 29.7, AMER-N 11.85, EURO-S 11.31, EURO-W 9.46, AFRI-N 8.57, EURO-N 4.9, AMER-C 3.55, AFRI-E 3.55, AFRI-S 3.16	BRA 12.51, USA 11.85, COL 7.61, MAR 7.05, ITA 6.54, FXX 5.05, ESP 3.34, VEN 3.31, ZAF 3.16
■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■□□□□■■■■■■■				
50 (H3) 777777777720771	16 (7.34)	0.47	AMER-S 18.16, EURO-W 17.54, AMER-N 17.54, EURO-S 11.53, EURO-E 5.51, EURO-N 5.45, AFRI-N 4.25, AFRI-S 4.04, CARI 3.48, ASIA-W 3.21	USA 17.51, BRA 7.52, FXX 6.87, AUT 6.07, ITA 5.43, ESP 5.43, PER 4.72, ZAF 4.04, CZE 3.66
■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■				
SIT64 (LAM6) 777777607560771	6 (2.75)	1.6	AMER-S 49.33, AMER-N 25.07, EURO-W 6.4, EURO-S 4.8, ASIA-W 3.2	BRA 38.4, USA 25.07, GUF 6.13, PRT 3.73
■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■□■■■□□□□■■■■■■■				
SIT47 (H1) 777777774020771	5 (2.29)	0.32	EURO-W 20.29, AMER-N 15.51, EURO-S 13.47, AMER-S 12.64, EURO-N 10.47, EURO-E 7.21, ASIA-W 4.02, AFRI-N 3.64	USA 15.19, ITA 8.23, AUT 8.04, BRA 7.34, FXX 6.64, FIN 6.0, CZE 3.77, ESP 3.57, SWE 3.38, PER 3.06
■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■				
SIT60 (LAM4) 777777607760731	5 (2.29)	1.17	AFRI-S 38.08, AMER-S 21.5, EURO-W 7.24, AFRI-N 7.01, AFRI-W 6.31, EURO-S 5.61, AMER-N 4.4	ZAF 38.08, BRA 14.72, FXX 5.14, USA 4.44, MAR 4.44, GMB 3.97, ITA 3.74, VEN 3.51
■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■□□□□■■■□■■■				
SIT73 (T) 777737777760731	5 (2.29)	1.94	EURO-S 17.05, EURO-W 13.95, AMER-N 13.95, AMER-S 11.24, AFRI-S 10.85, AFRI-E 7.36, ASIA-E 4.65, AMER-C 3.88	ITA 14.34, USA 13.95, ZAF 10.85, FXX 7.75, BRA 6.59, CHN 4.65, MOZ 3.88, MEX 3.1
■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■				
4 (Unknown) 000000007760771	4 (1.83)	1.08	EURO-S 16.49, AMER-S 14.32, AMER-N 12.43, EURO-W 10.81, ASIA-W 10.54, AFRI-S 8.11, AFRI-E 8.11, EURO-N 6.22, EURO-E 5.68	USA 9.73, ITA 8.92, BRA 8.92, ZAF 8.11, TUR 7.84, BGR 5.41, ETH 4.32, FXX 4.05, ALB 4.05
□□□□□□□□□□□□□□□□□□□□□□□□■■■■■■■□□□□■■■■■■■				
SIT17 (LAM2) 677737607760771	4 (1.83)	0.6	AMER-S 59.58, AMER-N 17.95, CARI 8.9, EURO-S 5.58	BRA 28.36, VEN 27.0, USA 17.95, ESP 4.37, HTI 3.32, GLP 3.32
■■□■■■■■■■■□■■■■■■■□□□□■■■■■■■□□□□■■■■■■■				
SIT33 (LAM3) 776177607760771	4 (1.83)	0.35	AFRI-S 28.76, AMER-S 25.31, AMER-N 14.07, EURO-S 12.57, EURO-W 7.26, AMER-C 4.78	ZAF 28.76, USA 14.07, BRA 12.04, ESP 7.88, PER 6.02, ARG 5.04, FXX 4.69, ITA 4.07, HND 3.81

Table 1. Cont.

SIT (Lineage) Octal Number; Spoligotype Description	Number (%) in study	% in study vs. database	Distribution in Regions with ≥3% of a given SITs *	Distribution in countries with ≥3% of a given SITs **
■■■■■■■■□□□■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■				
SIT3907 (T1) 777703777760631	4 (1.83)	100	AMER-S 100	BRA 100
■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■■□□□□■■□□■■■				
SIT306 (T1) 777777601560771	3 (1.38)	11.54	EURO-W 38.46, AMER-N 26.92, AMER-S 19.23, EURO-N 7.69, AFRI-M 7.69	USA 26.92, BEL 26.92, BRA 15.39, FXX 11.54, GBR 7.69, CAF 7.69, GUF 3.85
■■■■■■■■■■■■■■■■■■■■□□□□□□■■□■■■□□□□■■■■■■■				
SIT828 (LAM4) 377777607760731	3 (1.38)	9.38	AMER-S 90.63, EURO-S 3.13, AFRI-W 3.13, AFRI-S 3.13	BRA 84.38, PRY 6.25, ZAF 3.13, ITA 3.13, GNB 3.13,
□■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■□■■■				
SIT1711 (LAM2) 677337607760771	3 (1.38)	37.5	AMER-S 75.0, EURO-S 12.5, AMER-C 12.5	BRA 37.5, VEN 25.0, MEX 12.5, ESP 12.5, COL 12.5,
■■□■■■■■□■■□■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■				
SIT2498 (H3) 777760077620771	3 (1.38)	27.27	AMER-S 100	BRA 100
■■■■■■■■■■■■■■□□□□□□□■■■■■■■■□□■□□□□■■■■■■■				
SIT3908 (LAM2) 677730207760771	3 (1.38)	75	AMER-S 100	BRA 100
■■□■■■■■■■■■□■■□□□□□■□□□□□■■■■■■■■□□□□■■■■■■■				

*Worldwide distribution is reported for regions with more than 3% of a given SITs as compared to their total number in the SITVIT2 database. The definition of macro-geographical regions and sub-regions (http://unstats.un.org/unsd/methods/m49/m49regin.htm) is according to the United Nations; Regions: AFRI (Africa), AMER (Americas), ASIA (Asia), EURO (Europe), and OCE (Oceania), subdivided in: E (Eastern), M (Middle), C (Central), N (Northern), S (Southern), SE (South-Eastern), and W (Western). Furthermore, CARIB (Caribbean) belongs to Americas, while Oceania is subdivided in 4 sub-regions, AUST (Australasia), MEL (Melanesia), MIC (Micronesia), and POLY (Polynesia). Note that in our classification scheme, Russia has been attributed a new sub-region by itself (Northern Asia) instead of including it among rest of the Eastern Europe. It reflects its geographical localization as well as due to the similarity of specific TB genotypes circulating in Russia (a majority of Beijing genotypes) with those prevalent in Central, Eastern and South-Eastern Asia.

**The 3 letter country codes are according to http://en.wikipedia.org/wiki/ISO_3166-1_alpha-3; countrywide distribution is only shown for SITs with ≥3% of a given SITs as compared to their total number in the SITVIT2 database.

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Table 2. Allelic diversity of 24 MIRU-VNTRs loci on 218 *Mycobacterium tuberculosis* strains isolated from pulmonary tuberculosis patients in Rio de Janeiro, Brazil.

	Genotype families by Spoligotyping			
MIRU-VNTR *loci*	**LAM**	**H**	**T**	**All families**
MIRU02	0.362	0.148	0.353	0.325
MIRU04	0.061	0.153	0.225	0.139
MIRU10	0.56	0.687	0.692	0.692
MIRU16	0.636	0.243	0.439	0.544
MIRU20	0.081	0.499	0.24	0.27
MIRU23	0.541	0.529	0.584	0.688
MIRU24	0.021	0.101	0.081	0.071
MIRU26	0.723	0.559	0.687	0.639
MIRU27	0.314	0.145	0.105	0.227
MIRU31	0.429	0.357	0.51	0.445
MIIRU39	0.138	0.251	0.027	0.124
MIRU40	0.517	0.623	0.76	0.689
ETR-A	0.14	0.417	0.625	0.537
ETR-B	0.407	0.237	0.396	0.389
ETR-C	0.357	0.447	0.573	0.541
MTUB04	0.612	0.53	0.68	0.716
MTUB21	0.436	0.587	0.673	0.624
MTUB29	0.253	0.432	0.266	0.397
MTUB30	0.269	0.494	0.652	0.591
MTUB34	0.617	0.305	0.617	0.452
MTUB39	0.391	0.573	0.391	0.577
QUB11	0.697	0.702	0.697	0.737
QUB26	0.384	0.63	0.384	0.522
QUB4156	0.842	0.842	0.842	0.84

doi:10.1371/journal.pone.0107747.t002

The S family. Eleven isolates were classified as belonging to the S family and four of these exhibit SIT4, that in SpolDB4 was classified as LAM3-S Convergent, having absence of spacers 1–24 and 33–34 (The characteristic pattern of *S* family is absence of spacers 9–10, and 33–34). Among the others isolates, we observed SITs 53/n = 1, 102/n = 1, 378/n = 1, 2500/n = 1, 3907/n = 2 and 3909/n = 1; only two of these had the characteristic of S family (SIT3909/LAM8 and SIT2500/Unknown by SITVIT2 and H1 by Spotclust). Isolates of the S family shared their copy number in six loci, being one copy of MIRU24 and MTUB 21, two copies each of MIRU20 and MIRU39 and three copies MIRU10 and MIRU27.

RD^{Rio}, RD174 and *fbpC*^{103} analysis

The genotypes defined by the presence of RD^{Rio}, RD174 and SNP *fbp*C^{103} were added to the classification based on 24-MIRU-VNTR typing (Table S2). Thirty-six isolates (16.5%) were excluded from the final analysis either because of showing genotypes suggestive for multiple infection of because of failure in at least one of the three genotype procedures. The results of 182

Table 3. Frequencies of strains according to classification by Spoligotyping (SITVIT2) and 24 loci MIRU-VNTR (MIRUVNTRPlus).

Lineage	**Spoligotyping (%)**		**24 loci MIRU-VNTR (%)**	
LAM	95	(43.58)	136	(62.39)
T	76	(34.86)	21	(9.63)
H	40	(18.35)	47	(21.56)
S	0	0	11	(5.05)
X	1	(0.46)	1	(0.46)
EAI	5	(2.29)	1	(0.46)
BEIJING	1	(0.46)	1	(0.46)

doi:10.1371/journal.pone.0107747.t003

MIRU-VNTR 24 *loci*[2] \ Spoligotyping[1]	LAM	T	Haarlen	S	X	EAI	Beijing	Total
LAM	91	31	11	0	0	3	0	136
T	0	20	1	0	0	0	0	21
Haarlem	3	16	26	0	1	1	0	47
S	1	9	1	0	0	0	0	11
X	0	0	1	0	0	0	0	1
EAI	0	0	0	0	0	1	0	1
Beijing	0	0	0	0	0	0	1	1
Total	95	76	40	0	1	5	1	218

[1] Classification according to the SITIVIT2. For unknown Spoligotypes, we used the SpotClust.
[2] The patterns were classified based on MIRU-VNTRPlus tool that allows construction of a Neighbor-Joining based phylogenetic tree, visualizing proximity of a particular genotype with that of a set of reference strains to the genotype family level.

MIRU-VNTR 24 *loci* vs Spoligotying	
Positive Predictive Value (PPV) or Precision	0.7433
Accuracy (AAC)	0.6376
True positive rate (TPR) or sencivity	0.8176
Erro Rate	0.3623

	LAM	T	Haarlen
Positive Predictive Value (PPV) or Precision	0.6691	0.9523	0.5531
Accuracy (AAC)	0.7752	0.7385	0.8394
True positive rate (TPR) or sencivity	0.9578	0.2631	0.6500
True Negative Rate (TNR) or Specificity	0.4193	0.9929	0.8820
Negative Predictive Value (NPV)	0.9512	0.7157	0.9181
Positive Predictive Value (PPV)	0.669	0.9523	0.5531
Erro Rate	0.2247	0.2614	0.3500

Figure 1. Confusion Matrix comparing the classifications obtained by Spoligotyping and MIRU-VNTR. [1] Classification according to SITIVIT2. For unknown Spoligotypes, we used SpotClust. [2] Patterns were classified based on a VNTR*plus* database that allows construction of a Neighbor-Joining based phylogenetic tree, visualizing proximity of a particular genotype with that of a set of reference strains to the genotype family level.
doi:10.1371/journal.pone.0107747.g001

strains are summarized in Table 3 and for simplification of interpretation, we defined three groups, being LAM (n = 77), LAM-like (n = 33) and non-LAM (n = 72) as determined by spoligotyping and MIRU-VNTR typing.

The SNP *fbpC*[103] was observed in 107 (58.8%) of the isolates, including 97.3% (74/77) of LAM, 69.6% (23/29) of "LAM-like" and 13.9% (10/72) of non-LAM. The total frequency of RD^{Rio} was 11% (20/182), with 20.7% (16/77) among LAM, 6.0% (2/29) among "LAM-like" and 2.7% (2/72) among non-LAM isolates. The overall frequency of RD174 was 15.3% (28/182), being 33.7% (25/77) in the LAM genotype and 6.8% (2/29) in "LAM-like". All LAM/RD^{Rio} isolates presented the SNP *fbpC*[103] (Table 4 and Table 5), but not all were RD174; two isolates classified as LAM2 SIT3908 were not had RD174 (isolated from different patients). The frequency of RD174 (n = 25) was therefore higher than that of RD^{Rio} (32.5% vs 20.7%; p = 0.053 and $X^2 = 2{,}69$) in LAM. Eleven LAM isolates (14.3%) presented RD174 but not RD^{Rio}, all were positive for the *fbpC*[103].

The allelic diversity of the 24 loci MIRU-VNTR loci in LAM/RDRio isolates (Figure S2) showed that the copy number of combining of MIRU04, MIRU20, MIRU24, MIRU31, ETR-A, MTUB21 and MTUB30 loci was a signature of this genotype (2213231) (Table 4). In general, these loci present low variability in LAM, except for MTUB21, is being moderately variable in such isolates (table 2). Upon comparing 24 MIRU-VNTR signatures of LAM, LAM-like and non-LAM strains (Table 4), we observed two isolates that presented the hypothetical ancestral MIRU-VNTR signature (224226153321) for RD^{Rio} that was suggested by Lazzarini et al. (2007) [2]. One isolate (C2009) was classified as LAM1 SIT2539 and the other (C1966) as H3 SIT50 by spoligotyping and "LAM-like" by 24 MIRU-VNTR; both presented SNP *fbp*C[103] and were deleted for RD^{Rio} and RD174. Among the LAM/RD^{Rio} strains, frequency of LAM subtypes as defined by spoligotyping using SITVIT2 was 31.5% of LAM2, 25% of LAM9, 12.5% each of LAM6 and LAM5 and 6.3% each of LAM4 and LAM1. Figure 2 is a graphical representation of these three markers in the LAM strains as defined by 24 loci MIRU-VNTRs.

Table 4. Descripition of RD^{Rio} by 24 loci MIRU-VNTRs, *fbpC*^{103} and RD174.

									24 MIRU-VNTRs																								
									MIRU													ETR			MTUB							QUB		
									12 MIRU-VNTRs**													Additional 12 MIRU-VNTRs												
Strain	**Year**	**Spoligotype Description**	**SITVIT2**	**SIT2**	**Lineage***	**RD^{RIO}**	**RD174**	***fbpC*^{103}**	**2**	**2**	**4**	**2**	**2**	**6**	**1**	**5**	**3**	**3**	**2**	**1**	**2**	**1**	**4**	**4**	**3**	**4**	**1**	**3**	**2**	**3**	**4**	**2**
									2	**4**	**10**	**16**	**20**	**23**	**24**	**26**	**27**	**31**	**39**	**40**	**A**	**B**	**C**	**4**	**21**	**29**	**30**	**34**	**39**	**11**	**26**	**4156**
C0537A2	2009	■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM9	42	**LAM**	+	+	+	1	**2**	**4**	3	**2**	**6**	**1**	4	**3**	3	**2**	**1**	*2*	*1*	*4*	3	*3*	*4*	*1*	5	2	*2*	7	3
C0996	2008	■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM9	42	**LAM**	+	+	+	**2**	**2**	3	2	**2**	**6**	**1**	4	**3**	3	**2**	**1**	*2*	*1*	*4*	4	*3*	5	*1*	5	2	4	5	*2*
C2105	2008	■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM9	42	**LAM**	+	+	+	**2**	**2**	2	2	**2**	**6**	**1**	4	**3**	3	**2**	**1**	*2*	*1*	*4*	4	*3*	*4*	*1*	6	2	4	*	*2*
C1231A2	2008	■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■□□□□□□	LAM4	1106	**LAM**	+	+	+	**2**	**2**	**4**	1	**2**	**6**	**1**	3	2	3	**2**	**1**	*2*	*1*	*4*	4	*3*	*4*	*1*	*3*	2	*3*	1*6	*2*
C2314	2008	■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■□■■■□□□□■■■■■■■	LAM6	64	**LAM**	+	+	+	**2**	**2**	3	1	**2**	**6**	**1**	4	2	3	**2**	**1**	*2*	*1*	*4*	0	*3*	*4*	*1*	5	0	*3*	8	*2*
C0097	2009	■■■■■■■■■■■■■■■■■■■■■■□□□□■■□□□□□□□□□□□□□■■■	Unknow	132	**LAM**	+	+	+	**2**	**2**	3	1	**2**	**6**	**1**	4	2	3	**2**	**1**	*2*	*1*	*4*	3	*3*	*4*	*1*	4	2	2	8	*2*
C6689	2008	■■■■■■■■■■■■■■■■■■■■■■□□□□□■■■■■■■■□□□□■■■■■■■	LAM9	1800	**LAM**	+	+	+	**2**	**2**	**4**	3	**2**	**6**	**1**	**5**	3	2	1	3	*2*	2	*4*	*4*	*3*	6	*1*	*3*	2	2	7	*2*
C6582	2008	■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■□□□□□□□□■■□■■■	LAM6	1066	**LAM**	+	+	+	**2**	**2**	2	1	**2**	4	**1**	4	2	**3**	**2**	**1**	*2*	*1*	*4*	*4*	*3*	*4*	*1*	5	2	4	7	*2*
C0817	2008	■■■■■■■■■■■■□■■□□□□■□□□□■■■■■■■■□□□□■■■■■■■	LAM5	Orphan	**LAM**	+	+	+	**2**	**2**	4	**2**	**2**	5	**1**	**5**	**3**	**3**	**2**	**1**	*2*	2	*4*	*4*	*3*	*4*	*1*	2	2	*3*	4	*2*
C1893	2009	■■■■■■■■■■■■□□□□□□■■□□□□■■■■■■■■□□□□■■■■■■■	LAM5	1337	**LAM**	+	+	+	**2**	**2**	2	**2**	**2**	**6**	**1**	**5**	**3**	**3**	**2**	**1**	*2*	*1*	*4*	*4*	*3*	*4*	*1*	4	1	2	1	*2*
C2559	2009	■■□■■■■■■■■□■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM2	17	**LAM**	+	+	+	**2**	**2**	**4**	**2**	**2**	5	**1**	6	**3**	**3**	**2**	**1**	*2*	2	5	*4*	*3*	*4*	*1*	*3*	*2*	2	6	*2*
C3554	2009	■■□■■■■■■■■□■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM2	17	**LAM**	+	+	+	**2**	**2**	**4**	**2**	**2**	5	**1**	6	**3**	**3**	**2**	**1**	*2*	2	*4*	*4*	*3*	*4*	*1*	*3*	*2*	2	6	*2*
C2020	2009	■■□■■■■■■■■□■■□□□□■□□□□■■■■■■■■□□□□■■■■■■■	LAM2	3908	**LAM**	+	−	+	**2**	**2**	**4**	**2**	**2**	5	**1**	**5**	**3**	**3**	**2**	**1**	*2*		*4*	*4*	*3*		*1*		*2*	*3*	*4*	*2*
C2046	2009	■■□■■■■■■■■□■■□□□□■□□□□■■■■■■■■□□□□■■■■■■■	LAM2	3908	**LAM**	+	−	+	**2**	**2**	**4**	**2**	**2**	5	**1**	**5**	**3**	**3**	**2**	**1**	*2*	2	*4*	*4*	*3*	*4*	*1*	2	*2*	*3*	*4*	*2*
C2017	2008	■■□■■■■■■■■□■■□□□□■□□□□■■■■■■■■□□□□■■■■■■■	LAM2	Orphan	**LAM**	+	+	+	**2**	**2**	**4**	**2**	**2**	5	**1**	**5**	**3**	**3**	**2**	**1**	*2*	2	*4*	*4*	*3*	*4*	*1*	2	*2*	*3*	*4*	*2*
C2009	2009	■■□■■■□■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	LAM1	2539	**LAM**	+	+	+	**2**	**2**	**4**	**2**	**2**	5	**1**	**5**	**3**	**3**	**2**	**1**	*2*	2	*4*	1	*3*	5	*1*	*3*	*2*	2	3	*2*
C1966	2008	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	H3	50	LAM-like	+	+	+	**2**	**2**	**4**	**2**	**2**	**6**	**1**	**5**	**3**	**3**	**2**	**1**	*2*	*1*	*4*	*4*	*3*	*4*	*1*	5	*2*	*3*	6	2
C0669	2009	■■■■■■■■□■■■□■■■■■■□■■■■■■■■□□□□■■□□■■■	T1	Orphan	LAM-like	+	−	−	**2**	**2**	**4**	*	**2**	5	**1**	5	**3**	**3**	**2**	**1**	3	*1*	*4*	1	4	*4*	*1*	*	2	2	8	*2*

Table 4. Cont.

									24 MIRU-VNTRs																							
									MIRU												ETR			MTUB						QUB		
									12 MIRU-VNTRs**												Additional 12 MIRU-VNTRs											
Strain	**Year**	**Spoligotype Description**	**SITVIT2**	**SIT2**	**Lineage***	**RD^{RIO}**	**RD174**	***fbpC*^{103}**	**2**	**2**	**4**	**2**	**2**	**6**	**1**	**5**	**3**	**3**	**2**	**1**	**2**	**1**	**4**	**4**	**3**	**4**	**1**	**3**	**2**	**3**	**4**	**2**
									2	**4**	**10**	**16**	**20**	**23**	**24**	**26**	**27**	**31**	**39**	**40**	**A**	**B**	**C**	**4**	**21**	**29**	**30**	**34**	**39**	**11**	**26**	**4156**
C2142A2	2009	■■■■■■■■■■■■■■■■■■■■■■■■ ■■■■■■□■□□□□■■■■■■■	H3	50	H	+	–	–	3	**2**	**4**	3	1	2	**1**	2	**3**	**3**	**2**	2	3	2	3	2	2	2	4	3	3	4	*	2
C5817	2008	□□□□□□□□□□□□□□□□□□□□□□□□ ■■■■■■■■□□□□■■■■■■■	Unknow	4	S	+	–	+	3	3	**4**	2	2	5	**1**	6	**3**	2	**2**	2	4	2	*4*	3	1	*4*	2	3	0	3	7	2

*Classification based on construction of phylogenetic tree using the N-J Algorithm and evaluating proximity of particular isolate with a set of 182 reference strains in the MIRU-VNTRPlus. Note: Strains with RD^{Rio} (LAM, Like-LAM and Non LAM).
**In bold the same number of copy of hypothetic Ancestral RD^{Rio} as suggested by lazzarini *et al*, 2007 [2] and n the probable number of copy of hypothetic Ancestral RD^{Rio} in the additional 12 *loci*.
doi:10.1371/journal.pone.0107747.t004

Discussion

Rio de Janeiro is the capital of the state of Rio de Janeiro, located in the southeast of Brazil, has a population of 16 million habitants, six and a half million of these living in the capital, being the second largest city and a major touristic attraction in Brazil (Census 2010 http://cidades.ibge.gov.br/xtras/perfil.php?lang=&codmun=330455 accessed 12/18/2013). According to the Ministry of Health, 11.639 new TB cases were recorded in 2011 in the state with an incidence of 72.3/100.000 habitants and the highest mortality rate (5.1/100.000 habitants) at the national level [1]. Rio de Janeiro city has strong economic and social contrasts, with a large portion of the population living in numerous suburbs, consisting of "communities", urban areas where housing conditions, health, education and security are extremely precarious. These factors are directly related to the number of TB cases detected.

In the present study, we performed spoligotyping and 24 MIRU-VNTR typing and characterized a SNP in *fbpC*^{103} and the status of RD174 and RD^{Rio}, to decipher the population structure and the phylogenetic relationships of the MTBC strains of TB cases in this particular population that attended a single reference center in the city of Rio de Janeiro. *Mycobacterium tuberculosis* is classified into six phylogenetic lineages, each of which can be divided into sublineages [32]. Members of the Euro- American lineages represented by the LAM, H, T, S and X Spoligotyping families, which are genetically closely related are the most common in South America [19], [20], [21] and this was confirmed recently also in Brazil [22] and in different states of the country [8], [43], [44], [45], [46], [47] [48], but differences in the frequency of these families are observed, theses difference could also be due to differences in population and immigration history in each region or in period associated genotype frequencies or in differences in sample size. We here confirm the predominance of the Euro-American lineage (also known as lineage 4) with only two isolates classified as Indo-Oceanic lineage (EAI5) and East Asian lineage (Beijing), the first being more prevalent in east Africa, southeast Asia and in south India and the second in east Asia, Russia and South Africa. [32]. Recently, the frequency of such strains in Brazil was described as being less than 1% except for the higher frequency in the state of Pará, north Brazil [22].

The most prevalent families as defined by spoligotyping were LAM (43.6%), T (34.9%) and H (18.3%); however, classification based on 24-MIRU-VNTR and Neighbor-Joining based phylogenetic tree building using the database tool (www.miruvntrplus.org) showed considerable difference with that obtained by spoligotyping, being respectively 62.4%, 9.6% and 21.6% (error rate of 0.36). Among the isolates with discordant results, mostly isolates initially classified as T (n = 31), H (n = 11) and EAI (n = 3) by spoligotyping were classified as LAM by 24 MIRU-VNTRs typing, for isolates that did not show LAM prototype (absence of spacers 21–24 and 33–36), conveniently named LAM-like. Subsequently, 78.3% these isolates confirmed to be LAM by the presence of the LAM-specific SNP *fbpC*^{103} [7], [38] and when considering the presence of this SNP as an absolute marker for LAM family the frequency of this lineage is 58.9%. We also have preliminary data showing that the supposed LAM-specific marker *ligB*^{404} was observed in isolates that had been defined by spoligotyping as being T or H (data not shown). Very recently, Mokrousov et al. reported difference in classification of LAM strains as defined by spoligotyping and SNP analysis (*fbpC*^{103} and *ligB*^{404}) [49] although both SNPs were previously validated in different collection of clinical isolates and reference strains as to be specific for the LAM family [7], [38].

Table 5. The frequency of *fbpC*^{103}, RD^{Rio} and RD174 in LAM, LAM-like and Non LAM isolates, as designated by spoligotyping and 24 MIRU-VNTR typing.

	LAM (%)	LAM-Like (%)	Non LAM (%)	Total Frequency (%)
SNP and RD	**(n = 77)**	**(n = 29)**	**(n = 75)**	**(n = 182)**
fbpC^{103}	74 (97.3)	23 (79.3)	10 (13.3%)	107 (58.8)
RD^{Rio}	16 (20.7)	2 (6.9%)	2 (2.6%)	20 (11)
RD174	25 (32.5)	2 (6.9%)	1(1.3%)	28 (15.4)

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It is now common knowledge that spoligotyping has limitations as a tool prediction of the exact phylogenetic relationships between strains of the MTBC, particularly in modern strains (Euro American, East Asian and Indian e East African) [16], [18], [24], [48], [49], [50], [51] [52], mainly due to homoplasy [16], [24]. The accuracy of the phylogenetic grouping by MIRU-VNTR is more exact than that of spoligotyping but depends on the number of loci included in the analysis [49] and classification errors are reduced when analyzing 24 loci [16]. Indeed, several authors have suggested that SNPs are more suitable than spoligotyping and MIRU-VNTR settings for phylogenetic classification [16], [38], [53], [54], [55], [56]. The *fbpC*^{103} is described as a good marker for the LAM family [7], [38], [49], [57], [58], [59], and our original intention was to evaluate if strains RD^{Rio} was still prevalent in Rio de Janeiro as seen previously by Lazzarini in clinical isolates collected between 2002 and 2003 [2], for this purpose we believed only a marker that could differentiate LAM and non-LAM associated with the 24 MIRU-VNTR and Spoligotyping could be sufficient, however the scenario was observed more complex.

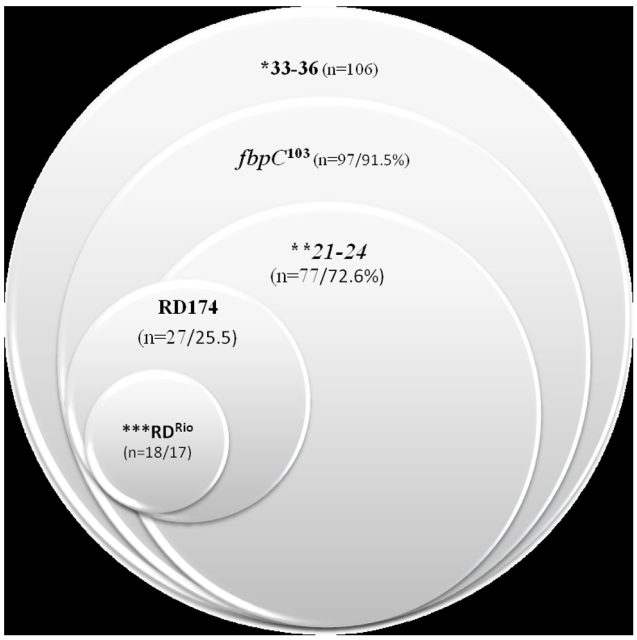


Figure 2. Venn diagram illustrating the different markers in isolated classified as LAM by 24 loci MIRU-VNTR. Notes: The Venn diagram was constructed based on LAM isolates defined by 24 loci MIURU-VNTR. The sizes of the circles is not proportional to the real frequency of these markers. Twenty isolates classified with LAM by MIRU-VNTRs were removed from the final analysis because of showing a mixed genotype or failure in at least one of the three genotype procedures. * absence of spacers 33–36 in the spoligotyping profile, ** absence of spacers 21–24 in the spoligotyping profile, ***Two isolates RD^{Rio} but not RD174 (LAM2 SIT3908).
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We here present the first data comparing classification by spoligotyping and MIRU-VNTRs and *fbpC*^{103} in Euro American lineage prevalent in Rio de Janeiro and Brazil. Among these different types of markers, we observed four major groups: (i) strains classified as LAM by spoligotyping and MIRU-VNTRs 24 loci without the LAM-characteristic SNP *fbpC*^{103}, (ii) strains not classified as LAM by spoligotyping and MIRU-VNTRs 24 loci but carrying the *fbpC*^{103} SNP, (iii) strains classified by spoligotyping as non-LAM but as LAM by MIRU-VNTRs 24 loci (LAM-like) and with SNP *fbpC*^{103} and (iv), strains classified by spoligotyping as non-LAM and LAM by MIRU-VNTRs 24 loci (LAM-like) but not presenting the SNP *fbpC*^{103}. These different scenarios could be explained by convergent evolution of spoligotypes and of MIRU-VNTRs loci (even including 24 alleles) because a limited number of loci were evaluated that might evolve rapidly and therefore susceptible to pronounced convergence [53] and/or because the existence of ancestral progenitor of Euro- American lineages containing SNP *fbpC*^{103}. In addition, a possible important limitation of the current classification based on MIRU-VNTRs and their similarity with genotypes present in MIRU-VNTRplus is that, despite including well characterized strains, the database contains a limited number of strains that does not reflect the real genetic diversity of isolates belonging to the MTBC; another limitation of this study is that no additional specific SNPs for H, T, S and X and T were investigated. The Whole Genome Sequencing (WGS) is superior to conventional genotyping for MTBC [60] and has been used in areas not yet studied, from global (phylogeography) for site (transmission chains and diversity of circulating strains), for single patient (clonal diversity) and the bacterium itself (evolutionary studies) [61]. We intend to compare through WGS (developing) these isolates to a better comprehension of the evolution of lineages Euro American, such as the development of new methodologies that allow a more rapid and accurate typing.

Analyzing the data obtained in this study, the spoligotypes of the T family showed the largest number of divergent results when compared to classification by 24-MIRU (TPR = 0,26/ TNR = 0,99). The prototype of the T family is characterized by the absence of spacers 33–36 only [48] and have been observed in almost every country, representing 20% of all isolates deposited in the database SITVITWEB. Despite the high frequency, this genotype family is still considered as "ill-defined" and includes non-monophyletic groups [54] [55]. In South America, the frequency of this family is 26.7% and in Brazil 18.6% (370/ 1991), with the T1 SIT53 subfamily being the most prevalent SIT [22], as observed also in this study. Here, among the 76 isolates classified as T by spoligotyping, only 21 (27.6%) were confirmed

by 24 MIRU-VNTRs typing, the rest was reclassified as LAM (n = 31), S (n = 9) and H (n = 16). Interestingly, SIT53 was associated with mixed infection in a study conducted in South Africa, a country characterized by a high prevalence of TB [57] and Lazzarini *et al*. [62], using a computational approach, showed that this is the most frequent false spoligotype derived from mixed infections. However, among isolates with this SIT, we did not observe double signals during 24 MIRU typing indicative for mixed infections. We also observed that spoligotypes, indicative for the T family, were sometimes grouped with spoligotypes of the H family by MIRU-VNTR typing. This could be related with the fact that the prototype spoligotype defining T1 SIT53 and H3 SIT 50 differ only in the absence of the spacer 31. We also observed that in our population, the absence of spacer 31 is not crucial for classification as being either H or T; what differentiates between the two is the number of copies of ETR-A, ETR-B, ETR-C. The H3 subfamily is characterized by the combination 323 of these alleles while T strains present considerable diversity of these loci (one to three copies of ETR-A, two or three copies of ETR-B and three to five copies of ETR-C).

The RD nominated RD^{Rio} was first reported as new *M. tuberculosis* lineage in Rio de Janeiro in 2007, Lazzarini *et al*. [2] and is a deletion of 26.3 kb restricted to the LAM family and in particular, in subfamilies LAM1, LAM2, LAM4, LAM5, LAM6 and LAM9. This deletion affects 10 genes, including two genes encoding Proline-proline-glutamic Acid Proteins (PPE) [2] and association between RD^{Rio} strains and high prevalence may be related to virulence and/or adaptation specifies the Latin American and European population-based epidemiological and clinical characteristics; however, studies have proven to be inconclusive or contradictory [4], [63], [64]. The lineage RD^{Rio}, was identified in different countries [5], [6], [7], [49] and in Brazil, has been described in different states, including Rio de Janeiro, Rio Grande do Sul, Minas Gerais, Espírito Santo and Rio Grande do Sul [3], [8], [63], [64]. The frequency ranges from 30 to 38% of isolates tested and was associated with MRD-TB [4], [63], [64] and with genotype clustering [5],[63], indicating a higher rate of recent infection and transmissibility. Another deletion, RD174, initially described as a marker for the LAM family and as a co-marker for RD^{Rio} [7], [8] was associated with high transmissibility [10].

The frequency of strains RD^{Rio} in the present study, with an overall frequency of 11% and 20.7% in LAM, is lower than that observed in other studies and even when including the eight isolates that showed mixed RD^{Rio}/WT signals, resulting frequencies of 14.7% and 28.2% still lower than previously observed. This difference could be related with the relative low frequency of LAM1, LAM2, LAM5, LAM6 and LAM9 related subfamilies in our study sample. Earlier studies on classification of RD^{Rio} strains was based on genotypes defined by spoligotyping and/or 12 MIRUs only [2], [5], [6], [7], [8], [63], [64] and again, this is the first study that used 24 MIRU-VNTR typing to conduct a more detailed phylogenetic analysis. We verified the signature of MIRU-VNTR loci for RD^{Rio} and RD174, as compared with that of the hypothetical ancestral of RD^{Rio} as defined by 12 MIRUs [2] and that, besides sharing two copies of MIRU04 and MIRU20, they also share one copy of MIRU24, three copies of MIRU31, two copies of ETR-A, three copies of MTUB21 and one copy of MTUB30, yielding 2213231 as fingerprint for RD^{Rio}. All LAM/RD174 isolates, with or without RD^{Rio}, carried two copies of MIRU20 and ETRA and one copy of MTUB31. We observed that LAM3 has two copies of MTUB30 (2213232) and we propose that this subfamily that do not carry RD^{Rio}, has evolved independently. We also observed RD^{Rio} in two isolates (2.6%) with a spoligotype not indicative for being LAM; a small number of such cases have also been observed by other research groups [5], [7], [64]. One of these isolates that had been classified by spoligotyping as H3 SIT53 was reclassified by 24 MIRU as being "LAM-Like" and called attention because it had the MIRU signature of the hypothetical ancestor of RD^{Rio} and carried the SNP $fbpC^{103}$ and RD174. Overall, we observed four scenarios: (i) isolates with the RD^{Rio} and RD174, (ii) isolates showing only RD^{Rio} (iii) isolates showing only RD174 and (iv) isolates that did not carry any of the deletions, suggesting that both markers evolved on different time points. This is different from earlier data [7] that claim that RD174 is an absolute co-marker for RD^{Rio} and therefore, studies that use the presence of RD174 to infer the presence of RD^{Rio} [8] may overestimate the frequency of the latter. In 2007, Lazzarini et al. [2] suggested that RD^{Rio} arose by homologous recombination between genes and although all neighboring sequences were identical, such event could have happened more than once. This suggests that the RD174 deletion occurred before RD^{Rio} but this needs to be confirmed as we also observed RD^{Rio} strains that had intact RD174. In Figure S3, we propose a possible evolution of members of the Euro-American lineages but with the limitation that the spoligotype defined lineages S, X and other are not represented and this concerns a sampling only from Rio de Janeiro.

In a recent study, Hill *et al*. (2012) [53], mentions the difficulty in studying the evolution of the Euro-American lineage (LAM, Haarlem, T, X and S) using spoligotyping due to the large number of IS*6110* copies in such strains that may result in IS*6110* mediated deletions in the DR locus. This might be the reason why bacterial evolution exclusively based on spoligotyping is not robust and the wide range of profiles reported as unclassified in SITVITWEB. Our approach, combining spoligotyping, MIRU-VNTRs, SNPs and RDs allowed the reclassification of 13 SITs that did not rank in SITVITWEB, allowing definition of 29 new spoligotypes and refine classification of isolates belonging to Euro-American lineage. Our data are also support the idea that absence of spacers 21–24 is not sufficient for classification as LAM and of spacer 31 to differentiate T and H, the latter indicative for subfamilies H3 SIT50 and T1 SIT53. Possible explanations are that ancestral lineages are currently circulating (plesiomorphic state) or that the isolates are suffering homoplasic evolution and reversion into the plesiomorphic state.

Supporting Information

Figure S1 Dendrogram constructed with BioNumerics software version 6.6 with the results of MIRU-VNTRs 24 *loci* and spoligotyping by similarity coefficient for categorical data and the neighbor-joining algorithm. 1st column (after spoligotypes): number of isolated label; 2nd column: patients who have more than one isolate in the study (n = 27) received numbering 1–27, and the different strains present the same numbering; 3rd column: International Spoliotype Types (SIT); 4th column: classification obtained through SITVITWEB (family and subfamily).
(DOC)

Figure S2 Allelic diversity of the 24 loci MIRU-VNTR loci in LAM/RDRio isolates.
(DOC)

Figure S3 Possible evolution of *M. tuberculosis* lineage Euro-American (LAM, T and H) according to the markers analyzed in this study. The Euro-American Ancestral evolved into two distinct groups: LAM ancestral and T/H ancestral, characterized by absences of spacers 33–36 and one copy of MIRU24 that is common to all Euro-American lineages. The ancestral LAM strains have $fbpC^{103}$ and this was the basis of LAM A (LAM9), with additional absence of spacers 21–24, one copy of MTUB30 and two copies of MIRU04 and ETR-A. LAM A on its turn is the basis for two other groups: LAM B (LAM9-LAM4, LAM1-LAM2-LAM5 and LAM6) and LAM C (LAM3). The LAM B evolved from LAM B1, characterized by a deleted RD174 and on its turn to LAM B2, with both deleted RD174 and RD^{Rio}. The H/T Ancestral lineage is the origin of both groups H and T (difference only in MIRU-VNTR copies), showing absence of spacers 33–36; additional loss of spacer 31 led to subtype H A, observed in high frequency in this study.
(DOC)

Table S1 Detailed genotyping results and associated demographic, epidemiologic and nomenclature information on 218 Mycobacterium tuberculosis strains isolated from pulmonary tuberculosis patients in Rio de Janeiro, Brazil.
(XLS)

Table S2 Detailed genotyping results of $fbpC^{103}$, RD174 and RD^{Rio} on 182 M. tuberculosis strains isolated from pulmonary tuberculosis patients in Rio de Janeiro, Brazil.
(XLS)

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Author Contributions

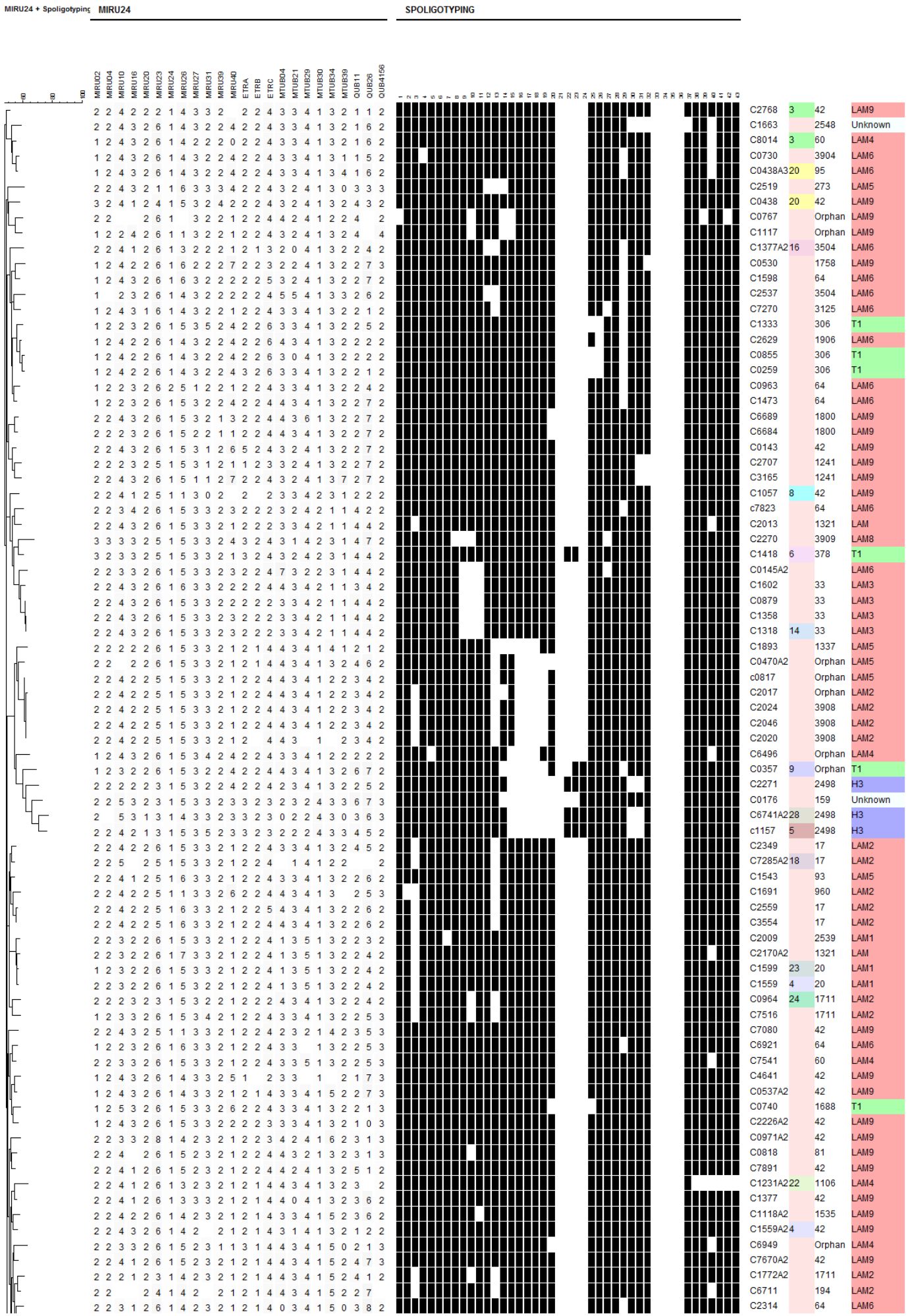
Conceived and designed the experiments: SEGV HMG ARS NB PNS. Performed the experiments: SEGV HMG ARS NB PNS. Analyzed the data: SEGV CCA HMG LLG ECC MIA DC MKG. Contributed reagents/materials/analysis tools: PNS KVL MLL FT PCSC NR CS. Wrote the paper: SEGV CCA PNS NR CS.

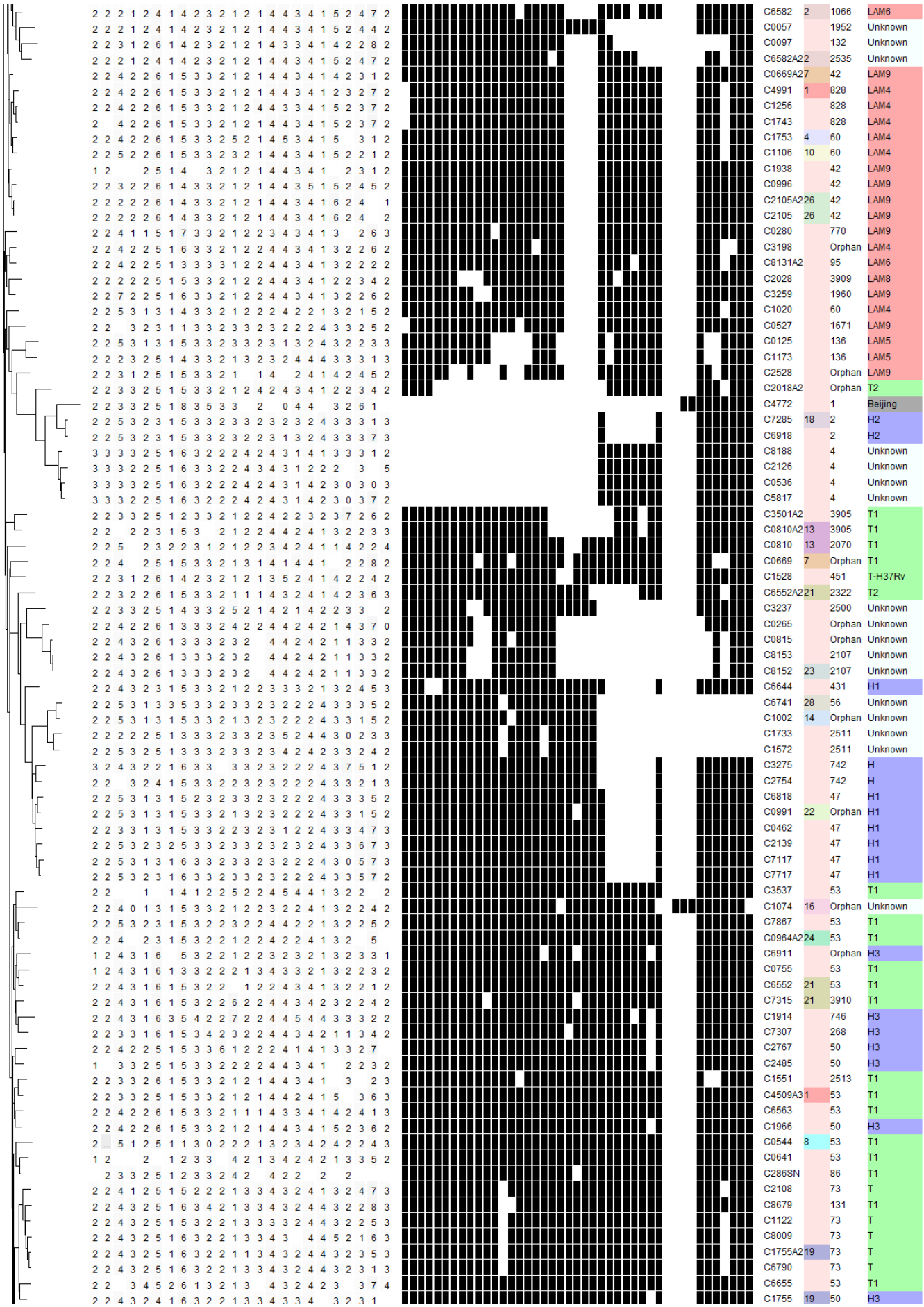
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Figure S1: Dendrogram constructed with BioNumerics software version 6.6 with the results of MIRU-VNTRs 24 loci and spoligotyping by similarity coefficient for categorical data and the neighbor-joining algorithm. 1st column (after spoligotypes): number of isolated label; 2nd column: patients who have more than one isolate in the study (n = 27) received numbering 1–27, and the different strains present the same numbering; 3rd column: International Spoliotype Types (SIT); 4th column: classification obtained through SITVITWEB (family and subfamily).





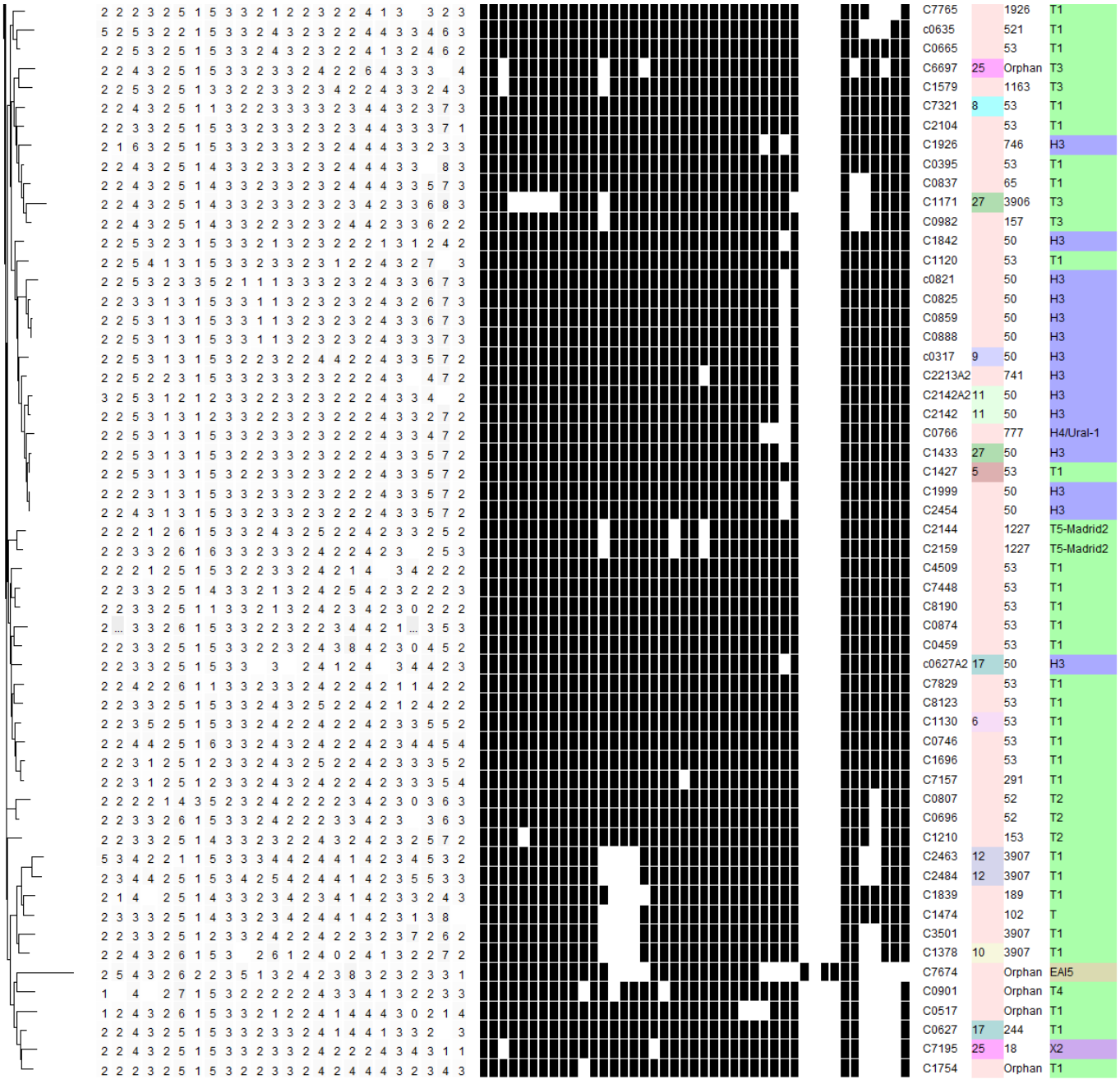


Figure S2: Allelic diversity of the 24 loci MIRU-VNTR loci in LAM/RDRio isolates.

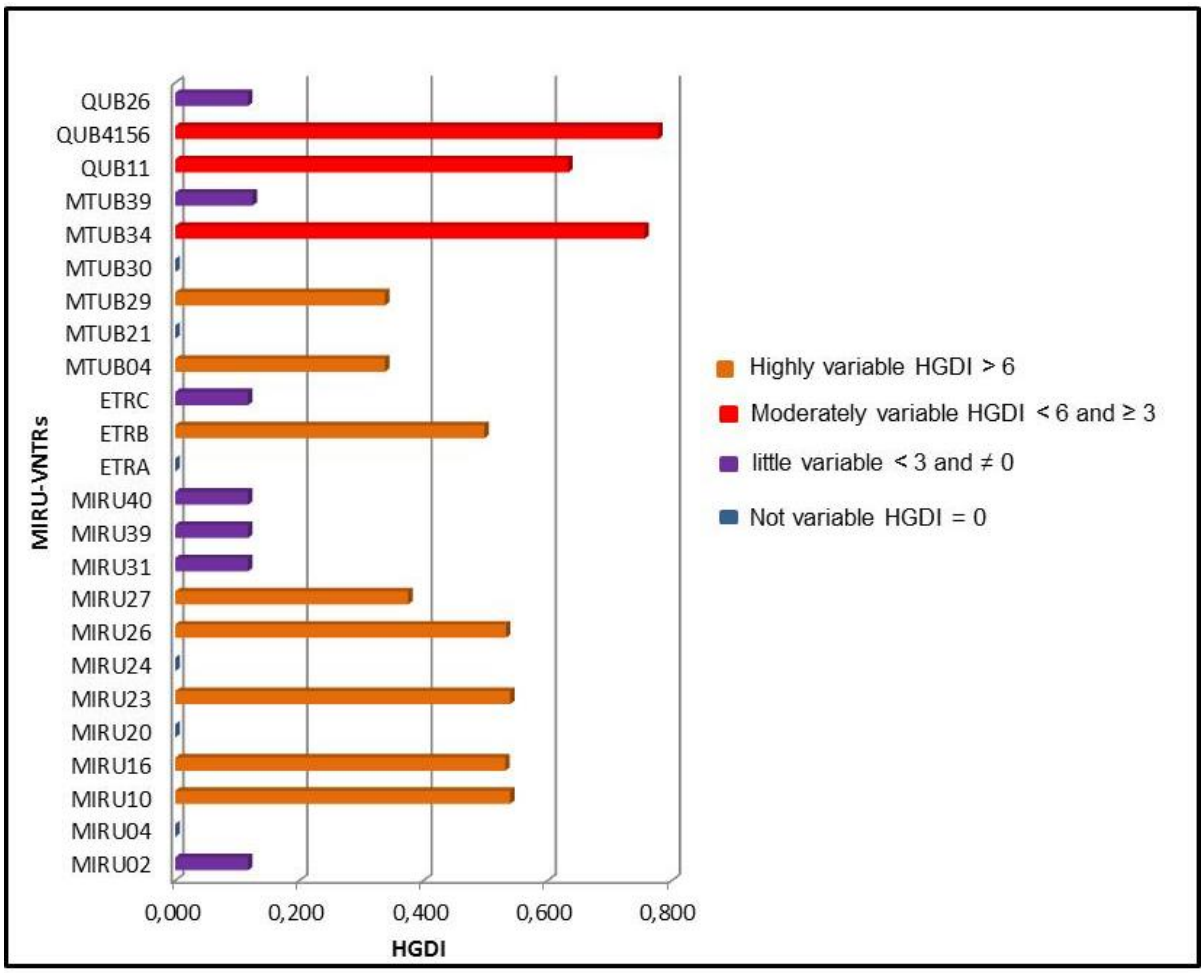
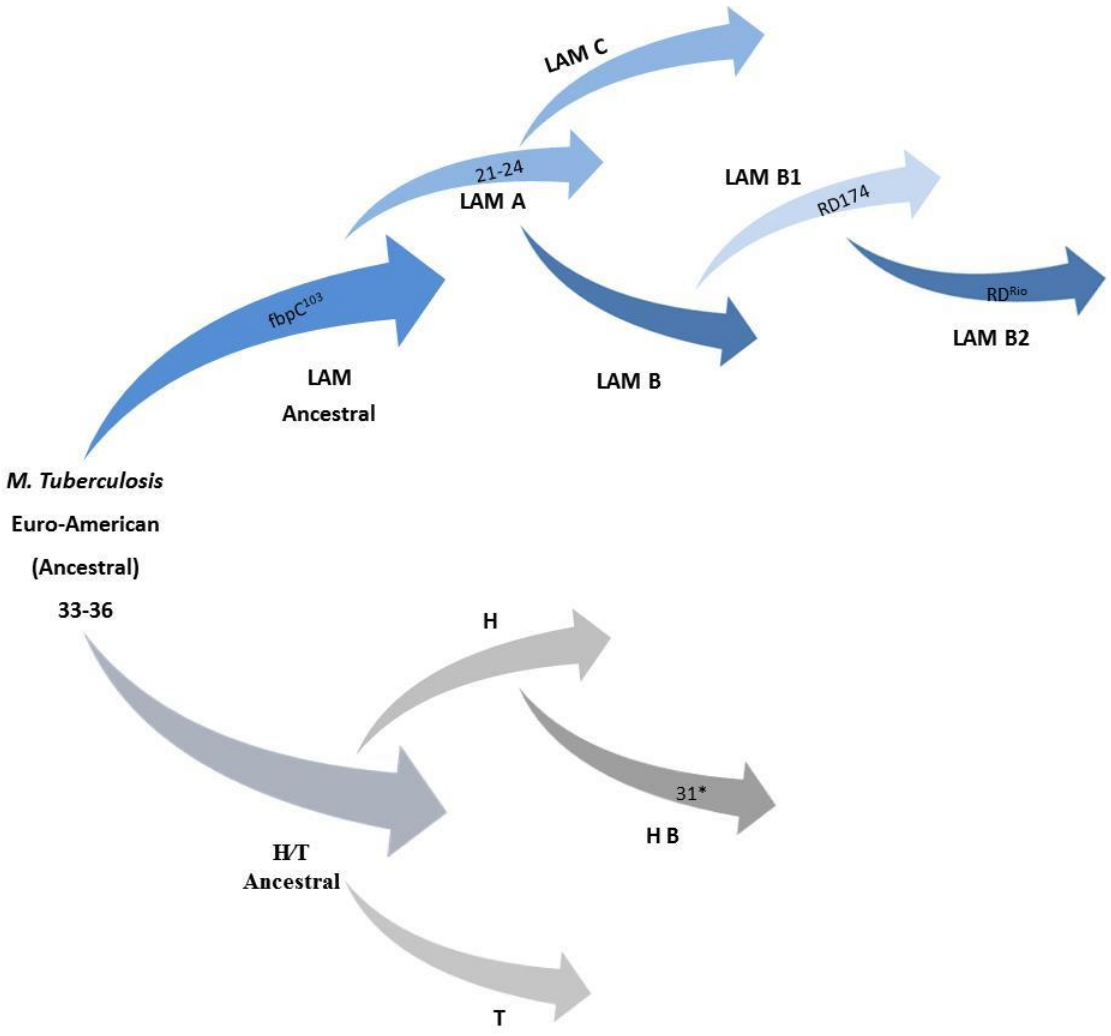


Figure S3: Possible evolution of *M. tuberculosis* lineage Euro-American (LAM, T and H) according to the markers analyzed in this study. The Euro-American Ancestral evolved into two distinct groups: LAM ancestral and T/H ancestral, characterized by absences of spacers 33–36 and one copy of MIRU24 that is common to all Euro-American lineages. The ancestral LAM strains have fbpC103 and this was the basis of LAM A (LAM9), with additional absence of spacers 21–24, one copy of MTUB30 and two copies of MIRU04 and ETR-A. LAM A on its turn is the basis for two other groups: LAM B (LAM9-LAM4, LAM1-LAM2-LAM5 and LAM6) and LAM C (LAM3). The LAM B evolved from LAM B1, characterized by a deleted RD174 and on its turn to LAM B2, with both deleted RD174 and RDRio. The H/T Ancestral lineage is the origin of both groups H and T (difference only in MIRU-VNTR copies), showing absence of spacers 33–36; additional loss of spacer 31 led to subtype H A, observed in high frequency in this study.



Supplemental Table S1: Detailed genotyping results and associated demographic, epidemiologic and nomenclature information on 218 *M. tuberculosis* strains isolated from pulmonary tuberculosis patients in Rio de Janeiro, Brazil.

IsoNumber	Year	Strain	Spoligotype Description	Octal code	SIT SITVIT2	Clade SITVIT2	SpotClust	MIRU-VNTR	VNTR	5-VIT	MIRU12	12-MIT	MIRU15	15-MIT	MIRU24	24-MIT	Drug-R Code	Sex/Age	MIT	VIT	MLVA 15-9
BRA1620090C4772	2009	C4772	□□□□□□□□□□□□□□□□	000000000003771	1	BEIJING	ND	BEIJING	32323	102	124326153424	Orphan	243544242223312	Orphan	132615342424334122	Orphan	0	M/13	84	ND	ND
BRA1620080C7674	2008	C7674	■■■■■■■■■■■■■□□□	777741777413600	Orphan	EAI5	EAI5	EAI-5	33422	491	234226153221	Orphan	342531243724312	Orphan	122615332121443415	Orphan	0	M	64	ND	ND
BRA1620090C2754	2009	C2754	■■■■■■■■■■■■■■■■	777777770020771	742	H	ND	H	32323	102	222226143321	1660	222431244-14312	Orphan	222614332121443416	Orphan	0	M	ND	97	ND
BRA1620090C3275	2009	C3275	■■■■■■■■■■■■■■■■	777777770020771	742	H	ND	H	32323	102	224-26152321	Orphan	24-531243134312	Orphan	4-261523212244321321	Orphan	0	M	ND	97	ND
BRA1620080C0462	2008	C0462	■■■■■■■■■■■■■■■■	777777774020771	47	H1	ND	H	21423	99	225313153323	42	253533332331342	Orphan	331315332332313243	Orphan	0	F/28	ND	97	ND
BRA1620082C2139	2008	C2139	■■■■■■■■■■■■■■■■	777777774020771	47	H1	ND	H	24255	Orphan	224226113323	Orphan	242133344222221	Orphan	122611332332422411	Orphan	2	F	ND	97	ND
BRA1620080C6818	2008	C6818	■■■■■■■■■■■■■■■■	777777774020771	47	H1	ND	H	32423	21	224226153321	25	242531144133312	Orphan	122615332111433414	Orphan	0	F	ND	97	ND
BRA1620081C7117	2008	C7117	■■■■■■■■■■■■■■■■	777777774020771	47	H1	ND	H	32423	21	224326153321	1286	243531224423321	Orphan	132615332122334211	Orphan	1	M	ND	97	ND
BRA1620080C7717	2008	C7717	■■■■■■■■■■■■■■■■	777777774020771	47	H1	ND	H	33422	491	124-27153222	Orphan	24-522242333312	Orphan	4-271532222243341322	Orphan	0	F	ND	97	ND
BRA1620080C6644	2008	C6644	■■■□□■■■■■■■■■■	717777774020771	431	H1	ND	LAM	32323	102	223326153321	224	23353124-234313	Orphan	33261533212144341-3	Orphan	0	M	ND	177	ND
BRA1620080C0991	2008	C0991	■■■■■■■■■■■■■■■■	777777734020771	Orphan	H1	H1	H	22323	92	223325123324	1650	233234242622227	Orphan	325123324224223237	Orphan	0	M/25	174	97	ND
BRA1620080C6918	2008	C6918	□□□□□□□□□□□□□□□□	000000004020771	2	H2	ND	H	32423	21	224326153322	1062	243532224423321	Orphan	132615332222334211	Orphan	0	F/35	43	177	ND
BRA1620080C7285	2008	C7285	□□□□□□□□□□□□□□□□	000000004020771	2	H2	ND	H	32523	55	124226162227	Orphan	242627232732212	Orphan	122616222723224132	Orphan	0	M/43	43	97	ND
BRA1620080c0821	2008	c0821	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	LAM	22223	105	222124142321	1648	221431244724312	584	2124142321214434152	232	0	M/39	ND	ND	ND
BRA1620080C1755	2008	C1755	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	T	22423	9	224225163321	130	242631242624312	598	1225163321224434132	234	0	F/43	ND	ND	ND
BRA1620080C0825	2008	C0825	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22223	105	22--24142-21	Orphan	2--4-12427-4312	Orphan	1--24142-2121443415224	Orphan	0	F	ND	97	ND
BRA1620082C0859	2008	C0859	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22223	105	214-25143323	Orphan	14-433432434123	Orphan	4-251433234234142333	Orphan	2	M	41	97	ND
BRA1620080C0888	2008	C0888	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22321	Orphan	223325113321	Orphan	233131342222320	Orphan	332511332132423023	Orphan	0	M	41	97	ND
BRA1620080C1433	2008	C1433	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22423	9	223325153323	116	233533333712343	Orphan	332515332332334433	Orphan	0	F/26	810	197	6904-76
BRA1620080C1842	2008	C1842	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22423	9	224325163221	949	243621341633-42	Orphan	432516322133443452	Orphan	0	M	ND	97	ND
BRA1620080C1999	2008	C1999	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	22423	9	234425153425	Orphan	344545445334125	Orphan	1442515345424414235	Orphan	0	F/52	ND	97	ND
BRA1620090C2142	2009	C2142	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	24423	488	224126132321	579	241331243-24312	Orphan	4126132321214434132	Orphan	0	M	ND	97	ND
BRA1620090C2142A2	2009	C2142A2	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	2-220	Orphan	224126132221	1460	241321232422012	Orphan	1126132221213204132	Orphan	0	M	ND	97	ND
BRA1620090C2454	2009	C2454	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	32322	109	224226142321	1658	242431243623312	Orphan	1226142321214334152	Orphan	0	M	240	97	ND
BRA1620080c0627A2	2008	c0627A2	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	H	21423	99	225413153323	Orphan	254533337-31242	Orphan	5413153323323122432	Orphan	0	F	ND	ND	ND
BRA1620090C2485	2009	C2485	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	LAM	32323	102	12422614324	1659	242424262223012	Orphan	1226143224226304132	Orphan	0	M	ND	ND	ND
BRA1620090C2767	2009	C2767	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	LAM	32323	102	223226143321	10	232431244524312	Orphan	1226143321214435152	Orphan	0	M	ND	229	ND
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BRA1620080C1966	2008	C1966	■■■■■■■■■■■■■■■■	777777777720771	50	H3	ND	LAM	22423	9	233325143323	1379	3334334438-4121	Orphan	3325143323424414231	Orphan	0	M/26	25	198	ND
BRA1620080C7307	2008	C7307	■■■■■■■■■■■■■■■■	777777677720771	268	H3	T1	LAM	32523	55	124326163222	328	243622252723212	Orphan	1326163222225324132	Orphan	0	M/28	ND	235	ND
BRA1620090C2213A2	2009	C2213A2	■■■■■■■■■■■■■■■■	777777757720771	741	H3	ND	H	2-423	489	224326133323	251	243333243324221	599	4326133232-4424211	235	0	M	607	97	ND
BRA1620082C1926	2008	C1926	■■■■■■■■■■■■■■■■	777777777520771	746	H3	ND	H	22423	9	227225163321	Orphan	272631242624312	Orphan	7225163212244341322	Orphan	2	F	ND	184	ND
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BRA1620082C6741A2	2008	C6741A2	■■■■■■■■■■■■■■□□	777760077620771	2498	H3	ND	H	32423	21	224226153321	25	242531244523312	Orphan	1226153321224334132	Orphan	2	F	ND	ND	ND
BRA1620080C2271	2008	C2271	■■■■■■■■■■■■■■□□	777760077620771	2498	H3	ND	LAM	31423	121	223126142321	1262	231431242823312	Orphan	1126142321214334142	Orphan	0	F	ND	191	ND
BRA1620080C6911	2008	C6911	■■■■■■■■■■■■■■■■	777776737720771	Orphan	H3	T1	LAM	32423	21	224326153126	1663	243516542723212	Orphan	1326153126524324132	Orphan	0	M	ND	230	5320-766
BRA1620090C0766	2009	C0766	■■■■■■■■■■■■■■■■	777777777420771	777	H4/Ural-1	ND	H	21423	99	225323153323	43	253533233731343	Orphan	3231533233233132433	Orphan	0	F	42	97	ND
BRA1620090C2170A2	2009	C2170A2	■■□■■■■■■■■■■■■	677777607760731	1321	LAM	ND	LAM	2-423	489	224326133323	251	243333243324221	599	4326133232-4424211	235	0	M	ND	9	ND
BRA1620080C2013	2008	C2013	■■□■■■■■■■■■■■■	677777607760731	1321	LAM	ND	LAM	22424	112	333225163322	Orphan	332632443-5312-	Orphan	3225163322434312221	Orphan	0	F	ND	229	1386-259
BRA1620090C145A2	2009	C0145A2	■■■■■■■■□□□□■■■■	776177606760771	2310	LAM	ND	LAM	1242-	Orphan	525322153324	Orphan	253534336322243	Orphan	3225153324323224433	Orphan	0	F	236	9	MLVA15-9
BRA1620080C1559	2008	C1559	■■□■■■■■■■■■■■■	677777607760771	20	LAM1	ND	LAM	22423	9	224225153321	127	242531243424312	597	42251533212-443-1-23	Orphan	0	F	492	191	ND
BRA1620080C1599	2008	C1599	■■□■■■■■■■■■■■■	677777607760771	20	LAM1	ND	LAM	22423	9	224325153221	1652	243521332533242	Orphan	1325153221333324432	Orphan	0	F	ND	9	ND
BRA1620090C2009	2009	C2009	■■□■■■□■■■■■■■■	673777607760771	2539	LAM1	LAM1/LAM9	LAM	22424	112	333325153324	397	333534344723121	Orphan	3325153324324314231	Orphan	0	M	128	9	ND
BRA1620083C2349	2008	C2349	■■□■■■■■■■■□■■■	677737607760771	17	LAM2	ND	LAM	32313	117	223126142321	1262	231431243820310	Orphan	1126142321214034150	Orphan	3	M	25	9	ND
BRA1620090C2559	2009	C2559	■■□■■■■■■■■□■■■	677737607760771	17	LAM2	ND	LAM	32323	102	124326143224	425	243424241523311	Orphan	1326143224224334131	Orphan	0	F/29	130	ND	ND
BRA1620090C3554	2009	C3554	■■□■■■■■■■■□■■■	677737607760771	17	LAM2	ND	LAM	32323	102	12322615321	Orphan	232531242421312	224	1226153321224135132	Orphan	0	NI	130	9	ND
BRA1620080C7285A2	2008	C7285A2	■■□■■■■■■■■□■■■	677737607760771	17	LAM2	ND	LAM	32523	55	122326163321	Orphan	223631242533312	Orphan	3326163321224334132	Orphan	0	M/24	ND	9	ND
BRA1620080C6711	2008	C6711	■■□■■■■■■■■□■■■	677737607760731	194	LAM2	ND	LAM	32422	118	224226153325	Orphan	24253524312531-	Orphan	4226153321214534152	Orphan	0	F/35	ND	ND	ND
BRA1620090C1691	2009	C1691	■□□■■■■■■■□■■■	477737607760771	960	LAM2	ND	LAM	22423	9	224-25153321	Orphan	24-531342821412	Orphan	4-251533213141441-23	Orphan	0	M	ND	9	ND
BRA1620080C0964	2008	C0964	■■□■■■■■■□■■□■■■	673337607760771	1711	LAM2	ND	LAM	22323	92	224325113321	Orphan	243131243532312	Orphan	1325113321224232142	Orphan	0	M/54	ND	225	ND
BRA1620090C1772A2	2009	C1772A2	■■□■■■■■■■□■■■	677337607760771	1711	LAM2	ND	LAM	22423	9	224325163221	949	243621143533242	Orphan	1325163221134324432	Orphan	0	M	ND	198	ND
BRA1620080C7516	2008	C7516	■■□■■■■■■■□■■■	677337607760771	1711	LAM2	ND	LAM	33322	490	22--261-3221	Orphan	2---21244-24212	Orphan	1--261-32212244241224	Orphan	0	F/22	ND	235	ND
BRA1620080C2024	2008	C2024	■■□■■■■■■■■□■■□	677730207760771	3908	LAM2	LAM1/LAM2	LAM	224E3	Orphan	225125113022	Orphan	251102232432322	Orphan	3125113022213234242	Orphan	0	M	127	9	ND
BRA1620090C2046	2009	C2046	■■□■■■■■■■■□■■□	677730207760771	3908	LAM2	LAM1/LAM2	LAM	22522	487	124316133222	Orphan	243322142323312	Orphan	3161332221343321322	Orphan	0	F	127	9	ND
BRA1620090C2020	2009	C2020	■■□■■■■■■■■□■■□	677730207760771	3908	LAM2	LAM1/LAM2	LAM	224E2	Orphan	333325163222	1654	333622443123113	Orphan	3325163224243141332	Orphan	0	F/6	127	ND	ND
BRA1620081C2017	2008	C2017	■■□■■■■■■■■□■■□	677710207760771	Orphan	LAM2	LAM1/LAM2	LAM	22424	112	333225163222	Orphan	332622443723120	Orphan	3225163222424314230	Orphan	1	M/35	127	9	ND
BRA1620080C0879	2008	C0879	■■■■■■■■□□□■■■■■	776177607760771	33	LAM3	ND	LAM	22223	105	224115173321	Orphan	24173123263431-	Orphan	4115173321223434132	Orphan	0	F/68	ND	229	ND
BRA1620080C1318	2008	C1318	■■■■■■■■□□□■■■■■	776177607760771	33	LAM3	ND	LAM	22422	94	222225153321	1197	222531243424312	Orphan	1225153321224434122	Orphan	0	F	213	229	ND
BRA1620080C1358	2008	C1358	■■■■■■■■□□□■■■■■	776177607760771	33	LAM3	ND	LAM	22422	94	222325153121	Orphan	223511132723212	Orphan	3251531211233241322	Orphan	0	M	213	229	ND
BRA1620090C1602	2009	C1602	■■■■■■■■□□□■■■■■	776177607760771	33	LAM3	ND	LAM	22423	9	224325153323	33	243533343-42243	Orphan	4325153323324226433	Orphan	0	F	ND	9	ND
BRA1620080C1020	2008	C1020	■■■■■■■■■■■■■■■■	777777607760731	60	LAM4	ND	LAM	22421	415	222225133323	498	222333332335240	Orphan	1225133323323524430	Orphan	0	M	ND	229	ND
BRA1620080C1106	2008	C1106	■■■■■■■■■■■■■■■■	777777607760731	60	LAM4	ND	LAM	22422	94	225325133223	Orphan	253323332434243	Orphan	3251332323323422433	Orphan	0	M	ND	198	ND
BRA1620080C1753	2008	C1753	■■■■■■■■■■■■■■■■	777777607760731	60	LAM4	ND	LAM	22423	9	224125163321	1403	241631242623312	Orphan	1125163321224334132	Orphan	0	F	ND	198	ND
BRA1620080C7541	2008	C7541	■■■■■■■■■■■■■■■■	777777607760731	60	LAM4	ND	LAM	33422	491	223326153322	289	233532323533421	Orphan	3261533223234421C	Orphan	0	NI	224	9	ND
BRA1620083C8014	2008	C8014	■■■■■■■■■■■■■■■■	777777607760731	60	LAM4	ND	LAM	42433	32	22-345261321	Orphan	2-363134374322-	Orphan	-3452613213-432423-3	Orphan	3	M	ND	191	ND
BRA1620090C1256	2009	C1256	□■■■■■■■■■■■■■■■	377777607760731	828	LAM4	ND	LAM	22422	94	222125153223	Orphan	2215233422221-4	Orphan	2125153223324214-342	Orphan	0	F	25	ND	ND
BRA1620080C1743	2008	C1743	□■■■■■■■■■■■■■■■	377777607760731	828	LAM4	ND	LAM	22423	9	323325153321	1653	233531344423221	Orphan	3251533213243242312	Orphan	0	M/16	ND	ND	ND
BRA1620080C4991	2008	C4991	□■■■■■■■■■■■■■■■	377777607760731	828	LAM4	ND	LAM	32323	102	125326153326	Orphan	253536242133312	Orphan	3261533262243413 2	Orphan	0	M	25	198	ND
BRA1620080C1231A2	2008	C1231A2	■■■■■■■■■■■■■■■■	777777607760400	1106	LAM4	ND	LAM	22422	94	224125152221	Orphan	241521344733212	Orphan	1125152221334324132	Orphan	0	M	579	198	ND
BRA1620080C6949	2008	C6949	■■■■■■■■■■■■■■■■	777777407760731	Orphan	LAM4	LAM9	LAM	32423	21	224326153323	213	243533224423321	603	3261533232223434211	236	0	M/29	ND	157	ND
BRA1620090C3198	2009	C3198	■■■■■■■■■■■■■■■■	777775607760711	Orphan	LAM4	LAM9	LAM	32323	102	223326152311	Orphan	233531342134310	Orphan	3261523113144341502	Orphan	0	F	130	9	ND
BRA1620080C6496	2008	C6496	■■■■□■■■■■■■■■□□	757760607760731	Orphan	LAM4	LAM9	LAM	32323	102	222226153321	1199	222531242124311	Orphan	1226153321214434141	Orphan	0	M	ND	235	ND
BRA1620080C1543	2008	C1543	■■■■■■■■■■■■■□■■	777737607760771	93	LAM5	ND	LAM	22423	9	224225153321	127	242531243424312	597	1225153321224434122	233	0	F/25	ND	9	ND
BRA1620080C0125	2008	C0125	■■■■■■■■■■□□□□□□	777603405760471	136	LAM5	ND	H	12222	Orphan	325312123322	Orphan	253232334-22243	Orphan	5312123322323222433	Orphan	0	F	42	97	ND
BRA1620080C1173	2008	C1173	■■■■■■■■■■□□□□□□	777603405760471	136	LAM5	ND	H	22422	94	224325143323	30	243433336832323	Orphan	3325143323323234233	Orphan	0	M/29	ND	97	ND
BRA1620090C2519	2009	C2519	■■■■■■■■■■□□□■■	777617607760771	273	LAM5	ND	LAM	32323	102	124226143224	1659	242424262224312	Orphan	1226143224226434132	Orphan	0	M	ND	9	ND
BRA1620090C1893	2009	C1893	■■■■■■■■■■■□□□□□	777700607760771	1337	LAM5	ND	LAM	22423	9	224325163421	Orphan	243641342833242	Orphan	1325163421334324432	Orphan	0	F	ND	198	ND
BRA1620090C0470A2	2009	C0470A2	■■■■■■■■■■■■■■■□	777730007760771	Orphan	LAM5	LAM9	LAM	21423	99	225313153223	810	253523245724243	Orphan	3131533233224422433	Orphan	0	F	ND	198	ND
BRA1620080c0817	2008	c0817	■■■■■■■■■■■■■■□□	777730207760771	Orphan	LAM5	LAM1/LAM2	LAM	22223	105	22214142321	1648	221431244424312	Orphan	2124142321214434152	Orphan	0	M/55	127	9	ND

BRA1620080C6921	2008	C6921	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	32423	21	224326153323	213	243533224423321	603	!3261533232223342111	236	0	F	ND	9	ND
BRA1620084C0963	2008	C0963	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	22322	106	224225113326	Orphan	24213624253431-	Orphan	!2251133262244341 3-:	Orphan	4	M	ND	191	ND
BRA1620090C1473	2009	C1473	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	22423	9	223325153321	401	23353124363421-	Orphan	!3251533212144241 5-:	Orphan	0	M	831	191	6904-76
BRA1620080C1598	2008	C1598	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	22423	9	224325153323	33	243533342-31413	Orphan	!3251533233241441 33	Orphan	0	F	ND	ND	6565
BRA1620080C2314	2008	C2314	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	322E3	Orphan	223126142321	1262	231431232425212	Orphan	!1261423212135241 42	Orphan	0	M/61	ND	198	ND
BRA1620080c7823	2008	c7823	■■■■■■■■■■■■■■■■	777777607560771	64	LAM6	ND	LAM	3-423	492	22--1-141225	Orphan	2--425242-25412	Orphan	'--1-1412252454413 22	Orphan	0	F	ND	229	ND
BRA1620080C0438A3	2008	C0438A3	■■■■■■■■■■■■■■■■	777777607560731	95	LAM6	ND	LAM	21423	99	224213153523	Orphan	242553334522243	Orphan	!2131535233232224 33	Orphan	0	M/49	425	191	ND
BRA1620080C8131A2	2008	C8131A2	■■■■■■■■■■■■■■■■	777777607560731	95	LAM6	ND	LAM	42434	33	254326223513	64	543253223313822	Orphan	!3262235132423832 32	Orphan	0	F	ND	9	ND
BRA1620080C6582	2008	C6582	■■■■■■■■■■■■■■□■	777767607560771	1066	LAM6	ND	LAM	32323	102	223326153323	236	23353244427321	Orphan	!3261533233247322 31	Orphan	0	M	ND	198	ND
BRA1620090C2629	2009	C2629	■■■■■■■■■■■■■■■■	777777605560771	1906	LAM6	ND	LAM	32323	102	124326143325	Orphan	243435121733312	Orphan	43261433251-233-1-21	Orphan	0	M	ND	224	ND
BRA1620080C7270	2008	C7270	■■■■■■■■■■■■■□■■	777737606560771	3125	LAM6	LAM9	LAM	32433	23	22-226153321	Orphan	2-2531244624312	Orphan	-226153321214434132	Orphan	0	M/43	ND	191	ND
BRA1620080C1377A2	2008	C1377A2	■■■■■■■■■■■■□□■■	777637607560771	3504	LAM6	LAM9	LAM	22422	94	223125153321	771	231531-4452-212	Orphan	3125153321-14-24142	Orphan	0	M	ND	214	ND
BRA1620090C2537	2009	C2537	■■■■■■■■■■■■□□■■	777637607560771	3504	LAM6	LAM9	LAM	32323	102	124326143321	Orphan	243431242733312	Orphan	!3261433212143341 52	Orphan	0	M/68	ND	ND	ND
BRA1620090C0730	2009	C0730	■■■□■■■■■■■■■■■■	737777607560731	3904	LAM6	LAM9	LAM	21423	99	224-23153221	Orphan	24-52124-5-2212	Orphan	4-2315322122422413 2	Orphan	0	F	425	191	ND
BRA1620080C2028	2008	C2028	■■■■■■■□□□■■■■■■	774377606760771	3909	LAM8	ND	LAM	224F2	Orphan	123325153322	1655	233532242324312	Orphan	!3251533222244341-2:	Orphan	0	M/30	ND	9	4163-328
BRA1620080C2270	2008	C2270	■■■■■■■■□□□■■■■■	774377606760771	3909	LAM8	ND	S	31423	121	124326142220	Orphan	243420241623312	600	!3261422022433413 2	Orphan	0	M	397	23	ND
BRA1620090C0537A2	2009	C0537A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	21423	99	225313153321	174	253531331522243	595	!3131533213232224 33	230	0	F/21	ND	198	ND
BRA1620080C1559A2	2008	C1559A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22423	9	224225153321	127	242531243424312	597	!2251533212244341 22	233	0	F	ND	198	ND
BRA1620090C2226A2	2009	C2226A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	2-423	489	224326133323	251	243333243324221	599	!3261333232-4424211 2	235	0	M/57	ND	177	ND
BRA1620092C0143	2009	C0143	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	12321	Orphan	22422214332-	Orphan	24243-241123312	Orphan	!2224314332-2243341 32	Orphan	2	F/27	ND	ND	ND
BRA1620084C0438	2008	C0438	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	21423	99	224013153321	Orphan	240531232422212	Orphan	!0131533212232412 4	Orphan	4	M/49	ND	191	ND
BRA1620090C0669A2	2009	C0669A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	21423	99	222323153221	Orphan	223521222424312	Orphan	!3231532212224341 32	Orphan	0	F	25	198	ND
BRA1620080C0971A2	2008	C0971A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22323	92	223125123324	436	231234353522223	Orphan	!1251233243252242 33	Orphan	0	M/35	ND	177	ND
BRA1620080C0996	2008	C0996	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22323	92	223325123321	Orphan	233231242622227	Orphan	!3251233212242233 37	Orphan	0	M	10	198	ND
BRA1620090C1057	2009	C1057	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22422	94	224225133331	Orphan	242331242224312	Orphan	!2251333312244341 32	Orphan	0	F	174	ND	ND
BRA1620080C1377	2008	C1377	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22422	94	222325153321	838	22353123323221-	Orphan	!3251533212232241 3-:	Orphan	0	M	ND	198	124-462
BRA1620090C1938	2009	C1938	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22423	9	223325183533	84	233853--61-04-2	Orphan	!3325183533-2-044-326	Orphan	0	M	ND	198	ND
BRA1620080C2105	2008	C2105	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22622	97	223316153423	Orphan	233543243424321	Orphan	!3161534232244341 12	Orphan	0	M	ND	198	ND
BRA1620080C2105A2	2008	C2105A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	22622	97	22431615322-	Orphan	24352-122124312	Orphan	!3161533222433413 2	Orphan	0	M	ND	198	ND
BRA1620094C2768	2009	C2768	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	32323	102	224326143224	Orphan	243424241623312	Orphan	!3261432242243341 32	Orphan	4	F	ND	9	ND
BRA1620090C4641	2009	C4641	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	32323	102	124326153322	991	243532231033312	Orphan	!3261533222233341 32	Orphan	0	F/85	ND	ND	ND
BRA1620080C7080	2008	C7080	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	32423	21	224326153-26	Orphan	2435-6142720212	Orphan	!3261533-26124024132 2	Orphan	0	M/48	ND	9	ND
BRA1620080C7670A2	2008	C7670A2	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	33422	491	132326143222	Orphan	323422242625513	Orphan	!3261432222245541 33	Orphan	0	M	163	198	ND
BRA1620080C7891	2008	C7891	■■■■■■■■■■■■■■■■	777777607760771	42	LAM9	ND	LAM	42432	71	225-23223121	Orphan	25-211232244214	Orphan	5-2322312122342411 47	Orphan	0	M	163	9	ND
BRA1620080C0818	2008	C0818	■■■■■■■■■□■■■■■■	777737607760771	81	LAM9	ND	LAM	22223	105	222124142321	1648	221431244724312	584	!1241423212144341 52	232	0	F/35	ND	9	4136-17
BRA1620092C0280	2009	C0280	■■■■■■■■■■■■□■■■	777677607760771	770	LAM9	ND	LAM	21322	136	225313152323	1580	253533333522243	593	!3131523233232224 33	Orphan	2	M	ND	177	ND
BRA1620090C2707	2009	C2707	■■■■■■■■■■■■■■■■	777777607700771	1241	LAM9	LAM9	LAM	32323	102	222226143321	1660	222431244-24312	Orphan	!2261433212144341 62	Orphan	0	F	ND	ND	ND
BRA1620090C3165	2009	C3165	■■■■■■■■■■■■■■■■	777777607700771	1241	LAM9	LAM9	LAM	32323	102	222326152211	Orphan	223521242724312	Orphan	!3261522112244341 32	Orphan	0	M	ND	ND	ND
BRA1620090C1118A2	2009	C1118A2	■■■■■■■■■■□■■■■■	777577607760771	1535	LAM9	ND	LAM	22422	94	223325143323	121	233433245723222	Orphan	!3251433232432423 22	Orphan	0	F/20	ND	198	ND
BRA1620080C0527	2008	C0527	□■■■■■■■■■■■■■■■	377767607760771	1671	LAM9	ND	H	21423	99	225313153311	41	253531336732343	572	!3131533113232324 33	Orphan	0	M/31	ND	97	ND
BRA1620090C0530	2009	C0530	■■■■■■■■■■■■■■■■	777777607540771	1758	LAM9	ND	LAM	21423	99	225313153311	41	253531333732343	Orphan	!3131533113232324 33	Orphan	0	M/49	ND	230	ND
BRA1620080C6684	2008	C6684	■■■■■■■■■■■■■■■■	777777407760771	1800	LAM9	ND	LAM	32323	102	223426153323	Orphan	234533224223221	Orphan	!4261533223223241 12	Orphan	0	F	ND	191	ND
BRA1620080C6689	2008	C6689	■■■■■■■■■■■■■■■■	777777407760771	1800	LAM9	ND	LAM	32325	Orphan	224226153321	25	242531243124312	Orphan	!2261533212144341 42	Orphan	0	NI	ND	191	ND
BRA1620090C3259	2009	C3259	■■■■■■■■■□□■■■■■	777177607760771	1960	LAM9	ND	LAM	32323	102	224126152321	163	241531245124212	Orphan	!1261523212244241 32	Orphan	0	M	ND	9	ND
BRA1620080C0767	2008	C0767	□■■■■■■■■□■■■□□■	377347607760661	Orphan	LAM9	LAM9	LAM	21423	99	225323153323	43	253533333132343	Orphan	!3231533233232433 32	Orphan	0	F	ND	191	1278-76
BRA1620090C1117	2009	C1117	■■■■■■■■■□■■■□□■	777347607760771	Orphan	LAM9	LAM9	LAM	22422	94	222325143321	1552	223431333132443	Orphan	!3251433213233244 33	Orphan	0	F/60	ND	191	ND
BRA1620090C2528	2009	C2528	■■■■■■□□■□□□■□□■	771047607760671	Orphan	LAM9	LAM9	LAM	32323	102	124326143224	425	243424241623314	Orphan	!3261432242243413 42	Orphan	0	M	771	ND	ND
BRA1620080C1755A2	2008	C1755A2	■■■■■■■■■■■■□■■■	777737777760731	73	T	ND	T	22423	9	224225163321	130	242631242624312	598	!2251633212244341 32	234	0	F/43	ND	ND	ND
BRA1620090C1122	2009	C1122	■■■■■■■■■■■■□■■■	777737777760731	73	T	ND	T	22422	94	223325143321	796	233431342232522	Orphan	!3251433213242542 32	Orphan	0	F/48	ND	ND	ND
BRA1620080C2108	2008	C2108	■■■■■■■■■■■■□■■■	777737777760731	73	T	ND	T	22625	Orphan	224316153226	1656	243526242424322	Orphan	!3161533226224342 32	Orphan	0	F	ND	ND	ND
BRA1620082C6790	2008	C6790	■■■■■■■■■■■■□■■■	777737777760731	73	T	ND	T	32423	21	224226153321	25	242531242724313	Orphan	!2261533212144341 23	Orphan	2	NI/33	ND	ND	ND
BRA1620083C8009	2008	C8009	■■■■■■■■■■■■□■■■	777737777760731	73	T	ND	T	42432	71	225323253323	Orphan	253533336732343	531	!3232533233232243 33	Orphan	3	F	ND	ND	ND
BRA1620080C1474	2008	C1474	■■■■■■■■■■■■□□□□	777703777760771	102	T	ND	S	22423	9	223325153324	125	233534354222222	Orphan	!3251533243252242 12	Orphan	0	F	ND	32	ND
BRA1620090C0544	2009	C0544	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	21423	99	225313153223	810	253523335722243	596	!3131532233232224 33	231	0	NI	ND	ND	ND
BRA1620080C0665	2008	C0665	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	21423	99	222123142321	Orphan	221431244124312	Orphan	!1231423212144341 52	Orphan	0	F/20	46	97	ND
BRA1620090C1120	2009	C1120	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	22422	94	223325143325	118	233435243-22123	Orphan	!3251433252142142 23	Orphan	0	F/41	ND	97	ND
BRA1620080C1427	2008	C1427	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	22423	9	223325153321	401	233531223424312	Orphan	!3251533212424341 22	Orphan	0	M/26	810	197	ND
BRA1620082C2104	2008	C2104	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	22523	Orphan	124316143221	Orphan	243421242123312	Orphan	!3161432212243341 32	Orphan	2	M/55	116	97	4163-328
BRA1620080C7321	2008	C7321	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	H	33321	Orphan	224326163322	Orphan	243632243424321	Orphan	!3261633222244341 12	Orphan	0	M/39	ND	ND	ND
BRA1620090C0641	2009	C0641	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	21423	99	22-323113323	Orphan	2-3133332522243	Orphan	-3231133233232224 33	Orphan	0	M	ND	208	ND
BRA1620080C0755	2008	C0755	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	21423	99	225323153321	1404	253531332422211	Orphan	!3231533213232213 12	Orphan	0	M/69	ND	ND	ND
BRA1620080C0874	2008	C0874	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	22223	105	216325153323	1649	163533332332443	Orphan	!3251533233232444 33	Orphan	0	M/28	ND	ND	ND
BRA1620080C0964A2	2008	C0964A2	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	22323	92	224325113223	Orphan	243123333732342	Orphan	!3251132233332344 32	Orphan	0	M/54	ND	191	ND
BRA1620090C3537	2009	C3537	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	32323	102	123226153224	1662	232524246724312	Orphan	!2261532242244341 32	Orphan	0	M	ND	191	ND
BRA1620080C4509A3	2008	C4509A3	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	32323	102	124326153321	Orphan	243531242141440	Orphan	!3261533212241440 32	Orphan	0	M	401	198	ND
BRA1620082C6552	2008	C6552	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	32323	102	223226153221	492	232521242421312	Orphan	!2261533221241351 32	Orphan	2	M	ND	ND	ND
BRA1620080C6563	2008	C6563	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	32323	102	223226153321	128	232531143633212	Orphan	!2261533211143241 42	Orphan	0	M	25	240	ND
BRA1620080C7829	2008	C7829	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	42313	Orphan	12--2-1233-4	Orphan	2--234233524223	Orphan	'--2-1233-421342421 33	Orphan	0	M	ND	21	ND
BRA1620080C7867	2008	C7867	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	42432	71	22432-163221	Orphan	2436213431-33-2	Orphan	432-163221334334-32:	Orphan	0	M	693	191	ND
BRA1620080C8123	2008	C8123	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	LAM	42433	32	122326251221	Orphan	223521242423312	Orphan	!3262512212243341 32	Orphan	0	M	125	55	ND
BRA1620090C0459	2009	C0459	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	S	21423	99	224313153323	240	243533335722243	594	!3131533233232224 33	Orphan	0	F/33	15	21	ND
BRA1620080C0746	2008	C0746	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	21423	99	225323153323	43	253533336732343	531	!3231533233232243 33	Orphan	0	M	ND	21	ND
BRA1620080C1130	2008	C1130	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	22422	94	224325143323	30	24343333--32443	Orphan	!3251433233232444 33	Orphan	0	M/68	ND	9	ND
BRA1620080C1696	2008	C1696	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	22423	9	225325153324	46	253534334622212	Orphan	!3251533243232241 32	Orphan	0	M/62	436	555	ND
BRA1620080C4509	2008	C4509	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	32323	102	123326153421	Orphan	233541242533312	Orphan	!3261534212243341 32	Orphan	0	M/13	ND	112	4643-111
BRA1620080C6655	2008	C6655	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	32323	102	223326153321	224	233531242533312	Orphan	!3261533212243351 32	Orphan	0	F	ND	ND	ND
BRA1620080C7448	2008	C7448	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	33322	490	223226173321	1664	232731242421312	Orphan	!2261733212241351 32	Orphan	0	M	796	21	ND
BRA1620080C8190	2008	C8190	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	T	-2423	Orphan	224316354227	Orphan	243527243224543	Orphan	!3163542272244544 33	Orphan	0	ND	ND	21	ND
BRA1620090C0395	2009	C0395	■■■■■■■■■■■■■■■■	777777777760771	53	T1	ND	X	213E0	Orphan	223313153311	Orphan	233531336732342	Orphan	!3131533113232324 32	Orphan	0	F	30	97	ND
BRA1620080C0837	2008	C0837	■■■■■■■■■■■■■■■■	777777777760471	65	T1	ND	H	22223	105	22-324153322	Orphan	2-3532332132243	Orphan	-3241533223232224 33	Orphan	0	M	30	97	ND
BRA1620090C286SN	2009	C286SN	■■■■■■■■■■■■■■■■	777777737760771	86	T1	ND	T	32323	102	224326151127	Orphan	243517242723217	Orphan	!3261511272243241 37	Orphan	0	M/46	ND	ND	ND
BRA1620080C8679	2008	C8679	■■■■■■■■■■■■□□■■	777717777760771	131	T1	ND	T	-2-25	Orphan	124316-53221	Orphan	243521233312312	Orphan	!4316-532212232321 32	Orphan	0	ND	ND	ND	ND
BRA1620080C1839	2008	C1839	■■■■■■■■■■■■■□□□	777741777760771	189	T1	ND	H	22423	9	224325163221	949	243621343133242	Orphan	!3251633213343243 22	Orphan	0	F	ND	ND	ND
BRA1620080C0627	2008	C0627	■■■■■■■■■■■■■■■■	777777777760601	244	T1	ND	LAM	21423	99	225313153223	810	253523335722243	596	!3131532233232224 33	231	0	F	33	21	ND
BRA1620083C7157	2008	C7157	■■■■■■■■■■■■■■■■	777777677760771	291	T1	ND	T	32423	21	224326153213	Orphan	243523242724312	Orphan	!3261532132244361 32	Orphan	3	NI	436	21	ND
BRA1620090C0855	2009	C0855	■■■■■■■■■■■■■■■■	777777601560771	306	T1	ND	LAM	22223	105	324124153242	Orphan	241522244323212	Orphan	!1241532422243241 32	Orphan	0	M	ND	224	ND

BRA1620090C0259	2009	C0259	■■■■■■■■■■■■■■■■■■	777777601560771	306	T1	ND	LAM	13422	485	225313123322	Orphan	253232332722243	Orphan	3131232322323222433	Orphan	0	M	ND	ND	291-31
BRA1620093C1333	2009	C1333	■■■■■■■■■■■■■■■■■■	777777601560771	306	T1	ND	LAM	22422	94	222325153223	1651	223523343432442	Orphan	3252153223324244432	Orphan	3	F	ND	ND	124-462
BRA1620080C1418	2008	C1418	■■■■■■■■■■■■■■■■■■	777777667760771	378	T1	ND	S	22422	94	2233251533-3	Orphan	233533-442312-4	Orphan	33251533-3-24124-344	Orphan	0	M/41	ND	21	ND
BRA1620080c0635	2008	c0635	■■■■■■■■■■■■■■■■■■	777777777760611	521	T1	ND	H	21423	99	225313163323	612	253633335732240	Orphan	3131633233232224303	Orphan	0	M/27	ND	97	ND
BRA1620090C0740	2009	C0740	■■■■■■■■■■■■■■■■■■	777777403760771	1688	T1	ND	LAM	21423	99	225223153323	607	2525333347224-	Orphan	3223153323323222434	Orphan	0	M	ND	9	ND
BRA1620080C7765	2008	C7765	■■■■■■■■■■■■■■■■■■	777777777760701	1926	T1	ND	LAM	33424	Orphan	223328142321	Orphan	233431233134212	Orphan	3328142321223424162	Orphan	0	M/21	833	177	5812-31
BRA1620080C0810	2008	C0810	■■■■■■■■■■■■■■■■■■	777777637760771	2070	T1	ND	LAM	2142-	486	22-223153-21	Orphan	2-25-1242334212	Orphan	-223153-21224424132	Orphan	0	M/54	ND	ND	ND
BRA1620080C1551	2008	C1551	■■■■■■■■■■■■■■■■■□	777767777760471	2513	T1	ND	LAM	22423	9	22422153321	127	242531243424312	597	1225153321224434122	233	0	M	224	198	6862-111
BRA1620080C0810A2	2008	C0810A2	■■■■■■■■■■■■■■■■■■	777777001660771	3905	T1	LAM9	LAM	214F3	Orphan	225323163323	1295	253633335722243	Orphan	3232163323323222433	Orphan	0	M/54	ND	191	ND
BRA1620092C3501A2	2009	C3501A2	■■■■■■■■■■■■■■■■■■	777777001660771	3905	T1	LAM9	T	32323	102	122326153224	836	223524242724312	Orphan	3261532242244341324	Orphan	2	F	ND	9	ND
BRA1620080C1378	2008	C1378	■■■■■■■■■■■■■□□□□□	777703777760631	3907	T1	T1	LAM	22422	94	223325153322	15	233532344523820	Orphan	3252153322324384230	Orphan	0	F/39	ND	ND	ND
BRA1620090C2463	2009	C2463	■■■■■■■■■■■■■□□□□□	777703777760631	3907	T1	T1	S	32322	109	224326142-21	Orphan	2434-1241223112	Orphan	4326142-21214314132	Orphan	0	M/53	ND	32	ND
BRA1620090C2484	2009	C2484	■■■■■■■■■■■■■□□□□□	777703777760631	3907	T1	T1	S	32322	109	124226143224	1659	242424362123312	Orphan	1226143224326334132	Orphan	0	M/53	ND	33	ND
BRA1620092C3501	2009	C3501	■■■■■■■■■■■■□□□□□	777703777760631	3907	T1	T1	T	32323	102	122326153524	1661	223554626523312	Orphan	3261535242263341324	Orphan	2	M	ND	9	ND
BRA1620080C7315	2008	C7315	■■■■■■■■■■■□■■■■■■	777577737760771	3910	T1	T1	LAM	32622	Orphan	223326163323	Orphan	23363334253222-	Orphan	3326163323324224233	Orphan	0	F	ND	191	ND
BRA1620080C1754	2008	C1754	■■■■■■■■■■□■■■■■■■	777577777760601	Orphan	T1	T1	H	22423	9	224225163321	130	242631252624312	Orphan	1225163321225434132	Orphan	0	M	ND	112	ND
BRA1620080C0357	2008	C0357	■■■■■■■■■■■■■■■□□□	777740237560771	Orphan	T1	X1	LAM	21323	137	223313153322	1646	233532334731243	Orphan	3131533223231224334	Orphan	0	F/41	ND	191	ND
BRA1620090C0669	2009	C0669	■■■■■■■■■■□■■■□■■■	777357677760631	Orphan	T1	T1	LAM	21423	99	222223153224	Orphan	22252424522312	Orphan	2223153224224234132	Orphan	0	F	ND	157	ND
BRA1620090C0517	2009	C0517	■■■■■■■■■■■■■■■■■■	777777776160601	Orphan	T1	T1	LAM	21423	99	225313153323	42	253533334722243	152	3131533233232224334	Orphan	0	M/31	ND	9	ND
BRA1620090C0696	2009	C0696	■■■■■■■■■■■■■■■■■■	777777777760731	52	T2	ND	LAM	21423	99	224323153321	1647	243531234533312	Orphan	3232153321223332132	Orphan	0	M/45	18	229	ND
BRA1620090C0807	2009	C0807	■■■■■■■■■■■■■■■■■■	777777777760731	52	T2	ND	LAM	2142-	486	225323153223	693	253523242524212	Orphan	3232153223224422132	Orphan	0	M	ND	229	ND
BRA1620092C1210	2009	C1210	■■■■■□■■■■■■■■■■■■	757777777760731	153	T2	ND	T	22422	94	12--2514-321	Orphan	2--431243124312	Orphan	'--2514-3212144341-23	Orphan	2	F	121	9	ND
BRA1620080C6552A2	2008	C6552A2	■■■■■■■■■■■■■■■■■■	777777760160731	2322	T2	ND	LAM	32323	102	223226153321	128	232531242321312	601	1226153321224135132	Orphan	0	M	128	240	ND
BRA1620080C2018A2	2008	C2018A2	■■■■□□□□□□□□□□□□□□	740000003760731	Orphan	T2	T1	LAM	2242-	Orphan	333325163222	1654	333622443033120	Orphan	3325163222424314230	Orphan	0	F/50	401	ND	4163-328
BRA1620080C0982	2008	C0982	■■■■■■■■■■■■■□■■■■	777737777760471	157	T3	ND	H	22323	92	223125123324	436	231234343542223	Orphan	3125123234324224233	Orphan	0	M	150	97	ND
BRA1620080C1579	2008	C1579	■■□■■■■■■■■■□■■■■	677737777760771	1163	T3	ND	H	22423	9	224225153361	Orphan	2425312227-4113	Orphan	4225153361222414133	Orphan	0	NI	ND	197	ND
BRA1620080C1171	2008	C1171	■■■□□□□□■■■■□■■■■	701737777740471	3906	T3	T1	H	22422	94	224325143322	150	243432336222423	Orphan	3252143322323244233	Orphan	0	M	30	97	ND
BRA1620082C6697	2008	C6697	■■□■■■■■■■■■□■■■■	677735777760551	Orphan	T3	T1	H	323-3	Orphan	224226153321	25	242531243723312	Orphan	1226153321244334152	Orphan	2	M	33	21	ND
BRA1620080C0901	2008	C0901	■■■■■■■■■■■□■■□■■■	777557377760601	Orphan	T4	T1	LAM	22322	106	22412511302-	Orphan	24110-222223321	Orphan	412511302-2-2334231	Orphan	0	M/35	ND	ND	ND
BRA1620090C2144	2009	C2144	■■■■■■■■■■■■■□■■■■	777737557760771	1227	T5-Madrid2	ND	T	2-423	489	224126133321	1657	241331243624012	Orphan	1126133321214404132	Orphan	0	F/27	ND	55	ND
BRA1620090C2159	2009	C2159	■■■■■■■■■■■■■□■■■■	777737557760771	1227	T5-Madrid2	ND	T	2-423	489	224226133324	Orphan	242334243704224	Orphan	1226133324224424214	Orphan	0	M	ND	21	ND
BRA1620080C1528	2008	C1528	■■■■■■■■■■■■■■■■■■	777777477760771	451	T-H37Rv	ND	LAM	22423	9	223525153324	Orphan	235534245522223	Orphan	3525153224224224233	Orphan	0	F	ND	208	ND
BRA1620090C0536	2009	C0536	□□□□□□□□□□□□□□□□□□	000000007760771	4	Unknown	T3	S	21423	99	225313153321	174	253533133152243	595	3131533213232224333	230	0	M/60	ND	71	ND
BRA1620092C2126	2009	C2126	□□□□□□□□□□□□□□□□□□	000000007760771	4	Unknown	T3	S	24223	Orphan	12242611322	Orphan	224121244-43212	Orphan	2426113221224324132	Orphan	2	M	ND	ND	ND
BRA1620080C5817	2008	C5817	□□□□□□□□□□□□□□□□□□	000000007760771	4	Unknown	T3	S	32323	102	222126153324	Orphan	221534352522223	Orphan	2126153324325224233	Orphan	0	M	ND	71	ND
BRA1620080C8188	2008	C8188	□□□□□□□□□□□□□□□□□□	000000007760771	4	Unknown	T3	S	-1423	Orphan	222214352324	Orphan	222534223632320	Orphan	2214352324222234230	Orphan	0	F/84	ND	71	ND
BRA1620082C6741	2008	C6741	■■■■■■■■■■■■□■■■■■	777737770000000	56	Unknown	T1	H	32422	118	224226153321	25	242531243624312	602	1226153321214434152	Orphan	2	F/35	ND	97	ND
BRA1620090C0097	2009	C0097	■■■■■■■■■■■■■■■■■■	777777606000031	132	Unknown	EAI	LAM	11423	132	534221153334	Orphan	342534445324124	Orphan	1221153334424414234	Orphan	0	M/50	ND	198	ND
BRA1620080C0176	2008	C0176	■■■■■■■■■■■■■□□□	777740017760771	159	Unknown	ND	H	13422	485	3243221633-3	Orphan	243633335122247	Orphan	43221633-3323222437	Orphan	0	M/27	43	97	ND
BRA1620091C0057	2009	C0057	■■■■■■■■■■■■■■■■■■	777777774000071	1952	Unknown	H1	LAM	11423	132	224321163334	Orphan	243634243333210	Orphan	3211633342243241304	Orphan	1	M/54	ND	198	ND
BRA1620080C8152	2008	C8152	■■■■■■■■■□□□■■■■■■	776177400000131	2107	Unknown	LAM7	LAM	43433	299	225313353323	Orphan	253533333522243	593	3133533233232224334	Orphan	0	F/54	251	ND	ND
BRA1620080C8153	2008	C8153	■■■■■■■■■□□□■■■■■■	776177400000131	2107	Unknown	LAM7	LAM	52421	Orphan	225323352111	Orphan	253511336732343	Orphan	3232352111333232433	Orphan	0	F	251	ND	ND
BRA1620092C3237	2009	C3237	■■■■■■■■■□□■■■■■■■	776377770000771	2500	Unknown	H1	S	32323	102	224126152321	163	241531244734312	Orphan	1126152321214434152	Orphan	2	F	118	198	4643-111
BRA1620080C1572	2008	C1572	■■■■■■■■■■■■■□■■■■	777736770000000	2511	Unknown	EAI	LAM	22423	9	224225153321	127	242531243424312	597	1225153321224434122	233	0	M/26	645	97	ND
BRA1620090C1733	2009	C1733	■■■■■■■■■■■■■□■■■■	777736770000000	2511	Unknown	EAI	LAM	22423	9	225-25153321	Orphan	25-53124--2-112	Orphan	'5-25153321224-14122	Orphan	0	M/53	498	97	ND
BRA1620080C6582A2	2008	C6582A2	■■■■■■■■■■■■■■■■■■	777777207600331	2535	Unknown	LAM9	LAM	32323	102	223326153324	18	23353422363332-	Orphan	3326153324222334233	Orphan	0	M	ND	198	ND
BRA1620080C1663	2008	C1663	■■■■■■■■■■■■■■■■■■	777777607600331	2548	Unknown	LAM9	LAM	22423	9	224325153323	33	243533343112244	Orphan	3251533233242243434	Orphan	0	M	ND	191	ND
BRA1620080C1002	2008	C1002	■■■■■■■■■■■■■■■□■■	777757770000000	Orphan	Unknown	EAI	H	22323	92	-23325123324	Orphan	23323424---2222	Orphan	3325123324-422-2-2-	Orphan	0	M	174	97	455-140
BRA1620080C1074	2008	C1074	■■■■■■■■■■■■■■■■■■	777777577747770	Orphan	Unknown	F33	H	22422	94	225325133323	645	253333332424223	Orphan	3251333233232424233	Orphan	0	M	ND	177	ND
BRA1620080C0265	2008	C0265	■■■■■■■■■□□■■■■■■■	777177400000371	Orphan	Unknown	LAM8	LAM	1-223	Orphan	225313143321	Orphan	253431221524212	Orphan	3131433212224221324	Orphan	0	F/31	ND	9	ND
BRA1620090C0815	2009	C0815	■■■■■■■■■■□□■■□■■■	777157400000131	Orphan	Unknown	LAM8	LAM	22222	98	2-5313143323	Orphan	-53433333630240	Orphan	3131433233232022430	Orphan	0	F	251	ND	ND
BRA1620080C7195	2008	C7195	■■□■■■■■■■■■■■■■■■	677776777760601	18	X2	X2	H	32423	21	225226153323	Orphan	252533242124312	Orphan	3226153323214434152	Orphan	0	F	33	21	ND

New patterns marked in yellow
Discrepancies in lineages marked in blue
Changes in SIT numbers vs. former labels

Drug-R Code

0 not specified
1 sensible
2 INH resistent
3 MDR
4 XDR

Suplemental table S2: Detailed genotyping results of *fbpC* [103], RD174 and RD[Rio] on 182 *M. tuberculosis* strains isolated from pulmonary tuberculosis patients in Rio de Janeiro, Brazil.

Strain	Spoligotype Description	MIRU-VNTR 24 loci	Clade SITVIT2	SIT SITVIT2	designation	fbpC[103]	DR174	RD[Rio]
C2170A2	■ ■ □ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 2 2 6 1 7 3 3 2 1 2 2 4 1 3 5 1 3 2 2 4 2	LAM	1321	LAM	+	-	-
C2013	■ ■ □ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 3 3 2 1 2 2 2 3 3 4 2 1 1 4 4 2	LAM	1321	LAM	+	-	-
C1559	■ ■ □ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 2 2 6 1 5 3 2 2 1 2 2 4 1 3 5 1 3 2 2 4 2	LAM1	20	LAM	+	+	-
C1599	■ ■ □ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 3 2 2 6 1 5 3 3 2 1 2 2 4 1 3 5 1 3 2 2 4 2	LAM1	20	LAM	+	+	-
C2009	■ ■ □ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 2 2 6 1 5 3 3 2 1 2 2 4 1 3 5 1 3 2 2 3 2	LAM1	2539	LAM	+	+	+
C2349	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 6 1 5 3 3 2 1 2 2 4 3 3 4 1 3 2 4 5 2	LAM2	17	LAM	+	-	-
C2559	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 6 3 3 2 1 2 2 5 4 3 4 1 3 2 2 6 2	LAM2	17	LAM	+	+	+
C3554	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 6 3 3 2 1 2 2 4 4 3 4 1 3 2 2 6 2	LAM2	17	LAM	+	+	+
C7516	■ ■ □ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 3 3 2 6 1 5 3 4 2 1 2 2 4 3 3 4 1 3 2 2 5 3	LAM2	1711	LAM	+	-	-
C1772A2	■ ■ □ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 1 2 3 1 4 2 3 2 1 2 1 4 4 3 4 1 5 2 4 1 2	LAM2	1711	LAM	+	+	-
C2024	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ □ □ □ □ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 5 3 3 2 1 2 2 4 4 3 4 1 2 2 3 4 2	LAM2	3908	LAM	+	+	-
C2046	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ □ □ □ □ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 5 3 3 2 1 2 2 4 4 3 4 1 2 2 3 4 2	LAM2	3908	LAM	+	-	+
C2017	■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ ■ □ □ □ □ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 5 3 3 2 1 2 2 4 4 3 4 1 2 2 3 4 2	LAM2	Orphan	LAM	+	+	+
C1602	■ ■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 6 3 3 2 2 2 2 4 4 3 4 2 1 1 3 4 2	LAM3	33	LAM	+	-	-
C0879	■ ■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 3 3 2 2 2 2 2 3 3 4 2 1 1 4 4 2	LAM3	33	LAM	+	-	-
C1318	■ ■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 3 3 2 3 2 2 2 3 3 4 2 1 1 4 4 2	LAM3	33	LAM	+	-	-
C1358	■ ■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 3 3 2 3 2 2 2 3 3 4 2 1 1 4 4 2	LAM3	33	LAM	+	-	-
C1106	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ □ ■ ■ □ ■ ■	2 2 5 2 2 6 1 5 3 3 2 3 2 1 4 4 3 4 1 5 2 2 1 2	LAM4	60	LAM	+	-	-
C1020	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ □ ■ ■ □ ■ ■	2 2 5 3 1 3 1 4 3 3 2 1 2 2 2 4 2 2 1 3 2 1 5 2	LAM4	60	LAM	+	-	-
C1256	□ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 6 1 5 3 3 2 1 2 4 4 3 3 4 1 5 2 3 7 2	LAM4	828	LAM	+	-	-
C4991	□ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 6 1 5 3 3 2 1 2 1 4 4 3 4 1 2 3 2 7 2	LAM4	828	LAM	+	+	-
C1231A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ □ □ □ □ □ □	2 2 4 1 2 6 1 3 2 3 2 1 2 1 4 4 3 4 1 3 2 3 2	LAM4	1106	LAM	+	+	+
C3198	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ □ ■ ■ □ ■ ■	2 2 4 2 2 5 1 6 3 3 2 1 2 2 4 4 3 4 1 3 2 2 6 2	LAM4	Orphan	LAM	+	+	-
C6949	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 3 2 6 1 5 2 3 1 1 3 1 4 4 3 4 1 5 0 2 1 3	LAM4	Orphan	LAM	+	-	-
C2519	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 1 1 6 3 3 3 4 2 2 4 3 2 4 1 3 0 3 3 3	LAM5	273	LAM	+	-	-
C0470A2	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ □ □ □ □ □ □ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 2 6 1 5 3 3 2 1 2 1 4 4 3 4 1 3 2 4 6 2	LAM5	Orphan	LAM	+	-	-
c0817	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ □ □ □ □ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 5 1 5 3 3 2 1 2 2 4 4 3 4 1 2 2 3 4 2	LAM5	Orphan	LAM	+	+	+
C0963	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 2 3 2 6 2 5 1 2 2 1 2 2 4 3 3 4 1 3 2 2 4 2	LAM6	64	LAM	+	+	-
C1598	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 4 3 2 6 1 6 3 2 2 2 2 2 5 3 2 4 1 3 2 2 7 2	LAM6	64	LAM	+	-	-
C1473	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 2 3 2 6 1 5 3 2 2 4 2 2 4 4 3 4 1 3 2 2 7 2	LAM6	64	LAM	+	-	-
C6921	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 2 3 2 6 1 6 3 3 2 1 2 2 4 3 3 1 3 2 2 5 3	LAM6	64	LAM	+	-	-
c7823	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 4 2 6 1 5 3 3 2 3 2 2 2 3 3 4 2 1 1 4 2 2	LAM6	64	LAM	+	-	-
C2314	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 1 2 6 1 4 2 3 2 1 2 1 4 0 3 4 1 5 0 3 8 2	LAM6	64	LAM	+	+	+
C0438A3	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 4 3 2 6 1 4 3 2 2 4 2 2 4 3 3 4 1 3 4 1 6 2	LAM6	95	LAM	+	-	-
C6582	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 1 2 4 1 4 2 3 2 1 2 1 4 4 3 4 1 5 2 4 7 2	LAM6	1066	LAM	+	+	+
C2629	■ □ □ □ □ ■ □ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 4 2 2 6 1 4 3 2 2 4 2 2 6 4 3 4 1 3 2 2 2 2	LAM6	1906	LAM	+	-	-
C2537	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 3 2 6 1 4 3 2 2 2 2 2 4 5 5 4 1 3 3 2 6 2	LAM6	3504	LAM	+	+	-
C1377A2	■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 1 2 6 1 3 2 2 2 1 2 1 3 2 0 4 1 3 2 2 4 2	LAM6	3504	LAM	+	-	-
C2028	■ ■ ■ ■ ■ ■ ■ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 2 2 5 1 5 3 3 2 1 2 2 4 4 3 4 1 2 2 3 4 2	LAM8	3909	LAM	+	-	-
C4641	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 4 3 2 6 1 4 3 3 2 5 1 2 3 3 1 2 1 7 3	LAM9	42	LAM	-	-	-
C0669A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 6 1 5 3 3 2 1 2 1 4 4 3 4 1 4 2 3 1 2	LAM9	42	LAM	-	-	-
C0143	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 3 1 2 6 5 2 4 3 2 4 1 3 2 2 7 2	LAM9	42	LAM	+	-	-
C2768	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 2 2 1 4 3 3 2 2 2 4 3 3 4 1 3 2 1 1 2	LAM9	42	LAM	+	-	-
C7891	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 1 2 6 1 5 2 3 2 1 2 2 4 4 2 4 1 3 2 5 1 2	LAM9	42	LAM	+	+	-
C1559A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 4 2 2 1 2 1 4 3 1 4 1 3 2 1 2 2	LAM9	42	LAM	+	-	-
C1377	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 1 2 6 1 3 3 3 2 1 2 1 4 4 0 4 1 3 2 3 6 2	LAM9	42	LAM	+	-	-
C1938	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 2 5 1 4 3 2 1 2 1 4 4 3 4 1 2 3 1 2	LAM9	42	LAM	+	-	-
C7670A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 1 2 6 1 5 2 3 2 1 2 1 4 4 3 4 1 5 2 4 7 3	LAM9	42	LAM	+	+	-
C0438	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	3 2 4 1 2 4 1 5 3 2 4 2 2 2 4 3 2 4 1 3 2 4 3 2	LAM9	42	LAM	+	-	-
C0537A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	1 2 4 3 2 6 1 4 3 3 2 1 2 1 4 3 3 4 1 5 2 2 7 3	LAM9	42	LAM	+	+	+
C0996	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 3 2 2 6 1 4 3 3 2 1 2 1 4 4 3 5 1 5 2 4 5 2	LAM9	42	LAM	+	+	+
C2105A2	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 2 2 6 1 4 3 3 2 1 2 1 4 4 3 4 1 6 2 4 1	LAM9	42	LAM	+	+	+
C2105	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 2 2 2 6 1 4 3 3 2 1 2 1 4 4 3 4 1 6 2 4 2	LAM9	42	LAM	+	+	+
C0818	■ ■ ■ ■ ■ ■ ■ ■ ■ □ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 2 6 1 5 2 3 2 1 2 2 4 4 3 2 1 3 2 3 1 3	LAM9	81	LAM	-	-	-
C3165	■ □ □ □ □ ■ ■ ■ ■ ■ ■ ■ ■ □ □ □ □ ■ ■ ■ □ ■ ■	2 2 4 3 2 6 1 5 1 1 2 7 2 2 4 3 2 4 1 3 7 2 7 2	LAM9	1241	LAM	+	-	-

C2707	■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■□□□□□□■■■■■■■	2	2	2	3	2	5	1	5	3	1	2	1	1	2	3	3	2	4	1	3	2	2	7	2	LAM9	1241	LAM	+	-	-
C1118A2	■■■■■■■■■■□■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	2	2	4	2	2	6	1	4	2	3	2	1	2	1	4	3	3	4	1	5	2	3	6	2	LAM9	1535	LAM	+	+	-
C6684	■■■■■■■■■■■■■■■■■■■□□□□□■■■■■■■■□□□□■■■■■■■	2	2	2	3	2	6	1	5	2	2	1	1	2	2	4	4	3	4	1	3	2	2	7	2	LAM9	1800	LAM	+	-	-
C6689	■■■■■■■■■■■■■■■■■■■□□□□□■■■■■■■■□□□□■■■■■■■	2	2	4	3	2	6	1	5	3	2	1	3	2	2	4	4	3	6	1	3	2	2	7	2	LAM9	1800	LAM	+	+	+
C3259	■■■■■■■■■□□■■■■■■■■■□□□□■■■■■■■■□□□□■■■■■■■	2	2	7	2	2	5	1	6	3	3	2	1	2	2	4	4	3	4	1	3	2	2	6	2	LAM9	1960	LAM	+	-	-
C2528	■■■■■■□□■□□□■□□■■■■■□□□□■■■■■■■■□□□□■■□■■■■	2	2	3	1	2	5	1	5	3	3	2	1		1	4		2	4	1	4	2	4	5	2	LAM9	Orphan	LAM	-	-	-
C0855	■■■■■■■■■■■■■■■■■■■■□□□□□□■■□■■■□□□□■■■■■■■	1	2	4	2	2	6	1	4	3	2	2	4	2	2	6	3	0	4	1	3	2	2	2	2	T1	306	LAM	+	-	-
C0740	■■■■■■■■■■■■■■■■■■■□□□□□□■■■■■■■□□□□■■■■■■■	1	2	5	3	2	6	1	5	3	3	2	6	2	2	4	3	3	4	1	3	2	2	1	3	T1	1688	LAM	+	-	-
C0097	■■■■■■■■■■■■■■■■■■■■□□□□■■□□□□□□□□□□□□□□■■■	2	2	3	1	2	6	1	4	2	3	2	1	2	1	4	3	3	4	1	4	2	2	8	2	Unknown	132	LAM	+	+	+
C8152	■■■■■■■■□□□■■■■■■■■□□□□□□□□□□□□□□□□□□□■□■■■	2	2	4	3	2	6	1	3	3	3	2	3	2		4	4	2	4	2	1	1	3	3	2	Unknown	2107	LAM	+	-	-
C8153	■■■■■■■■□□□■■■■■■■■□□□□□□□□□□□□□□□□□□□■□■■■	2	2	4	3	2	6	1	3	3	3	2	3	2		4	4	2	4	2	1	1	3	3	2	Unknown	2107	LAM	+	-	-
C6582A2	■■■■■■■■■■■■■■■■■■□■□□□□■■■■■□□□□□□□□■■□■■■	2	2	2	1	2	4	1	4	2	3	2	1	2	1	4	4	3	4	1	5	2	4	7	2	Unknown	2535	LAM	+	+	+
C1663	■■■■■■■■■■■■■■■■■■■■□□□□■■■■■□□□□□□□□■■□■■■	2	2	4	3	2	6	1	4	3	2	2	4	2	2	4	3	3	4	1	3	2	1	6	2	Unknown	2548	LAM	+	-	-
C0265	■■■■■■■■■□□■■■■■■■■□□□□□□□□□□□□□□□□□□■■■■■■	2	2	4	2	2	6	1	3	3	3	2	4	2	2	4	4	2	4	2	1	4	3	7	0	Unknown	Orphan	LAM	+	-	-
C0815	■■■■■■■■■□□■■□■■■■■□□□□□□□□□□□□□□□□□□□■□■■■	2	2	4	3	2	6	1	3	3	3	2	3	2		4	4	2	4	2	1	1	3	3	2	Unknown	Orphan	LAM	+	-	-
C2020	■■□■■■■■■■■■□■■□□□□■□□□□■■■■■■■■□□□□■■■■■■■	2	2	4	2	2	5	1	5	3	3	2	1	2		4	4	3		1		2	3	4	2	LAM2	3908	LAM	+	-	+
C8014	■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■■□□□□■■■□■■■	1	2	4	3	2	6	1	4	2	2	2	0	2	2	4	3	3	4	1	3	2	1	6	2	LAM4	60	LAM	+	-	-
C6496	■■■■□■■■■■■■■■□□□□■■□□□□■■■■■■■■□□□□■■■□■■■	1	2	4	3	2	6	1	5	3	4	2	4	2	2	4	3	3	4	1	2	2	2	2	2	LAM4	Orphan	LAM	+	-	-
C1893	■■■■■■■■■■■■□□□□□□■■□□□□■■■■■■■■□□□□■■■■■■■	2	2	2	2	2	6	1	5	3	3	2	1	2	1	4	4	3	4	1	4	1	2	1	2	LAM5	1337	LAM	+	+	+
C7270	■■■■■■■■■■■■□■■■■■■■□□□□■■□■□■■■□□□□■■■■■■■	1	2	4	3	1	6	1	4	3	2	2	1	2	2	4	3	3	4	1	3	2	2	1	2	LAM6	3125	LAM	+	-	-
C0730	■■■□■■■■■■■■■■■■■■■■□□□□■■■■□■■■□□□□■■■□■■■	1	2	4	3	2	6	1	4	3	2	2	4	2	2	4	3	3	4	1	3	1	1	5	2	LAM6	3904	LAM	+	-	-
C0259	■■■■■■■■■■■■■■■■■■■■□□□□□□■■□■■■□□□□■■■■■■■	1	2	4	2	2	6	1	4	3	2	2	4	3	2	6	3	3	4	1	3	2	2	1	2	T1	306	LAM	+	-	-
C1333	■■■■■■■■■■■■■■■■■■■■□□□□□□■■□■■■□□□□■■■■■■■	1	2	2	3	2	6	1	5	3	5	2	4	2	2	6	3	3	4	1	3	2	2	5	2	T1	306	LAM	+	-	-
C6644	■■■□□■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	4	3	2	3	1	5	3	3	2	1	2	2	3	3	3	2	1	3	2	4	5	3	H1	431	LAM LIKE	+	-	-
c0317	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	2	2	3	2	2	4	4	2	2	4	3	3	5	7	2	H3	50	LAM LIKE	-	-	-
C2485	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	1		3	3	2	5	1	5	3	3	2	2	2	2	4	4	3	4	1		2	2	3	2	H3	50	LAM LIKE	+	-	-
C1966	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	4	2	2	6	1	5	3	3	2	1	2	1	4	4	3	4	1	5	2	3	6	2	H3	50	LAM LIKE	+	+	+
C7307	■■■■■■■■■■■■■■■■■■■■□■■■■■■■■■□■□□□□■■■■■■■	2	2	3	3	1	6	1	5	3	4	2	3	2	2	4	4	3	4	2	1	1	3	4	2	H3	268	LAM LIKE	+	-	-
C1914	■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□■□□□□■■■■■■■	2	2	4	3	1	6	3	5	4	2	2	7	2	2	4	4	5	4	4	3	3	3	2	2	H3	746	LAM LIKE	+	-	-
C2271	■■■■■■■■■■■■■■□□□□□□□■■■■■■■■□□■□□□□■■■■■■■	2	2	2	2	2	3	1	5	3	2	2	4	2	2	4	2	3	4	1	3	2	2	5	2	H3	2498	LAM LIKE	+	-	-
C6911	■■■■■■■■■■■■■■■■■□■■■□■■■■■■■■□■□□□□■■■■■■■	1	2	4	3	1	6		5	3	2	2	1	2	2	3	2	3	2	1	3	2	3	3	1	H3	Orphan	LAM LIKE	+	-	-
C7867	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	5	3	2	3	1	5	3	2	2	3	2	2	4	4	2	2	1	3	2	2	5	2	T1	53	LAM LIKE	-	-	-
C0964A2	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4		2	3	1	5	3	2	2	1	2	2	4	2	2	4	1	3	2		5		T1	53	LAM LIKE	-	-	-
C0641	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	1	2			2		1	2	3	3		4	2	1	3	4	2	4	2	1	3	3	5	2	T1	53	LAM LIKE	-	-	-
C8123	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	3	2	5	1	5	3	3	2	4	3	2	5	2	2	4	2	1	2	4	2	2	T1	53	LAM LIKE	-	-	-
C3537	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2			1		1	4	1	2	2	5	2	2	4	5	4	4	1	3	2	2		2	T1	53	LAM LIKE	+	-	-
C0755	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	1	2	4	3	1	6	1	3	3	2	2	2	1	3	4	3	3	2	1	3	2	2	3	2	T1	53	LAM LIKE	+	-	-
C6552	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4	3	1	6	1	5	3	2	2		1	2	2	4	3	4	1	3	2	2	1	2	T1	53	LAM LIKE	+	-	-
C6563	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4	2	2	6	1	5	3	3	2	1	1	1	4	3	3	4	1	4	2	4	1	3	T1	53	LAM LIKE	+	-	-
C4509A3	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	3	2	5	1	5	3	3	2	1	2	1	4	4	2	4	1	5		3	6	3	T1	53	LAM LIKE	+	-	-
C0874	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2'S	3	3	2	6	1	5	3	3	2	2	3	2	2	3	4	4	2	1	12	3	5	3	T1	53	LAM LIKE	+	-	-
C0627	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■□□□□■	2	2	4	3	2	5	1	5	3	3	2	3	3	2	4	1	4	4	1	3	3	2		3	T1	244	LAM LIKE	-	-	-
C7765	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■□□□■	2	2	2	3	2	5	1	5	3	3	2	1	2	2	3	2	2	4	1	3		3	2	3	T1	1926	LAM LIKE	-	-	-
C0810	■■■■■■■■■■■■■■■■■■■■□□■■■■■■■■■■□□□□■■■■■■■	2	2	5		2	3	2	2	3	1	2	1	2	2	3	4	2	4	1	1	4	2	2	4	T1	2070	LAM LIKE	+	-	-
C1551	■■■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■□□□□■□□■■■■	2	2	3	3	2	6	1	5	3	3	2	1	2	1	4	4	3	4	1		3		2	3	T1	2513	LAM LIKE	+	-	-
C1378	■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■■□□□□■■□□■■■	2	2	4	3	2	6	1	5	3		2	6	1	2	4	0	2	4	1	3	2	2	7	2	T1	3907	LAM LIKE	+	-	-
C7315	■■■■■■■■■■□■■■■■■■■■■□■■■■■■■■■■□□□□■■■■■■■	2	2	4	3	1	6	1	5	3	2	2	6	2	2	4	4	3	4	2	3	2	2	4	2	T1	3910	LAM LIKE	+	-	-
C0669	■■■■■■■■■□■■■□■■■■■■□■■■■■■■■■■■□□□□■■□□■■■	2	2	4		2	5	1	5	3	3	2	1	3	1	4	1	4	4	1		2	2	8	2	T1	Orphan	LAM LIKE	-	-	+
C0357	■■■■■■■■■■■■■□□□□□□■□□■■■■■■□■■■□□□□■■■■■■■	1	2	3	2	2	6	1	5	3	2	2	4	2	2	4	4	3	4	1	3	2	6	7	2	T1	Orphan	LAM LIKE	+	-	-
C0517	■■■■■■■■■■■■■■■■■■■■■■■■■■□□□■■■□□□□■■□□□□■	1	2	4	3	2	6	1	5	3	3	2	1	2	2	4	1	4	4	4	3	0	2	1	4	T1	Orphan	LAM LIKE	+	-	-
C0807	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	2	2	1	4	3	5	2	3	2	4	2	2	2	2	3	4	2	3	0	3	6	3	T2	52	LAM LIKE	+	-	-
C0696	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	3	3	2	6	1	5	3	3	2	4	2	2	2	3	3	4	2	3		3	6	3	T2	52	LAM LIKE	+	-	-
C1528	■■■■■■■■■■■■■■■■■■■□□■■■■■■■■■■■□□□□■■■■■■■	2	2	3	1	2	6	1	4	2	3	2	1	2	1	3	5	2	4	1	4	2	2	4	2	T-H37Rv	451	LAM LIKE	+	-	-
C1733	■■■■■■■■■■■■□■■■■□■■■■■■□□□□□□□□□□□□□□□□□□□	2	2	2	2	2	5	1	3	3	3	2	3	3	2	3	5	2	4	4	3	0	2	3	3	Unknown	2511	LAM like	-	-	-
C1572	■■■■■■■■■■■■□■■■■□■■■■■■□□□□□□□□□□□□□□□□□□□	2	2	5	3	2	5	1	3	3	3	2	3	3	2	3	4	2	4	2	3	3	2	4	2	Unknown	2511	LAM like	-	-	-
C2754	■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□□■□□□□■■■■■■■	2	2		3	2	4	1	5	3	3	2	2	3	2	3	2	2	2	4	3	3	2	1	3	H	742	Non LAM	-	-	-
C3275	■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□□■□□□□■■■■■■■	3	2	4	3	2	2	1	6	3	3		3	3	2	3	2	2	2	4	3	7	5	1	2	H	742	Non LAM	+	-	-

C2139	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	5	3	2	3	2	5	3	3	2	3	3	2	3	2	3	2	4	3	3	6	7	3	H1	47	Non LAM	-	-	-
C0462	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	3	3	1	3	1	5	3	3	2	2	3	2	3	1	2	2	4	3	3	4	7	3	H1	47	Non LAM	-	-	-
C7117	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	5	3	1	3	1	6	3	3	2	3	3	2	3	2	2	2	4	3	0	5	7	3	H1	47	Non LAM	-	-	-
C7717	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	5	3	2	3	1	6	3	3	2	3	3	2	3	2	2	2	4	3	3	5	7	2	H1	47	Non LAM	-	-	-
C6818	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	2	3	2	3	3	2	3	2	2	2	4	3	3	3	5	2	H1	47	Non LAM	+	-	-
C0991	■■■■■■■■■■■■■■■■■■■■■□■■■□□□□□□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	3	2	1	3	2	3	2	2	2	4	3	3	1	5	2	H1	Orphan	Non LAM	-	-	-
C7285	□□□□□□□□□□□□□□□□□□□□□□□□■□□□□□□■□□□□■■■■■■■	2	2	5	3	2	3	1	5	3	3	2	3	3	2	3	2	3	2	4	3	3	3	1	3	H2	2	Non LAM	-	-	-
C1842	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	2	3	1	5	3	3	2	1	3	2	3	2	2	2	1	3	1	2	4	2	H3	50	Non LAM	-	-	-
c0627A2	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	3	3	2	5	1	5	3	3		3		2	4	1	2	4		3	4	4	2	3	H3	50	Non LAM	-	-	-
c0821	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	2	3	3	5	2	1	1	1	3	3	3	2	3	2	4	3	3	6	7	3	H3	50	Non LAM	-	-	-
C0825	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	3	3	1	3	1	5	3	3	1	1	3	2	3	2	3	2	4	3	2	6	7	3	H3	50	Non LAM	-	-	-
C0859	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	3	1	1	3	2	3	2	3	2	4	3	3	6	7	3	H3	50	Non LAM	-	-	-
C0888	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	3	1	1	3	2	3	2	3	2	4	3	3	3	7	3	H3	50	Non LAM	-	-	-
C2142	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	1	3	1	2	3	3	2	2	3	2	3	2	2	2	4	3	3	2	7	2	H3	50	Non LAM	-	-	-
C2454	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	4	3	1	3	1	5	3	3	2	3	3	2	3	2	2	2	4	3	3	5	7	2	H3	50	Non LAM	-	-	-
C1433	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	2	2	3	3	2	3	2	2	2	4	3	3	5	7	2	H3	50	Non LAM	-	-	-
C1755	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□□□□■■■■■■■	2	2	4	3	2	4	1	6	3	2	2	1	3	3	4	3	3	4		3	2	3	1		H3	50	Non LAM	-	-	-
C2213A2	■■■■■■■■■■■■■■■■■■■■■■□■■■■■■■□■□□□□■■■■■■■	2	2	5	2	2	3	1	5	3	3	2	3	3	2	3	2	2	2	4	3		4	7	2	H3	741	Non LAM	-	-	-
C1926	■■■■■■■■■■■■■■■■■■■■■■■■■■■■□■□■□□□□■■■■■■■	2	1	6	3	2	5	1	5	3	3	2	3	3	2	3	2	4	4	4	3	3	2	3	3	H3	746	Non LAM	-	-	-
c1157	■■■■■■■■■■■■■■□□□□□□□■■■■■■■■□□■□□□□■■■■■■■	2	2	4	2	1	3	1	5	3	5	2	3	3	2	3	2	2	2	4	3	3	4	5	2	H3	2498	Non LAM	-	-	-
C0766	■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	3	2	3	3	2	3	2	2	2	4	3	3	4	7	2	H4/Ural-1	777	Non LAM	-	-	-
C1173	■■■■■■■■■■■□□□□□■■■□□□□□■□■■■■■■□□□□■□□■■■■	2	2	2	3	2	5	1	4	3	3	2	1	3	2	3	2	4	4	4	3	3	3	1	3	LAM5	136	Non LAM	-	-	-
C0125	■■■■■■■■■■■□□□□□■■■□□□□□■□■■■■■■□□□□■□□■■■■	2	2	5	3	1	3	1	5	3	3	2	3	3	2	3	1	3	2	4	3	2	2	3	3	LAM5	136	Non LAM	+	-	-
C2270	■■■■■■■□□□■■■■■■■■■■□□□□■■□■■■■■□□□□■■■■■■■	3	3	3	3	2	5	1	5	3	3	2	4	3	2	4	3	1	4	2	3	1	4	7	2	LAM8	3909	Non LAM	+	-	-
C2108	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	4	1	2	5	1	5	2	2	2	1	3	3	4	3	2	4	1	3	2	4	7	3	T	73	Non LAM	-	-	-
C1122	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	4	3	2	5	1	5	3	2	2	1	3	3	3	3	2	4	4	3	2	2	5	3	T	73	Non LAM	-	-	-
C8009	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	4	3	2	5	1	6	3	2	2	1	3	3	4	3		4	4	5	2	1	6	3	T	73	Non LAM	-	-	-
C1755A2	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	4	3	2	5	1	6	3	2	2	1	1	3	4	3	2	4	4	3	2	3	5	3	T	73	Non LAM	-	-	-
C6790	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	4	3	2	5	1	6	3	2	2	1	3	3	4	3	2	4	4	3	2	3	1	3	T	73	Non LAM	-	-	-
C1474	■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	3	3	3	2	5	1	4	3	3	2	3	4	2	4	4	1	4	2	3	1	3	8	?	T	102	Non LAM	-	-	-
C0665	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	5	3	2	5	1	5	3	3	2	4	3	2	3	2	2	4	1	3	2	4	6	2	T1	53	Non LAM	-	-	-
C7321	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4	3	2	5	1	1	3	2	2	3	3	3	3	2	3	4	4	3	2	3	7	3	T1	53	Non LAM	-	-	-
C2104	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	3	2	5	1	5	3	3	2	3	3	2	3	2	3	4	4	3	3	3	7	1	T1	53	Non LAM	-	-	-
C0395	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4	3	2	5	1	4	3	3	2	3	3	2	3	2	4	4	4	3	3		8	3	T1	53	Non LAM	-	-	-
C1120	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	5	4	1	3	1	5	3	3	2	3	3	2	3	1	2	2	4	3	2	7		3	T1	53	Non LAM	-	-	-
C1427	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	5	3	1	3	1	5	3	2	2	3	3	2	3	2	2	2	4	3	3	5	7	2	T1	53	Non LAM	-	-	-
C0459	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	3	2	5	1	5	3	3	2	2	3	2	4	3	8	4	2	3	0	4	5	2	T1	53	Non LAM	-	-	-
C6655	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2		3	4	5	2	6	1	3	2	1	3		4	3	2	4	2	3		3	7	4	T1	53	Non LAM	-	-	-
C0746	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	4	4	2	5	1	6	3	3	2	4	3	2	4	2	2	4	2	3	4	4	5	4	T1	53	Non LAM	-	-	-
C1130	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	5	2	5	1	5	3	3	2	4	2	2	4	2	2	4	2	3	3	5	5	2	T1	53	Non LAM	-	-	-
C1696	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	1	2	5	1	2	3	3	2	4	3	2	5	2	2	4	2	3	3	3	5	2	T1	53	Non LAM	-	-	-
C4509	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	2	1	2	5	1	5	3	2	2	3	3	2	4	2	1	4		3	4	2	2	2	T1	53	Non LAM	-	-	-
C7448	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	3	3	2	5	1	4	3	3	2	1	3	2	4	2	5	4	2	3	2	2	2	3	T1	53	Non LAM	+	-	-
C0837	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■□□■■■■	2	2	4	3	2	5	1	4	3	3	2	3	3	2	3	2	4	4	4	3	3	5	7	3	T1	65	Non LAM	-	-	-
C286SN	■■■■■■■■■■■■■■■■■■■■■□■■■■■■■■■■□□□□■■■■■■■		2	3	3	2	5	1	2	3	3	2	4	2		4	2	2		2		2				T1	86	Non LAM	-	-	-
C1839	■■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■□□□□■■■■■■■	2	1	4		2	5	1	4	3	3	2	3	4	2	3	4	1	4	2	3	3	2	4	3	T1	189	Non LAM	+	-	-
C7157	■■■■■■■■■■■■■■■■■■■■□■■■■■■■■■■■□□□□■■■■■■■	2	2	3	1	2	5	1	2	3	3	2	4	3	2	4	2	2	4	2	3	3	3	5	4	T1	291	Non LAM	-	-	-
C1418	■■■■■■■■■■■■■■■■■■■■□■■□■■■■■■■■□□□□■■■■■■■	3	2	3	3	2	5	1	5	3	3	2	1	3	2	4	3	2	4	2	3	1	4	4	2	T1	378	Non LAM	-	-	-
c0635	■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■□□□■■	5	2	5	3	2	2	1	5	3	3	2	4	3	2	3	2	2	4	4	3	3	4	6	3	T1	521	Non LAM	-	-	-
C3501A2	■■■■■■■■■■■■■■■■■■□□□□□□□□■■■□■■□□□□■■■■■■■	2	2	3	3	2	5	1	2	3	3	2	1	2	2	4	2	2	3	2	3	7	2	6	2	T1	3905	Non LAM	-	-	-
C2463	■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■■□□□□■■□□■■■	5	3	4	2	2	1	1	5	3	3	3	4	4	2	4	4	1	4	2	3	4	5	3	2	T1	3907	Non LAM	-	-	-
C2484	■■■■■■■■■■■■□□□□■■■■■■■■■■■■■■■■□□□□■■□□■■■	2	3	4	4	2	5	1	5	3	4	2	5	4	2	4	4	1	4	2	3	5	5	3	3	T1	3907	Non LAM	-	-	-
C1754	■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■■■□□□□■■□□□□■	2	2	2	3	2	5	1	5	3	2	2	3	3	2	4	2	4	4	4	3	2	3	4	3	T1	Orphan	Non LAM	-	-	-
C1210	■■■■□■■■■■■■■■■■■■■■■■■■■■■■■■■■□□□□■■■□■■■	2	2	3	3	2	5	1	4	3	3	2	3	2	2	4	3	2	4	2	3	2	5	7	2	T2	153	Non LAM	-	-	-
C0982	■■■■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■□□■■■■	2	2	4	3	2	5	1	4	3	3	2	2	3	2	3	2	4	4	2	3	3	6	2	2	T3	157	Non LAM	-	-	-
C1579	■■□■■■■■■■■■□■■■■■■■■■■■■■■■■■■■□□□□■■■■■■■	2	2	5	3	2	5	1	3	3	2	2	3	3	2	3	4	2	2	4	3	3	2	4	3	T3	1163	Non LAM	-	-	-
C1171	■■■□□□□□■■■■□■■■■■■■■■■■■■■■■■■□□□□□■□□■■■■	2	2	4	3	2	5	1	4	3	3	2	3	3	2	3	2	3	4	2	3	3	6	8	3	T3	3906	Non LAM	-	-	-

C6697	■■□■■■■■■■■■□■■■□■■■■■■■■■■■■■■■■■□□□□■□■■□■■	2 2 4 3 2 5 1 5 3 3 2 3 3 2 4 2 2 6 4 3 3 3 4	T3	Orphan	Non LAM	-	-	-
C2144	■■■■■■■■■■■■□■■■■■■□■■□■■■■■■■■■■□□□□■■■■■■■	2 2 2 1 2 6 1 5 3 3 2 4 3 2 5 2 2 4 2 3 3 2 5 2	T5-Madrid2	1227	Non LAM	-	-	-
C2159	■■■■■■■■■■■■□■■■■■■□■■□■■■■■■■■■■□□□□■■■■■■■	2 2 3 3 2 6 1 6 3 3 2 3 3 2 4 2 2 4 2 3 2 5 3	T5-Madrid2	1227	Non LAM	-	-	-
C2126	□□□□□□□□□□□□□□□□□□□□□□□□■■■■■■■■□□□□■■■■■■■	3 3 3 2 2 5 1 6 3 3 2 2 4 3 4 3 1 2 2 2 ? 3 ? 5	Unknown	4	Non LAM	-	-	-
C0536	□□□□□□□□□□□□□□□□□□□□□□□□■■■■■■■■□□□□■■■■■■■	3 3 3 3 2 5 1 6 3 2 2 2 4 2 4 3 1 4 2 3 0 3 0 3	Unknown	4	Non LAM	-	-	-
C8188	□□□□□□□□□□□□□□□□□□□□□□□□■■■■■■■■□□□□■■■■■■■	3 3 3 3 2 5 1 6 3 2 2 2 4 2 4 3 1 4 1 3 3 3 1 2	Unknown	4	Non LAM	+	-	-
C5817	□□□□□□□□□□□□□□□□□□□□□□□□■■■■■■■■□□□□■■■■■■■	3 3 3 2 2 5 1 6 3 2 2 2 4 2 4 3 1 4 2 3 0 3 7 2	Unknown	4	Non LAM	+	-	+
C6741	■■■■■■■■■■■■□■■■■■■■■■■■□□□□□□□□□□□□□□□□□□□	2 2 5 3 1 3 3 5 3 3 2 3 3 2 3 2 2 2 4 3 3 3 5 2	Unknown	56	Non LAM	-	-	-
C0057	■■■■■■■■■■■■■■■■■■■■■■■■■□□□□□□□□□□□■■■■■■■	2 2 2 1 2 4 1 4 2 3 2 1 2 1 4 4 3 4 1 5 2 4 4 2	Unknown	1952	Non LAM	+	+	-
C3237	■■■■■■■■□□■■■■■■■■■■■■■■□□□□□□□□□□□□■■■■■■■	2 2 3 3 2 5 1 4 3 3 2 5 2 1 4 2 1 4 2 2 3 3 2	Unknown	2500	Non LAM	+	-	-
C1074	■■■■■■■■■■■■■■■■■■■□■■■■■■■■■■■□□■■■■■■■■■□	2 2 4 0 1 3 1 5 3 3 2 1 2 2 3 2 2 4 1 3 2 2 4 2	Unknown	Orphan	Non LAM	-	-	-
C1002	■■■■■■■■■■■■■□■■■■■■■■■■□□□□□□□□□□□□□□□□□□□	2 2 5 3 1 3 1 5 3 3 2 1 3 2 3 2 2 2 4 3 3 1 5 2	Unknown	Orphan	Non LAM	+	-	-
C7195	■■□■■■■■■■■■■■■■■□■■■■■■■■■■■■■■■■□□□□■■□□□□■	2 2 4 3 2 5 1 5 3 3 2 3 3 2 4 2 2 2 4 3 4 3 1 1	X2	18	Non LAM	-	-	-