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# Phylogenomic analysis of the species of the *Mycobacterium tuberculosis* complex demonstrates that *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*, *Mycobacterium microti* and *Mycobacterium pinnipedii* are later heterotypic synonyms of *Mycobacterium tuberculosis*

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## Abstract

The species within the *Mycobacterium tuberculosis* Complex (MTBC) have undergone numerous taxonomic and nomenclatural changes, leaving the true structure of the MTBC in doubt. We used next-generation sequencing (NGS), digital DNA–DNA hybridization (dDDH), and average nucleotide identity (ANI) to investigate the relationship between these species. The type strains of *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*, *Mycobacterium microti* and *Mycobacterium pinnipedii* were sequenced via NGS. Pairwise dDDH and ANI comparisons between these, previously sequenced MTBC type strain genomes (including '*Mycobacterium canettii*', '*Mycobacterium mungi*' and '*Mycobacterium orygis*') and *M. tuberculosis* H37Rv<sup>T</sup> were performed. Further, all available genome sequences in GenBank for species in or putatively in the MTBC were compared to H37Rv<sup>T</sup>. Pairwise results indicated that all of the type strains of the species are extremely closely related to each other (dDDH: 91.2–99.2%, ANI: 99.21–99.92%), greatly exceeding the respective species delineation thresholds, thus indicating that they belong to the same species. Results from the GenBank genomes indicate that all the strains examined are within the circumscription of H37Rv<sup>T</sup> (dDDH: 83.5–100%). We, therefore, formally propose a union of the species of the MTBC as *M. tuberculosis*. *M. africanum*, *M. bovis*, *M. caprae*, *M. microti* and *M. pinnipedii* are reclassified as later heterotypic synonyms of *M. tuberculosis*. '*M. canettii*', '*M. mungi*', and '*M. orygis*' are classified as strains of the species *M. tuberculosis*. We further recommend use of the infrasubspecific term 'variant' ('var.') and infrasubspecific designations that generally retain the historical nomenclature associated with the groups or otherwise convey such characteristics, e.g. *M. tuberculosis* var. *bovis*.

## INTRODUCTION

The species within the *Mycobacterium tuberculosis* Complex (MTBC) have undergone numerous taxonomic and nomenclatural changes, leaving the true structure of the MTBC in doubt.

At the time of writing, the species within the MTBC with validly published names are *Mycobacterium tuberculosis* (also the type species of the genus), *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*,

*Mycobacterium microti* and *Mycobacterium pinnipedii*, which are all very closely related [1, 2]. Even these species have undergone some taxonomic and nomenclatural changes. For example, the species most recently known as *M. caprae* was first proposed as *M. tuberculosis* subsp. *caprae* [3], then was later renamed as *M. bovis* subsp. *caprae* [4], and finally elevated to the rank of species [5]. These nomenclatural changes have resulted in equally valid basonyms for the same organism. Numerous other 'species' with similar properties have been identified but have not been

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**Keywords:** *Mycobacterium tuberculosis* complex; *Mycobacterium tuberculosis*; digital DNA–DNA hybridization; average nucleotide identity; species reclassification.

**Abbreviations:** ANI, average nucleotide identity; dDDH, digital DNA–DNA hybridization; GGD, genome-to-genome distance; ICNP, International Code of Nomenclature of Prokaryotes; MTBC, *Mycobacterium tuberculosis* Complex; NGS, next-generation sequencing; RD, regions of difference.

The GenBank accession numbers for the whole genome draft sequences are as follows: *Mycobacterium tuberculosis* var. *africanum* ATCC® 25420<sup>TM</sup> - MWXF01.1, *Mycobacterium tuberculosis* var. *bovis* ATCC® 19210<sup>TM</sup> - MWXE01.1, *Mycobacterium tuberculosis* var. *caprae* ATCC® BAA-824<sup>TM</sup> - MWXD01.1, *Mycobacterium tuberculosis* var. *microti* ATCC® 19422<sup>TM</sup> - MWXC01.1, *Mycobacterium tuberculosis* var. *pinnipedii* ATCC® BAA-688<sup>TM</sup> - MWXB01.1.

Eight supplementary tables are available with the online version of this article.

officially accepted into bacterial nomenclature: ‘*Mycobacterium canettii*’ [6], ‘*Mycobacterium mungi*’ [7], and ‘*Mycobacterium orygis*’ [8].

*M. tuberculosis* was first identified in 1882 [9] and publications describing species of the MTBC date as far back as 1957 for *M. microti* [10], 1969 for *M. africanum* [11], and 1970 for *M. bovis* [12]. While these species were no doubt characterized according to the best available methods of their respective generations, technology has clearly advanced considerably and now allows much greater analytical resolution, enabling the identification and delineation of species with greater accuracy. In particular, next-generation sequencing (NGS) and powerful bioinformatics tools allow the classification of species based upon the entirety of their genomes, rather than just a few potentially misleading phenotypic observations or even a small number of genomic loci (16S, *hsp65*, *rpoB*, etc.).

MTBC phylogeny is typically based on regions of difference (RDs) and SNPs [13]. Molecular strain typing methods currently used for the identification of species of MTBC include IS6110-RFLP, spoligotyping, mycobacterial interspersed repetitive units-variable number tandem repeats (MIRU-VNTR), repetitive-sequence-based PCR (rep-PCR) and whole-genome sequencing [14]. By characterizing species/strains of the MTBC using molecular typing techniques, the species/strains have been categorized into various lineages [13, 15–17]. Although the development of such phylogenetic lineages may have important clinical and epidemiological applications, conflating what are likely host-adapted ecotypes [18, 19] with actual species may have a negative and confounding effect on mycobacterial systematics, particularly taxonomy and nomenclature.

It was suggested as early as 1982 that the typically accepted species within the MTBC may actually represent a single species [20]. Recent research comparing the genomes of species of the MTBC determined that whole-genome similarities support this idea. For example, the work of Garcia-Betancur, *et al.* compared *M. tuberculosis* H37Rv<sup>T</sup> to nine other MTBC genomes and found the strains to be closely enough related to be considered as a single species. While their results are sound, their work compared non-type strains of members of the MTBC. Thus, their conclusion that ‘mycobacterial scientists should agree an accord that designates MTBC as a single species in the official taxonomic rules of nomenclature’ [21] is overstated. The applicability of their findings is inherently limited by the scope of the strains examined: their results indicate that those nine strains fall within the circumscription of *M. tuberculosis*. However, to suggest that the species *M. africanum*, *M. bovis*, and ‘*M. canettii*’ – and, by extension, those specific epithets – should be consolidated into *M. tuberculosis* is premature. Such a conclusion could only be reached by comparing the type strains of the species considered. To our knowledge, such an examination of the type strains of the MTBC has not been reported prior to the current work.

The use of DNA–DNA hybridization (DDH) has been considered the gold standard for the genomic circumscription of bacterial species, with 70 % relatedness generally considered the threshold for species delineation [22]. However, the technique is labour-intensive, error-prone and poorly reproducible [23]. A recently developed *in silico* adaptation of DDH, digital DDH (dDDH), that allows the pairwise calculation of similarly-scaled genome-to-genome distances (GGDs) from whole-genome DNA sequences [23, 24] has been shown to be useful in species-level identification of bacterial strains, the identification of subspecies [25], and the development of detailed phylogenies for difficult taxa such as *Escherichia* [25] the *Bacillus cereus* Group [26] and *Aeromonas* [27].

The current work uses NGS and phylogenomic analysis based on dDDH and average nucleotide identity (ANI) to investigate the genomic coherence among type strains of the MTBC.

## METHODS

### Bacterial strains and DNA extraction

We obtained the following type strains of currently recognized species of the MTBC from ATCC: *M. africanum* ATCC 25420<sup>T</sup>, *M. bovis* ATCC 19210<sup>T</sup>, *M. caprae* ATCC BAA-824<sup>T</sup>, *M. microti* ATCC 19422<sup>T</sup> and *M. pinnipedii* ATCC BAA-688<sup>T</sup>. DNA was extracted in BSL-3 conditions using BMBL-recommended safety precautions [28]. After verifying that the DNA extracts contained no viable organisms ( $\geq 28$  days), subsequent work was performed at BSL-2 conditions. Previously sequenced genomes from species in or putatively in the MTBC include *M. tuberculosis* H37Rv<sup>T</sup>, ‘*M. canettii*’ CIPT 140010059, ‘*M. mungi*’ BM22813, and ‘*M. orygis*’ 112400015. Because they are not validly published, no officially accepted type strains of ‘*M. canettii*’, ‘*M. mungi*’, and ‘*M. orygis*’ exist. The aforementioned strains are the earliest identified strains or the earliest published strains for which whole-genome sequencing data was available. For the purposes of this work, these strains were treated as type strains. *M. pseudoshottsii* L15<sup>T</sup> was used as an intermediate phylogenetic outlier, i.e. within *Mycobacterium* but outside the MTBC. *Nocardia asteroides* NBRC 15531<sup>T</sup> was used as an extragenomic phylogenetic outlier. The list of accession numbers for the genomes used is shown in Table 1.

### Next-generation sequencing

DNA was prepared using a KAPA Biosystems Hyper Prep Kit and sequenced using Illumina HiSeq 2500 (2×100 bp). Sequencing reads were quality assessed with FastQC, data were filtered using Sickle, and *de novo* contigs were assembled using Velvet 1.2.10.

### Calculation of genomic distance

MTBC type strain genomes sequenced during this work were combined with the previously sequenced genomes to compose the main dataset (Table 1). We calculated GGDs using dDDH via the Genome-to-Genome Distance

**Table 1.** Genomes of type (or treated as type) strains of the MTBC

Current organism name	Strain	Genome	Genome source
<i>M. tuberculosis</i>	H37Rv <sup>T</sup>	NC_000962.3	GenBank
<i>M. africanum</i>	ATCC 25420 <sup>T</sup>	MWXF01.1	This Work
<i>M. bovis</i>	ATCC 19210 <sup>T</sup>	MWXE01.1	This Work
<i>M. caprae</i>	ATCC BAA-824 <sup>T</sup>	MWXD01.1	This Work
<i>M. microti</i>	ATCC 19422 <sup>T</sup>	MWXC01.1	This Work
<i>M. pinnipedii</i>	ATCC BAA-688 <sup>T</sup>	MWXB01.1	This Work
' <i>M. canettii</i> '	CIPT 140010059	NC_015848.1	GenBank
' <i>M. mungi</i> '	BM22813	LXTB01.1	GenBank
' <i>M. orygis</i> '	112400015	APKD01.1	GenBank
<i>M. pseudoshottsii</i>	L15 <sup>T</sup>	BCND01.1	GenBank
<i>Nocardia asteroides</i>	NBRC 15531 <sup>T</sup>	BAFO02.1	GenBank

Calculator (GGDC) v2.1 using the recommended Formula 2 [23, 24]. GGDs between *M. tuberculosis* H37Rv<sup>T</sup> and the genomes published in GenBank were calculated using the same methods. The complete list of genomes analyzed is available together with the results in Tables S1–S6 (available in the online version of this article). In order to corroborate independently the dDDH results, we calculated GGDs via ANI between the type strains using OrthoANI v0.93 [29]. The species delineation thresholds used were 80 % for dDDH [25] and 96 % for ANI [30].

### Phylogenomic analysis

For a better phylogenetic context, the whole genomes of the sequenced type strains were compared to each other and to the whole genome FASTAs from other species ( $n=12$ ). After the GGD results from this larger pairwise whole-genome comparison were transformed into PHYLIP format, a phylogeny was inferred with FastME 2.0 using the BioNJ tree-building algorithm [31]. The resulting phylogenomic Newick tree was visualized using iTOL 3.5.3 and rooted with *Nocardia asteroides* NBRC 15531<sup>T</sup>. The accession numbers for the genomes used in this analysis are provided in Fig. 1.

### In silico spoligotyping and clade analysis

We calculated spoligotypes *in silico* for the available genomes of the strains of MTBC (limited to 10 strains of the species *M. tuberculosis*) using SpoTyping v2.0 [32]. The resulting spoligotypes were analyzed using the SITVITWEB database [33].

## RESULTS

### Genomic distances between the genomes of type strains

GGDs obtained from the analysis of the MTBC genomes are shown in Table 2. For the nine MTBC type (or treated as type) strains, the results from both pairwise comparison methods demonstrated that each strain is closely related to each of the other strains (dDDH: 91.2–98.9 %, ANI: 99.21–99.92 %), whereas genomic distances to the outgroups were

far lower (dDDH: 18.8–22.3 %, ANI: 70.75–79.37 %). In all cases, the results from comparisons to *M. tuberculosis* H37Rv<sup>T</sup> greatly exceed the respective dDDH or ANI species delineation thresholds, demonstrating that these all belong to the same species [22, 24, 25, 30]. Both sets of results show that the most distantly related member of the MTBC is '*M. canettii*', which is consistent with evidence suggesting that it is the likely progenitor from which the remaining MTBC members diverged [15].

### Phylogenomic analysis

The phylogenetic tree inferred from the pairwise whole-genome GGDs is shown in Fig. 1. The results clearly show that the members of the MTBC form an extremely tight clade that is very distant from all of the other species, further supporting the hypothesis that they represent a single species.

### Genomes in GenBank

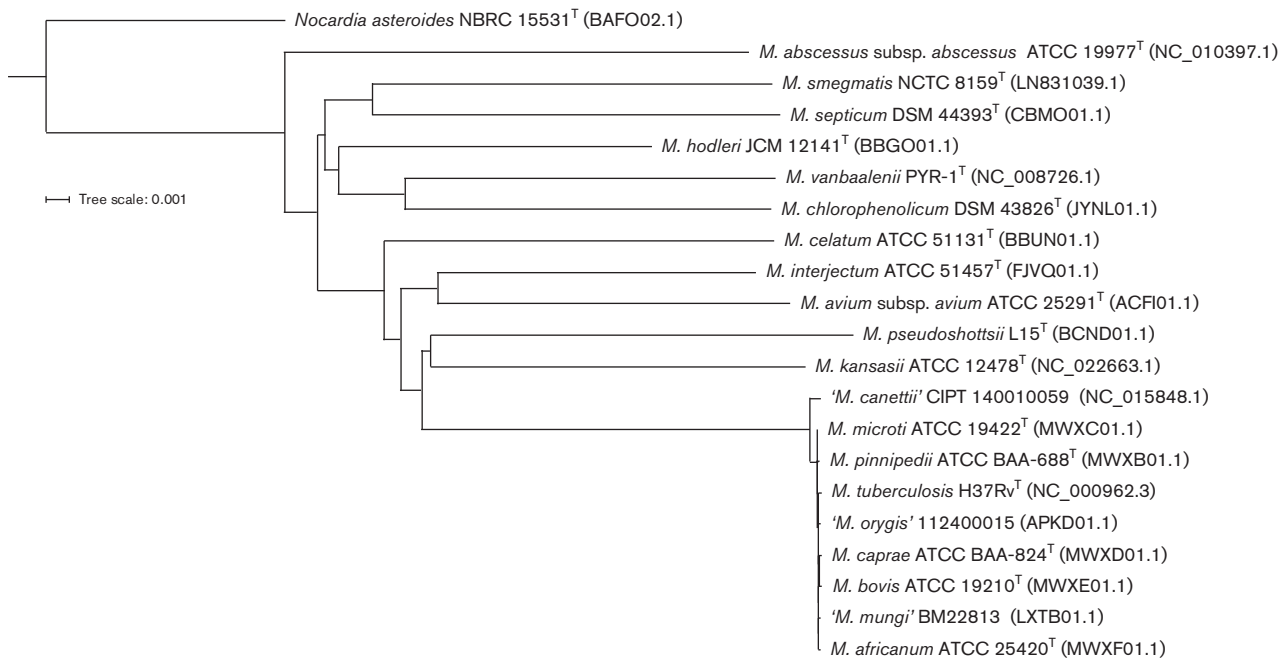
Table 3 summarizes the dDDH GGDs calculated from GenBank genomes, illustrating that all the strains showed a high similarity (83.5–100 %) to *M. tuberculosis* H37Rv<sup>T</sup>. (The complete data are shown in Tables S1–S6.) A single outlier represents a strain that has most likely been misclassified and is not included in Table 3; this strain was analyzed separately (see below).

### In silico spoligotyping and clade analysis

The spoligotypes calculated for the strains of the MTBC and their SITVITWEB clade classification are shown in Table S7.

### Outlier strain

When compared to *M. tuberculosis* H37Rv<sup>T</sup>, *M. tuberculosis* TTK-01-0051 (JLXW01.1) provided GGDs indicating it is not a strain of *M. tuberculosis* (dDDH: 22.2 %, ANI: 79.39 %). We, therefore, compared this genome to a reference genome set composed of all the available type strains of species/subspecies of the genus *Mycobacterium* ( $n=81$ ). These results demonstrate that strain TTK-01-0051 represents a strain of *M. colombiense* (dDDH: 81.3 %, ANI: 97.73 %; see Table S8).



**Fig. 1.** Phylogenomic tree showing the relationship between the whole genomes of type strains of species of MTBC and the type strains of various other species of the genus *Mycobacterium* with *Nocardia asteroides* as an outgroup. Bar, 0.001 substitutions per site.

## DISCUSSION

Pairwise GGDs for the nine type strains of the species in or putatively in the MTBC fall well within both the dDDH and ANI thresholds for delineation of bacterial species. It is also clear that (with the exception of a single misclassified strain) all genomes in GenBank deposited as *M. tuberculosis*, *M. africanum*, *M. bovis*, *M. caprae*, *M. microti* and '*M. canettii*' are genomically within the circumscription of *M. tuberculosis*.

Thus, our analysis of all the 'species' of MTBC demonstrates clearly that taxonomically they actually represent a single species. While this is not the first work to challenge the MTBC species concept [20, 21], our work provides sufficient justification in the form of comprehensive whole-genome comparisons showing extremely high similarities between the type strains of the members. NGS-based phylogenomic analysis supports reclassification of all the species of the MTBC as a single species. Were such a reclassification to occur, Rule 42 of the International Code of Nomenclature of Prokaryotes (ICNP) [34] requires that the oldest validly published specific epithet be retained, in this case *M. tuberculosis*.

In their review of past and future definitions of species of bacteria, Roselló-Móra and Amann have recommended a species concept that would allow 'unequivocal identification' into categories that circumscribe 'monophyletic, and genomically and phenotypically coherent populations of individuals that can be clearly discriminated from other

such entities by means of standardized parameters' [35]. Their analysis of genomes in the NCBI database shows some specific epithets applied to genomes are incorrect. Their results show a trimodal distribution: between the inter-species/intra-genus range and the intra-species range, the central mode represents a 'fuzzy zone' wherein organisms may represent either genomovars of the same species or different species based on the stability of differential phenotypes [35]. (Although their research used ANI as the measure of genomic similarity, a similar trend would be expected from data generated using dDDH.) Such phenotypes may be at odds with the genomic similarities observed. In this 'fuzzy zone', strains that should be considered a single 'genomosppecies' (e.g.  $\geq 80\%$  GGD) may still display stable differential phenotypes, essentially constituting different 'phenospecies'. One such example from the MTBC is '*M. canettii*', which phenotypically retains a smooth colony morphology unlike any of the other species of the MTBC, but is genomically well within the circumscription of *M. tuberculosis*.

There are defined characteristics (certain morphologies, SNPs, spoligotypes, etc.) that can differentiate the MTBC into various coherent lineages. At the same time, we observe that the overall genomic similarity within the MTBC is quite high – in most cases far higher than the 79–80% dDDH GGD threshold that would delineate bacterial subspecies [25]. Thus, considering the currently accepted species of the MTBC as genomovars or host-adapted ecotypes of a single species represents something of a compromise between the

**Table 2.** Genomic Distance Analysis of type strains of members of the MTBC

Pairwise genome-to-genome distances (GGDs) for the type strains of the species within the *Mycobacterium tuberculosis* complex ('MTBC') and two outgroups ('OUT'). Results from digital DNA–DNA hybridization (dDDH) are shown above the self-comparison diagonal, and average nucleotide identity (ANI) results are shown below the diagonal. Species delineation thresholds used were 80 % for dDDH and 96 % for ANI.

	Species/ Strain	dDDH ANI	MTBC1	MTBC2	MTBC3	MTBC4	MTBC5	MTBC6	MTBC7	MTBC8	MTBC9	OUT1	OUT2
MTBC1	<i>M. tuberculosis</i> H37Rv <sup>T</sup>		100	97.7	97.5	97.9	98.7	97.3	91.2	97.9	97.6	22.1	18.8
MTBC2	<i>M. africanum</i> ATCC® 25420 <sup>T</sup>		99.88	100	98	98.5	98.9	98.2	92.2	98.9	98.4	22.2	18.8
MTBC3	<i>M. bovis</i> ATCC® 19210 <sup>T</sup>		99.78	99.82	100	98.2	98.2	97.8	91.6	98.1	97.8	22.3	19
MTBC4	<i>M. caprae</i> ATCC® BAA-824 <sup>T</sup>		99.86	99.87	99.83	100	98.8	97.7	91.7	98.6	98.2	22.1	18.8
MTBC5	<i>M. microti</i> ATCC® 19422 <sup>T</sup>		99.89	99.89	99.79	99.91	100	99.2	93.3	99	98.9	22.3	18.9
MTBC6	<i>M. pinnipedii</i> ATCC® BAA-688 <sup>T</sup>		99.84	99.86	99.78	99.84	99.92	100	91.6	98.3	97.6	22.1	18.8
MTBC7	" <i>M. canettii</i> " CIPT 140010059		99.25	99.28	99.21	99.26	99.36	99.26	100	92.5	91.8	22.2	19
MTBC8	" <i>M. mungi</i> " BM22813		99.88	99.91	99.81	99.88	99.92	99.89	99.31	100	98.6	22.2	18.8
MTBC9	" <i>M. orygis</i> " 112400015		99.85	99.87	99.80	99.87	99.91	99.86	99.28	99.88	100	22.1	18.8
OUT1	<i>M. pseudoshottsii</i> L15 <sup>T</sup>		79.33	79.27	79.21	79.34	79.34	79.25	79.29	79.25	79.37	100	19.2
OUT2	<i>Nocardia asteroides</i> NBRC 15531 <sup>T</sup>		70.92	70.76	70.96	70.94	70.88	71.02	70.99	71.00	70.84	70.75	100

Color Key	
ANI	dDDH
Self-Comparison	Self-Comparison
96 – 100	80 – 100
< 96	< 80

classical/phenotypic species definitions and the reality of their global genomic similarities.

We, therefore, propose that the currently recognized species of the MTBC: *M. africanum* Castets et al. 1969 (Approved Lists 1980), *M. bovis* Karlson and Lessel 1970 (Approved Lists 1980), *M. caprae* (Aranaz et al. 1999) Aranaz et al. 2003, *M. microti* Reed 1957 (Approved Lists 1980), *M. pinnipedii* Cousins et al. 2003, and *M. tuberculosis* (Zopf 1883) Lehmann and Neumann 1896 (Approved Lists 1980) should be united as *M. tuberculosis*. Further, we propose that the taxa '*M. canettii*', '*M. mungi*', and '*M. orygis*', which have

not yet been validly published, be similarly considered as later heterotypic synonyms of *M. tuberculosis*.

However, due to the stability of certain differential phenotypic and/or genomic characteristics within lineages, we recommend that the MTBC lineages be considered infrasubspecific subdivisions (i.e. variants) of *M. tuberculosis*. Although infrasubspecific subdivisions are not governed by the ICNP, it is useful to discuss some of the associated issues. With respect to the appropriate infrasubspecific term, the nature of the differential characteristics between the variants should inform its selection. Some variants, e.g. '*M. canettii*' and the 'smooth tuberculosis bacilli' (STB), may be identified according to unique morphologies [17] and would best be considered morphovars. Others may be considered biovars according to differential biochemical or physiological properties. In many cases, lineages are separated primarily based upon RDs, SNPs, and/or spoligotyping; these would best be considered genomovars. As a single such term does not appear to be appropriate between all the lineages, we recommend the general infrasubspecific term 'variant' ('var.'). With respect to the appropriate infrasub-specific designations, we recommend the use of designations that generally retain the structure of the current lineages, the historical nomenclature associated with the groups, or otherwise convey such characteristics (Table 4). Use of the recommended variant designations, e.g. *M. tuberculosis* var. *bovis*, will be useful in minimizing the confusion that might otherwise arise. As infrasubspecific subdivisions are not governed by the ICNP, no formal proposals are made in the current work regarding their usage, but we believe that the

**Table 3.** dDDH Analysis of type strains of members of the MTBC

dDDH GGD values are between the GenBank genomes identified as respective species and the type strain of *M. tuberculosis* (H37Rv<sup>T</sup>).

GenBank organism identifier	n	dDDH GGD to <i>M. tuberculosis</i> , H37Rv <sup>T</sup> (%)		
		Minimum	Mean	Maximum
<i>M. africanum</i>	30	96.7	97.5	98.3
<i>M. bovis</i>	69	95.7	97.8	99.1
' <i>M. canettii</i> '	9	80.1	89.8	94.1
<i>M. caprae</i>	2	97.4	97.7	97.9
<i>M. microti</i>	1	97.1	97.1	97.1
<i>M. tuberculosis</i>	3631*	83.5	98.6	100.0

\*Excludes one single outlier which was examined separately (see text and Table S8).

**Table 4.** Recommended infrasubspecific designations and reference strains

Current Name	Recommended Name	Reference Strain
<i>M. tuberculosis</i>	<i>M. tuberculosis</i> var. <i>tuberculosis</i>	H37Rv <sup>T</sup> (ATCC 27294 <sup>T</sup> ) (type strain of species)
<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	ATCC 25420
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	ATCC 19210
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	–
<i>M. caprae</i>	<i>M. tuberculosis</i> var. <i>caprae</i>	ATCC BAA-824
<i>M. microti</i>	<i>M. tuberculosis</i> var. <i>microti</i>	ATCC 19422
<i>M. pinnipedii</i>	<i>M. tuberculosis</i> var. <i>pinnipedii</i>	ATCC BAA-688
' <i>M. canettii</i> '	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140010059
' <i>M. mungi</i> '	<i>M. tuberculosis</i> var. <i>mungi</i>	BM22813
' <i>M. orygis</i> '	<i>M. tuberculosis</i> var. <i>orygis</i>	112400015
' <i>M. suricattae</i> '*	<i>M. tuberculosis</i> var. <i>suricattae</i>	–
Dassie bacillus*	<i>M. tuberculosis</i> var. <i>dassie</i>	–
Chimpanzee bacillus*	<i>M. tuberculosis</i> var. <i>chimpanzee</i>	–

\*These organisms were not included in this study, but recommended infrasubspecific designations (based upon the typically used nomenclature for these organisms) are included for completeness. Note that the strains that were previously listed as the species type strains are now considered reference strains of the respective varieties.

use of infrasubspecific subdivisions as described above would be ideal.

From a nomenclatural standpoint, it can be expected that the proposal to reclassify the species of the MTBC as *M. tuberculosis* might initially seem unnecessarily disruptive; however, it is not without precedent. Among the key principles of the International Code of Nomenclature of Prokaryotes is that the governing nomenclatural system should aim to bring stability to the names used in prokaryotic microbiology [34]. Accordingly, systematic changes as potentially major as those proposed in the current work have been infrequent, though not unheard of. One of the most significant such changes – which bears important parallels to the current work – occurred to the genus *Salmonella*. After many decades of assigning species based upon serotyping, *Salmonella* nomenclature had become increasingly disorganized and disjointed. This led various groups to propose that a reorganization of the genus was necessary. After the five species listed in the Approved Lists [36] were found to form a single coherent genomospecies in DNA hybridization experiments, it was proposed that the various species be consolidated into a single species with a previously unused specific epithet, *enterica* [37]. In 1999, it was further proposed that the previously recognized type species *S. choleraesuis* had become ambiguous and was a source of confusion and should be rejected; instead it was proposed that *S. enterica* become the neotype species [38]. By 2005, the commonly used nomenclature had become independent of that recognized by official nomenclatural guidelines; however, both were still in use, causing even greater confusion. This led the Judicial Commission of the International Committee for Systematics of Prokaryotes to issue Opinion No. 80 which established *Salmonella enterica* as the type species of the genus *Salmonella* and conserved the specific

epithet *enterica* over all earlier epithets applied to the species [39]. One of the effects of these changes was to combine both pathogenic and nonpathogenic species of the genus *Salmonella* into a single subspecies, *S. enterica* subsp. *enterica*. The previously existing specific epithets however were retained as the designations for the various serovars, e.g. *Salmonella typhi*, the etiologic agent of typhoid fever, became *S. enterica* subsp. *enterica* serovar Typhi.

The taxonomic and nomenclatural changes made to the genus *Salmonella* are in some ways analogous to the changes to the *Mycobacterium tuberculosis* Complex proposed in the current work. Whole-genome sequencing has shown that the currently recognized species of the MTBC actually constitute a single genomospecies. Although this has been suspected taxonomically for several decades and proven for a variety of non-type strains, the current work has shown that the type strains of each of the species fall well within the circumscription of *M. tuberculosis*. So, the next prudent step is to align the relevant nomenclature with the taxonomy, in much the same way as with *Salmonella*.

As a final note, it is prudent to discuss the potential implications of changing the associated nomenclature to reflect better the genomic/taxonomic reality. According to Rule 56a of the ICNP, care should be exercised when considering 'a proposed change in the specific epithet of a nomenclature that is widely recognized to be contagious, virulent, or highly toxigenic' [34]. The species currently named *M. africanum*, *M. bovis*, *M. caprae*, *M. microti*, and *M. pinnipedii* are pathogenic, and changing these specific epithets could hypothetically result in a perilous name (*nomen periculosum*). However, the specific epithet *tuberculosis* is even more well-known and associated with human disease. If all the species within the MTBC were reclassified as *M. tuberculosis*, it seems unlikely that the application of

this epithet would be ‘likely to lead to accidents endangering health or life or both, or serious economic consequences’ [34]. Changing the name of these species to *M. tuberculosis* – an extremely recognizable name that immediately conveys a significant biohazard – would in fact make this much less likely.

Another important benefit to the proposed nomenclatural scheme is that biosafety regarding the handling of these organisms is likely to be enhanced. For example, current International Air Transport Association (IATA) regulations for shipping infectious substances classify only certain bacterial species as Category A ‘Infectious substances affecting humans’ (UN 2814). This list of items includes only *M. tuberculosis* and excludes the other currently recognized species of the MTBC, despite their ability to cause essentially the same disease in humans and/or animals. The explicit interpretation of these regulations suggests that other members of the MTBC can be shipped under the less stringent ‘Biological substance Category B’ (UN 3373) regulations, which is inappropriate. Although the regulations specify that the list is not exhaustive and professional judgement should be used to assign infectious substances to Category A [40], this introduces a potential ambiguity that could result in avoidable infections. Reclassification of the existing species of the MTBC as *M. tuberculosis* would result in all such bacteria explicitly being assigned to Category A (whether or not the variant was specified), resulting in safer shipment and handling of MTBC-associated materials.

Finally, as a preemption of potential criticism, it is recognized that there are numerous important facets to the classification of organisms, e.g. clinical, epidemiological, phylogeographic, legal/biosafety risk groups and prokaryotic systematics. The present study was in no way intended to downplay the coherence of the currently accepted lineages, differential phenotypic or genotypic characteristics of various strains, or the importance of maintaining the concept of such groups. Rather, the discussion within the current work is primarily restricted to prokaryotic systematics and the application of the most modern technological and bioinformatical methodologies to the taxonomic and nomenclatural classification of bacteria of the MTBC. Uniting the MTBC as *M. tuberculosis* with the currently recognized lineages as variants allows the reality of their overall genomic similarity to guide their systematics (as it should), whilst simultaneously retaining classification according to specific characteristics that are of clinical, epidemiological, phylogeographic, or host preference relevance.

### **Emended description of *Mycobacterium tuberculosis* (Zopf 1883) Lehmann and Neumann 1896 (Approved Lists 1980)**

*M. africanum*, *M. bovis*, *M. caprae*, *M. microti* and *M. pinnipedii* are reclassified as later heterotypic synonyms of *M. tuberculosis*. The strains described with the effectively but not validly published names ‘*M. canettii*’ [6], ‘*M. mungi*’

[7], and ‘*M. orygis*’ [8] are likewise reclassified as belonging to the species *M. tuberculosis*. The phylogenetic groups that correspond to the previously named species should be considered infrasubspecific subdivisions, i.e. variants. Thus, the characteristics described for the above previously named species are now included in the description of *M. tuberculosis*. Although infrasubspecific subdivisions are not governed by the rules of prokaryotic nomenclature, it is recommended that these infrasubspecific subdivisions retain the previous specific epithet as the infrasubspecific designations, e.g. *M. tuberculosis* var. *bovis* (see Table 4).

Morphological, biochemical, genetic (e.g. spoligotypes, RD patterns), and host-preference characteristics of the respective variants are as previously described for the previously named species. Thus, the current differential characteristics remain unchanged, but their specificity is now applied at a lower taxonomic level (variety) than previously accepted (species).

*M. tuberculosis* has a broad host range. The known variants likely represent host-adapted ecotypes and generally correlate with host range, though most are generally also capable of causing human disease, particularly among immunocompromised individuals. *M. tuberculosis* var. *tuberculosis*, *M. tuberculosis* var. *africanum*, and *M. tuberculosis* var. *canettii* are typically isolated from humans. *M. tuberculosis* var. *bovis* is typically isolated from cattle, other bovids, or humans. *M. tuberculosis* var. *caprae* is typically associated with goats, *M. tuberculosis* var. *microti* is typically isolated from voles and other rodents, *M. tuberculosis* var. *pinnipedii* is typically isolated from marine mammals, *M. tuberculosis* var. *mungi* is typically isolated from mongooses, and *M. tuberculosis* var. *orygis* is typically isolated from antelope species (oryxes). Although each of these variants causes the disease tuberculosis in the affected host species, variants may cause little or no disease outside of their adapted host.

As the 16S rRNA sequences of the various *M. tuberculosis* variants are essentially identical, molecular methods with greater resolution must be used to differentiate the variants from each other. Such methods include MLST, spoligotyping, MIRU-VNTR, and whole-genome sequencing-based comparisons such as dDDH or ANI.

The type strain of *Mycobacterium tuberculosis* is H37Rv<sup>T</sup> (=ATCC 27294<sup>T</sup>=NCTC 13114<sup>T</sup>). For the variants of *M. tuberculosis*, the genomes range in size from approximately 4.2–4.5 Mbp with a DNA G+C content of 65.0–65.6 mol%.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**Ethical statement**

No research was conducted on humans or animals.

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Table S1. dDDH GGDs Between Strains Deposited as *M. tuberculosis* in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 3,634)

Query genome	Reference genome	Formula 2	Model C.I.	Distance	Prob. DDH >= 70%	Notes
NC_000962.3	JLXV00000000.1	22.2	[19.9 - 24.6%]	0.1978	0	Outlier: IDs as <i>Mycobacterium colombiense</i> (See Table S8)
NC_000962.3	CPWZ00000000.1	25.5	[23.1 - 28%]	0.1707	0.01	Excluded: Genome is 12.7 Mbp, inconsistent with MTBC
NC_000962.3	CNDE00000000.1	74	[71 - 76.8%]	0.0307	84.55	Excluded: Assembly annotation (GCA_001397415.1) indicates poor sequence reliability
NC_000962.3	JKBG00000000.1	83.5	[80.7 - 86%]	0.0193	92.92	
NC_000962.3	CPD04886.1	91.4	[89.2 - 93.2%]	0.0106	96.24	
NC_000962.3	JKBH00000000.1	92.3	[90.2 - 93.9%]	0.0096	96.5	
NC_000962.3	CPD08971.1	93	[91 - 94.5%]	0.0089	96.69	
NC_000962.3	CPD08983.1	94.3	[92.6 - 95.6%]	0.0074	97.04	
NC_000962.3	CPD08969.1	94.4	[92.7 - 95.7%]	0.0073	97.05	
NC_000962.3	CPD05386.1	95	[93.4 - 96.3%]	0.0066	97.21	
NC_000962.3	CPD08979.1	95.1	[93.5 - 96.3%]	0.0066	97.22	
NC_000962.3	CNFT00000000.1	95.8	[94.3 - 96.9%]	0.0057	97.38	
NC_000962.3	LHK00000000.1	96.1	[94.8 - 97.2%]	0.0053	97.47	
NC_000962.3	JKVI00000000.1	96.5	[95.2 - 97.4%]	0.0049	97.54	
NC_000962.3	COWU00000000.1	96.6	[95.3 - 97.5%]	0.0048	97.56	
NC_000962.3	CPBF00000000.1	96.6	[95.4 - 97.5%]	0.0048	97.57	
NC_000962.3	CPAV00000000.1	96.7	[95.4 - 97.6%]	0.0047	97.58	
NC_000962.3	CPD08967.1	96.8	[95.7 - 97.7%]	0.0045	97.62	
NC_000962.3	CPDF00000000.1	96.8	[95.6 - 97.7%]	0.0046	97.6	
NC_000962.3	JKBN00000000.1	96.8	[95.6 - 97.7%]	0.0045	97.61	
NC_000962.3	CHWQ00000000.1	96.9	[95.7 - 97.8%]	0.0044	97.63	
NC_000962.3	CPD08965.1	96.9	[95.8 - 97.8%]	0.0044	97.64	
NC_000962.3	CCSJ00000000.1	97	[95.8 - 97.8%]	0.0044	97.64	
NC_000962.3	CPD07809.1	97	[95.9 - 97.9%]	0.0043	97.65	
NC_000962.3	CPZD00000000.1	97	[95.9 - 97.9%]	0.0043	97.66	
NC_000962.3	JKBM00000000.1	97.2	[96.1 - 98%]	0.0041	97.68	
NC_000962.3	JLLK00000000.1	97.2	[96.2 - 98%]	0.004	97.7	
NC_000962.3	JLHM00000000.1	97.2	[96.1 - 98%]	0.0041	97.69	
NC_000962.3	CHCJ00000000.1	97.3	[96.2 - 98.1%]	0.0039	97.71	
NC_000962.3	CHYA00000000.1	97.3	[96.2 - 98%]	0.004	97.7	
NC_000962.3	CHZC00000000.1	97.3	[96.2 - 98.1%]	0.0039	97.71	
NC_000962.3	COKZ00000000.1	97.3	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	CPBZ00000000.1	97.3	[96.2 - 98.1%]	0.004	97.71	
NC_000962.3	CPCE00000000.1	97.3	[96.2 - 98.1%]	0.004	97.71	
NC_000962.3	CPCT00000000.1	97.3	[96.2 - 98.1%]	0.004	97.71	
NC_000962.3	CPIG00000000.1	97.3	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	CSAE00000000.1	97.3	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	JKCY00000000.1	97.3	[96.2 - 98.1%]	0.0039	97.71	
NC_000962.3	JLKD00000000.1	97.3	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	JLWT00000000.1	97.3	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	CFJL00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	CNGL00000000.1	97.4	[96.3 - 98.1%]	0.0039	97.73	
NC_000962.3	CPD02885.1	97.4	[96.3 - 98.1%]	0.0039	97.72	
NC_000962.3	CPD10335.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	CPCC00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	CPFH00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	CPFY00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.73	
NC_000962.3	CPGY00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.73	
NC_000962.3	JLIW00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JLJK00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JLKS00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JLLT00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JXXH00000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	AZHK00000000.1	97.5	[96.4 - 98.2%]	0.0037	97.75	
NC_000962.3	CFIX00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CGBK00000000.1	97.5	[96.4 - 98.2%]	0.0038	97.75	
NC_000962.3	CHCP00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CIIV00000000.1	97.5	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	COGH00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	CPD02882.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CPD07803.1	97.5	[96.5 - 98.3%]	0.0036	97.76	
NC_000962.3	CPD10873.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	CPD12090.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CPBH00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CPCA00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CPDI00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	CPDN00000000.1	97.5	[96.4 - 98.2%]	0.0037	97.75	
NC_000962.3	CPDU00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	CPFD00000000.1	97.5	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JLXB00000000.1	97.5	[96.5 - 98.3%]	0.0036	97.76	
NC_000962.3	JLCU00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	JLID00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	JLIN00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	JLRO00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	JLKF00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	JLKG00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	JLKH00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	JLKO00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	JLKN00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	JLKO00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.76	
NC_000962.3	JLKT00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	JLKV00000000.1	97.5	[96.4 - 98.2%]	0.0037	97.75	
NC_000962.3	JLKY00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	JLJI00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	JLJO00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	JLLQ00000000.1	97.5	[96.5 - 98.2%]	0.0037	97.75	
NC_000962.3	JLMI00000000.1	97.5	[96.4 - 98.2%]	0.0038	97.74	
NC_000962.3	JNGE00000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76	
NC_000962.3	CCBK00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CFJJ00000000.1	97.6	[96.6 - 98.3%]	0.0035	97.78	
NC_000962.3	CFRV00000000.1	97.6	[96.6 - 98.3%]	0.0035	97.78	
NC_000962.3	CGEU00000000.1	97.6	[96.7 - 98.3%]	0.0035	97.78	
NC_000962.3	CHXT00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CHYJ00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CNID00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPD02871.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPD02884.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPD10336.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPAT00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPCB00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPCQ00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPDX00000000.1	97.6	[96.7 - 98.3%]	0.0035	97.78	
NC_000962.3	CPXA00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPFE00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPFZ00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPFI00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPGH00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78	
NC_000962.3	CPHU00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	
NC_000962.3	CPJU00000000.1	97.6	[96.5 - 98.3%]	0.0036	97.76	
NC_000962.3	CPIV00000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77	

Color Key	
dDDH Range	Interpretation†
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

†Meier-Kolthoff et al., 2014







































































NC_000962.3	ATSH00000000.1	99.8	[99.7 - 99.9%]	0.0004	98.24
NC_000962.3	ATSI00000000.1	99.8	[99.7 - 99.9%]	0.0005	98.24
NC_000962.3	ATSL00000000.1	99.8	[99.7 - 99.9%]	0.0004	98.25
NC_000962.3	ATSM00000000.1	99.8	[99.6 - 99.9%]	0.0005	98.24
NC_000962.3	ATSO00000000.1	99.8	[99.6 - 99.9%]	0.0005	98.23
NC_000962.3	ATST00000000.1	99.8	[99.6 - 99.9%]	0.0005	98.24
NC_000962.3	LJL00000000.1	99.8	[99.6 - 99.9%]	0.0005	98.23
NC_000962.3	LKMG00000000.1	99.8	[99.6 - 99.9%]	0.0005	98.24
NC_000962.3	ADHZ00000000.1	99.9	[99.7 - 99.9%]	0.0004	98.25
NC_000962.3	ADIB00000000.1	99.9	[99.8 - 100%]	0.0002	98.27
NC_000962.3	ATSA00000000.1	99.9	[99.7 - 99.9%]	0.0004	98.25
NC_000962.3	ATSP00000000.1	99.9	[99.8 - 100%]	0.0002	98.27
NC_000962.3	JKGC00000000.1	99.9	[99.9 - 100%]	0.0002	98.28
NC_000962.3	JLXH00000000.1	99.9	[99.9 - 100%]	0.0002	98.28
NC_000962.3	AJSF00000000.1	100	[99.9 - 100%]	0.0001	98.29
NC_000962.3	AORP00000000.1	100	[100 - 100%]	0	98.3
NC_000962.3	CP003248.2	100	[100 - 100%]	0	98.3
NC_000962.3	CP007027.1	100	[100 - 100%]	0	98.3
NC_000962.3	JREW00000000.1	100	[100 - 100%]	0.0001	98.29
NC_000962.3	JREX00000000.1	100	[99.9 - 100%]	0.0001	98.29
NC_000962.3	NC_000962.3	100	[100 - 100%]	0	98.3

Minimum*:	83.5
Mean*:	98.6
Maximum*:	100

\* Excludes the outlier examined separately (Table S8) and the two poor/inconsistent genomes.

**Table S2. dDDH GGDs Between Strains Deposited as *M. africanum* in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 30)**

		Formula 2			
Query genome	Reference genome	DDH	Model C.I.	Distance	Prob. DDH >= 70%
NC_000962.3	CP010334.1	96.7	[95.5 - 97.6%]	0.0046	97.6
NC_000962.3	JLAX000000000.1	97.1	[95.9 - 97.9%]	0.0042	97.67
NC_000962.3	NC_015758.1	97.2	[96 - 98%]	0.0041	97.68
NC_000962.3	JKZO000000000.1	97.3	[96.2 - 98.1%]	0.004	97.71
NC_000962.3	JLAT000000000.1	97.4	[96.3 - 98.1%]	0.0038	97.73
NC_000962.3	JKXO000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.73
NC_000962.3	JKXO000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.73
NC_000962.3	JLAM000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74
NC_000962.3	JLAF000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74
NC_000962.3	JKZX000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.74
NC_000962.3	JKYP000000000.1	97.4	[96.4 - 98.2%]	0.0038	97.73
NC_000962.3	JLAN000000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76
NC_000962.3	JLAY000000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76
NC_000962.3	JKZH000000000.1	97.5	[96.5 - 98.3%]	0.0036	97.76
NC_000962.3	JKYR000000000.1	97.5	[96.5 - 98.3%]	0.0037	97.76
NC_000962.3	JLAO000000000.1	97.6	[96.6 - 98.3%]	0.0035	97.78
NC_000962.3	JKXR000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77
NC_000962.3	JLAZ000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78
NC_000962.3	JLAC000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77
NC_000962.3	JLAB000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.78
NC_000962.3	JKZZ000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77
NC_000962.3	JKZQ000000000.1	97.6	[96.6 - 98.3%]	0.0035	97.78
NC_000962.3	JKZI000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77
NC_000962.3	JKYL000000000.1	97.6	[96.6 - 98.3%]	0.0036	97.77
NC_000962.3	CP014617.1	97.7	[96.8 - 98.4%]	0.0034	97.8
NC_000962.3	JKZU000000000.1	97.7	[96.7 - 98.3%]	0.0035	97.78
NC_000962.3	JKZW000000000.1	97.9	[97 - 98.5%]	0.0032	97.84
NC_000962.3	JLAE000000000.1	98.1	[97.3 - 98.7%]	0.0029	97.89
NC_000962.3	JKYH000000000.1	98.2	[97.3 - 98.7%]	0.0029	97.89
NC_000962.3	ACHQ000000000.1	98.3	[97.5 - 98.8%]	0.0027	97.92

Color Key	
dDDH Range	Interpretation†
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

†Meier-Kolthoff *et al.*, 2014

Minimum:	96.7
Mean:	97.5
Maximum:	98.3

**Table S3. dDDH GGDs Between Strains Deposited as *M. bovis* in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 69)**

Query genome	Reference genome	Formula 2	DDH	Model C.I.	Distance	Prob. DDH >= 70%
NC_000962.3	NZ_CP003494.1		95.7	[94.3 - 96.8%]	0.0058	97.37
NC_000962.3	NZ_CP009449.1		96.6	[95.3 - 97.5%]	0.0048	97.56
NC_000962.3	CP010331.1		96.6	[95.4 - 97.6%]	0.0047	97.57
NC_000962.3	NZ_CUWF00000000.1		96.9	[95.7 - 97.7%]	0.0045	97.62
NC_000962.3	NZ_CUWN00000000.1		97	[95.8 - 97.8%]	0.0043	97.64
NC_000962.3	NZ_CUWQ00000000.1		97	[95.9 - 97.9%]	0.0043	97.66
NC_000962.3	CP015773.2		97	[95.9 - 97.9%]	0.0043	97.66
NC_000962.3	NC_008769.1		97.1	[96 - 98%]	0.0041	97.68
NC_000962.3	NC_016804.1		97.1	[96 - 97.9%]	0.0042	97.67
NC_000962.3	NZ_AM412059.1		97.1	[96 - 97.9%]	0.0041	97.68
NC_000962.3	NZ_CP012095.1		97.1	[96 - 98%]	0.0041	97.68
NC_000962.3	NZ_CP013741.1		97.1	[96 - 97.9%]	0.0042	97.67
NC_000962.3	NC_002945.3		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NC_012207.1		97.2	[96.1 - 98%]	0.0041	97.68
NC_000962.3	NZ_CP008744.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NZ_CP009243.1		97.2	[96.1 - 98%]	0.0041	97.68
NC_000962.3	NC_012207.1		97.2	[96.1 - 98%]	0.0041	97.68
NC_000962.3	CP010332.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NZ_CUWH00000000.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NZ_CUWL00000000.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NZ_CUWO00000000.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NZ_CUWG00000000.1		97.2	[96.1 - 98%]	0.0041	97.69
NC_000962.3	NC_020245.2		97.3	[96.2 - 98.1%]	0.004	97.71
NC_000962.3	NZ_JNAF00000000.1		97.3	[96.2 - 98%]	0.004	97.7
NC_000962.3	NZ_CUWJ00000000.1		97.3	[96.2 - 98.1%]	0.0039	97.71
NC_000962.3	NZ_CUWM00000000.1		97.3	[96.2 - 98%]	0.004	97.7
NC_000962.3	NZ_CUWR00000000.1		97.3	[96.2 - 98.1%]	0.004	97.71
NC_000962.3	NZ_AEZE00000000.1		97.4	[96.3 - 98.1%]	0.0038	97.73
NC_000962.3	NZ_CUWP00000000.1		97.4	[96.3 - 98.1%]	0.0039	97.73
NC_000962.3	NZ_JXTK00000000.1		97.5	[96.5 - 98.2%]	0.0037	97.75
NC_000962.3	NZ_LFGY00000000.1		97.5	[96.5 - 98.2%]	0.0037	97.76
NC_000962.3	NZ_CUWE00000000.1		97.5	[96.5 - 98.2%]	0.0037	97.75
NC_000962.3	JLAP00000000.1		97.5	[96.5 - 98.2%]	0.0037	97.75
NC_000962.3	NZ_CUWI00000000.1		97.6	[96.6 - 98.3%]	0.0035	97.78
NC_000962.3	NZ_AEF00000000.1		97.7	[96.7 - 98.4%]	0.0035	97.79
NC_000962.3	NZ_AEZG00000000.1		97.7	[96.7 - 98.4%]	0.0035	97.8
NC_000962.3	NZ_CP011455.1		97.8	[96.8 - 98.4%]	0.0034	97.81
NC_000962.3	NZ_JQES00000000.1		97.9	[97.1 - 98.6%]	0.0031	97.85
NC_000962.3	MINA01.1		98	[97.1 - 98.6%]	0.0031	97.86
NC_000962.3	NZ_AWPL00000000.1		98	[97.1 - 98.6%]	0.0031	97.85
NC_000962.3	NZ_JQEQ00000000.1		98	[97.1 - 98.6%]	0.0031	97.85
NC_000962.3	NZ_CDHE00000000.1		98	[97.1 - 98.6%]	0.0031	97.86
NC_000962.3	NZ_JQEX00000000.1		98.1	[97.3 - 98.7%]	0.0029	97.88
NC_000962.3	NZ_CDFH00000000.1		98.1	[97.2 - 98.7%]	0.003	97.87
NC_000962.3	NZ_CDHH00000000.1		98.1	[97.2 - 98.7%]	0.003	97.87
NC_000962.3	NZ_JQEV00000000.1		98.2	[97.4 - 98.8%]	0.0028	97.9
NC_000962.3	NZ_JQEP00000000.1		98.2	[97.4 - 98.8%]	0.0028	97.9
NC_000962.3	NZ_JQEO00000000.1		98.2	[97.3 - 98.7%]	0.0029	97.89
NC_000962.3	NZ_LNOF00000000.1		98.2	[97.4 - 98.8%]	0.0028	97.9
NC_000962.3	NZ_CYST00000000.1		98.2	[97.4 - 98.8%]	0.0028	97.9
NC_000962.3	NZ_CUWK00000000.1		98.2	[97.4 - 98.8%]	0.0028	97.9
NC_000962.3	NZ_JQEW00000000.1		98.3	[97.5 - 98.8%]	0.0027	97.91
NC_000962.3	NZ_JQEU00000000.1		98.3	[97.5 - 98.8%]	0.0027	97.92
NC_000962.3	NZ_JPF00000000.1		98.4	[97.7 - 98.9%]	0.0025	97.94
NC_000962.3	NZ_JPFQ00000000.1		98.4	[97.6 - 98.9%]	0.0026	97.93
NC_000962.3	NZ_JQER00000000.1		98.4	[97.7 - 98.9%]	0.0025	97.95
NC_000962.3	NZ_JQEM00000000.1		98.4	[97.6 - 98.9%]	0.0026	97.93
NC_000962.3	JKAL00000000.1		98.5	[97.8 - 99%]	0.0024	97.97
NC_000962.3	NZ_AKYQ00000000.1		98.7	[98.1 - 99.1%]	0.0021	98
NC_000962.3	NZ_JPFR00000000.1		98.7	[98.1 - 99.1%]	0.0021	98
NC_000962.3	NZ_JQET00000000.1		98.7	[98.1 - 99.1%]	0.0021	98
NC_000962.3	NZ_JQEN00000000.1		98.7	[98.1 - 99.1%]	0.0021	98
NC_000962.3	JKAM00000000.1		98.7	[98.1 - 99.2%]	0.0021	98.01

Color Key	
dDDH Range	Interpretation†
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

†Meier-Kolthoff *et al.*, 2014

NC_000962.3	NZ_AKYT00000000.1	98.9	[98.3 - 99.2%]	0.0019	98.03
NC_000962.3	NZ_AKYV00000000.1	98.9	[98.4 - 99.3%]	0.0018	98.05
NC_000962.3	NZ_AVSW00000000.1	98.9	[98.3 - 99.3%]	0.0019	98.04
NC_000962.3	NZ_AKYR00000000.1	99	[98.5 - 99.3%]	0.0017	98.06
NC_000962.3	NZ_AKYU00000000.1	99	[98.4 - 99.3%]	0.0018	98.06
NC_000962.3	AKYS00000000.1	99.1	[98.5 - 99.4%]	0.0017	98.07

Minimum:	95.7
Mean:	97.8
Maximum:	99.1

**Table S4. dDDH GGDs Between Strains Deposited as "M. canettii" in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 9)**

Query genome	Reference genome	Formula 2 DDH	Model C.I.	Distance	Prob. DDH >= 70%
NC_000962.3	NC_019951.1	80.1	[77.2 - 82.7%]	0.0233	90.65
NC_000962.3	NC_019952.1	81.7	[78.8 - 84.2%]	0.0214	91.78
NC_000962.3	NC_019965.1	90.5	[88.2 - 92.3%]	0.0116	95.95
NC_000962.3	NC_015848.1	91.2	[89.1 - 93%]	0.0108	96.19
NC_000962.3	NZ_CAON000000000.1	92.5	[90.5 - 94.1%]	0.0094	96.57
NC_000962.3	NC_019950.1	92.7	[90.7 - 94.3%]	0.0092	96.61
NC_000962.3	NZ_CA0000000000.1	92.7	[90.7 - 94.3%]	0.0092	96.61
NC_000962.3	NZ_CAOM000000000.1	93	[91 - 94.5%]	0.0089	96.7
NC_000962.3	NZ_CAOL000000000.1	94.1	[92.3 - 95.5%]	0.0076	96.98

Color Key	
dDDH Range	Interpretation <sup>†</sup>
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

<sup>†</sup>Meier-Kolthoff *et al.*, 2014

Minimum:	80.1
Mean:	89.8
Maximum:	94.1

**Table S5. dDDH GGDs Between Strains Deposited as *M. caprae* in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 2)**

Query genome	Reference genome	Formula 2 DDH	Model C.I.	Distance	Prob. DDH >= 70%
NC_000962.3	NZ_CDHG00000000.1	97.9	[96.9 - 98.5%]	0.0033	97.83
NC_000962.3	CP016401.1	97.4	[96.4 - 98.2%]	0.0038	97.74

Minimum:	97.4
Mean:	97.7
Maximum:	97.9

Color Key	
dDDH Range	Interpretation <sup>†</sup>
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

<sup>†</sup>Meier-Kolthoff *et al.*, 2014



**Table S6. dDDH GGDs Between Strains Deposited as *M. microti* in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup> (n = 1)**

Query genome	Reference genome	Formula 2		Distance	Prob. DDH >= 70%
		DDH	Model C.I.		
NC_000962.3	CP010333.1	97.1	[95.9 - 97.9%]	0.0042	97.66

Color Key	
dDDH Range	Interpretation†
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

†Meier-Kolthoff *et al.*, 2014

**Table S7. Spoligotypes and SITVITWEB Clade Classifications for MTBC Genomes**

Type	(Type strains shown in <b>Bold</b> )					<i>In Silico</i> Spoligotyping with SpoTyping v2.0																SITVIT Results																												
	Current Species Name	Recommended Nomenclature (including infrasubspecific designation)	Strain Name	Genome Source	Genome Accession	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	Spoligotype43	Clade
<b>M. tuberculosis</b>	<b>M. tuberculosis</b>	<b>M. tuberculosis var. tuberculosis</b>	<b>H37Rv</b>	<b>GenBank</b>	<b>NC_000962.3</b>	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77777477760771	H37Rv	451		
	M. tuberculosis	M. tuberculosis var. tuberculosis	Haarlem	GenBank	NC_022350.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77577777760751	--	Orphan		
	M. tuberculosis	M. tuberculosis var. tuberculosis	H37Ra	GenBank	NC_009525.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	75777477760771	--	Orphan		
	M. tuberculosis	M. tuberculosis var. tuberculosis	CTRI-2	GenBank	NC_017524.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77777607760771	LAM9	42		
	M. tuberculosis	M. tuberculosis var. tuberculosis	KZN 1435	GenBank	NC_012943.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77777607760731	LAM4	60		
	M. tuberculosis	M. tuberculosis var. tuberculosis	KZN 4207	GenBank	NC_016768.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77777607760731	LAM4	60		
	M. tuberculosis	M. tuberculosis var. tuberculosis	KZN 605	GenBank	NC_018078.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77777607760731	LAM4	60		
	M. tuberculosis	M. tuberculosis var. tuberculosis	F11	GenBank	NC_009565.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77617607760771	LAM3	33		
	M. tuberculosis	M. tuberculosis var. tuberculosis	CDC1551	GenBank	NC_002755.2	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	70007675760771	X3	549		
	M. tuberculosis	M. tuberculosis var. tuberculosis	CDC5180	GenBank	NC_017522.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	00000000003771	Beijing	1		
	M. tuberculosis	M. tuberculosis var. tuberculosis	W-148	GenBank	NZ_CP012090.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	00000000003771	Beijing	1		
<b>M. africanum</b>	M. africanum	M. tuberculosis var. africanum	MAL010129	GenBank	JKZW01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77177777777671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010112	GenBank	JLAE01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77277777777671	--	Orphan		
	<b>M. africanum</b>	M. tuberculosis var. africanum	<b>ATCC 25420<sup>T</sup></b>	<b>This Work</b>	<b>MWXF01</b>	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	25	GenBank	CP010334.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	MAL020148	GenBank	JKX001	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	MAL010102	GenBank	JLAM01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	MAL010081	GenBank	JLAT01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	GM041182	GenBank	NC_015758.1	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777671	AFRI_1	181		
	M. africanum	M. tuberculosis var. africanum	MAL020136	GenBank	JKZH01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	37077777777671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010137	GenBank	JKZQ01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077577777671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010100	GenBank	JLAN01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777777271	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010070	GenBank	JLAZ01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077577777671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL020135	GenBank	JKZI01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	77077777765671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL020107	GenBank	JKZ001	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707774777671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010131	GenBank	JKZU01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707777766671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	MAL010120	GenBank	JLAB01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707777765671	--	Orphan		
	M. africanum	M. tuberculosis var. africanum	K85	GenBank	ACHQ01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707770777671	AFRI_1	326		
	M. africanum	M. tuberculosis var. africanum	MAL020185	GenBank	JKYL01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707770777671	AFRI_1	326		
	M. africanum	M. tuberculosis var. africanum	MAL020176	GenBank	JKYP01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707770777671	AFRI_1	326		
	M. africanum	M. tuberculosis var. africanum	MAL020173	GenBank	JKYR01	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	7707770777671	AFRI_1	326		

	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010128	GenBank	JKZX01		7707770777671	AFRI_1	326
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010111	GenBank	JLAF01		7707770777671	AFRI_1	326
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010099	GenBank	JLAA01		7707770777671	AFRI_1	326
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010084	GenBank	JKXR01		7707770777401	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	K85	GenBank	JLCY01		77077707774671	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	UT307	GenBank	NZ_CP014617.1		77077707774671	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL020193	GenBank	JKYH01		77077703437671	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010123	GenBank	JKZZ01		17077060777671	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010118	GenBank	JLAC01		77400000777071	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010071	GenBank	JLAY01		77075600006671	--	Orphan
	<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>	MAL010074	GenBank	JLAX01		500000007176051	--	Orphan
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	D-10-02315	GenBank	MINA01		67677377777600	BOV_1	482
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	SP38	GenBank	NZ_CP015773.2		67677367777600	BOV_1	481
	<b><i>M. bovis</i><sup>T</sup></b>	<i>M. tuberculosis</i> var. <i>bovis</i>	<b>ATCC 19210<sup>T</sup></b>	<b>This Work</b>	<b>MWXE01</b>		65657337777600	BOV_1	670
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	30	GenBank	CP010332.1		656573377377600	--	Orphan
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	04-303	GenBank	AVSW01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	AN5	GenBank	AWPL01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	MB4	GenBank	CDHE01		676773674177600	BOV_1	696
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	09-1191	GenBank	JPPF01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	05-567	GenBank	JPFQ01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	05-566	GenBank	JPFR01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	534	GenBank	JQEM01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	09-1193	GenBank	JQEN01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	09-1192	GenBank	JQEO01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	45-08B	GenBank	JQEP01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	18-08C	GenBank	JQEQ01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	32-08	GenBank	JQER01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	49-09	GenBank	JQES01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	08-08BF2	GenBank	JQET01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	50	GenBank	JQEU01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	0822-11	GenBank	JQEW01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	61-09	GenBank	JQEX01		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	W-1171	GenBank	JXTK01		66407377777600	BOV_2	683
<b>MTBC</b>	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	AF2122/97	GenBank	NC_002945.3		66407377777600	BOV_2	683
	<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	1595	GenBank	NZ_CP012095.1		66407377777600	BOV_2	683

<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	ATCC BAA-935	GenBank	NZ_CP009449.1		66407377773600	BOV_2	1855
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	MAL010093	GenBank	JLAP01		77077702005671	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	35	GenBank	JQEV01		664073776077600	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	MbURU-001	GenBank	LFGY01		640013777777600	BOV_3	479
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	B-3222	GenBank	LNOF01		664003777774600	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	MB3	GenBank	CDHH01		600001774000600	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	MB1	GenBank	CDHF01		674000000001600	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	B2 7505	GenBank	JKAL01		700000000006000	--	Orphan
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>	Bz 31150	GenBank	JKAM01		000000176000200	--	Orphan
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Frapplier	GenBank	AKYQ01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Phipps	GenBank	AKYT01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	26	GenBank	CP010331.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Birkhaug	GenBank	CUWE01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Connaught	GenBank	CUWF01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Danish	GenBank	CUWH01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Glaxo	GenBank	CUWJ01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Moreau	GenBank	CUWK01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Phipps	GenBank	CUWN01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Russia	GenBank	CUWO01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	BCG	GenBank	JNAF01		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	BCG Pasteur 1173P2	GenBank	NC_008769.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Tokyo 172	GenBank	NC_012207.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Mexico	GenBank	NC_016804.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Korea 1168P	GenBank	NC_020245.2		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Moreau RDJ	GenBank	NZ_AM412059.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	63839	GenBank	NZ_CP003494.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	3281	GenBank	NZ_CP008744.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Russia 368	GenBank	NZ_CP009243.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	BCG-1 (Russia)	GenBank	NZ_CP013741.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Tokyo 172 substr. TRCS	GenBank	NZ_CP014566.1		676773777777600	BOV_1	482
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	--	GenBank	CYST01		676773757777600	BOV_1	1181
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	ATCC 35733	GenBank	AEZF01		67677377373200	--	Orphan
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Sweden	GenBank	AKYV01		606773777777600	BOV_1	986
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	China	GenBank	AEZE01		67677375767000	--	Orphan
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Glaxo	GenBank	AKYR01		67677377760600	--	Orphan

	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	BCG-1	GenBank	NZ_CP011455.1		61677377731600	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	China	GenBank	CUWG01		67677377740200	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Frappier	GenBank	CUWI01		67677377740200	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Pasteur	GenBank	CUWL01		676773774037600	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Prague	GenBank	CUWM01		67677377740200	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Sweden	GenBank	CUWP01		67677377740200	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Tice	GenBank	CUWQ01		67677377740200	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	ATCC 35740	GenBank	AEZG01		650263777325600	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Prague	GenBank	AKYU01		422461376737600	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Japan	GenBank	CUWR01		676773760000000	--	Orphan
	<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG	Moreau	GenBank	AKYS01		000000000000000	ATYPIC	2669
	<i>M. caprae</i> <sup>T</sup>	<i>M. tuberculosis</i> var. <i>caprae</i>	ATCC BAA-824 <sup>T</sup>	This Work	MWXD01		200003777207600	BOV_4-CAPRAE	646
	<i>M. microti</i> <sup>T</sup>	<i>M. tuberculosis</i> var. <i>microti</i>	ATCC 19422 <sup>T</sup>	This Work	MWXC01		074000030000600	PINI1	641
	<i>M. pinnipedii</i> <sup>T</sup>	<i>M. tuberculosis</i> var. <i>pinnipedii</i>	ATCC BAA-688 <sup>T</sup>	This Work	MWXB01		074000033747400	--	Orphan
	"M. mungi"	<i>M. tuberculosis</i> var. <i>mungi</i>	BM22813	GenBank	LXTB01.1		672600000000671	--	Orphan
	"M. orygis"	<i>M. tuberculosis</i> var. <i>orygis</i>	112400015	GenBank	APKD01.1		600740007774671	--	Orphan
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140010059	GenBank	NC_015848.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070010	GenBank	NC_019951.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140060008	GenBank	NC_019950.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070017	GenBank	NC_019952.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070008	GenBank	NC_019965.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070002	GenBank	CAOL01.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070005	GenBank	CAOM01.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070013	GenBank	CAON01.1		000000000000000	ATYPIC	2669
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	CIPT 140070007	GenBank	CAOO01.1		000000040000000	--	Orphan
	"M. canettii"	<i>M. tuberculosis</i> var. <i>canettii</i>	NLA000701671	This Work			000000000000000	ATYPIC	2669
Non-MTBC Species (Negative Controls)	<i>M. pseudoshottsii</i> <sup>T</sup>	--	L15 <sup>T</sup>	GenBank	BCND01.1				
	<i>M. smegmatis</i> <sup>T</sup>	--	NCTC 8159 <sup>T</sup>	GenBank	LN831039.1				
	<i>Nocardia asteroides</i> <sup>T</sup>	--	NBRC 15531 <sup>T</sup>	GenBank	BAFO02.1				

**Table S8. dDDH GGDs Between *M. tuberculosis* TKK-01-0051 in GenBank vs. *M. tuberculosis* H37Rv<sup>T</sup>**

Query genome	Reference genome	Formula 2	DDH	Model C.I.	Distance	Prob. DDH >= 70%
JLXW01.1_Mtuberculosis	TS1_NC_010397.1_M_abscessus_abscessus		21.2	[18.9 - 23.6%]	0.2072	0
JLXW01.1_Mtuberculosis	TS2_AHAS01.1_M_abscessus_bollettii		19.5	[17.3 - 21.9%]	0.2252	0
JLXW01.1_Mtuberculosis	TS3_GH1_Mafricanum		22.1	[19.9 - 24.6%]	0.1982	0
JLXW01.1_Mtuberculosis	TS6_GH1_Malgericum		20.5	[18.3 - 23%]	0.2138	0
JLXW01.1_Mtuberculosis	TS11_JALN02.1_M_aromaticivorans		20.1	[17.9 - 22.6%]	0.2182	0
JLXW01.1_Mtuberculosis	TS14_CCB01.1_M_asiaticum		21.8	[19.5 - 24.2%]	0.2014	0
JLXW01.1_Mtuberculosis	TS15_GH1_Maubagnense		19.4	[17.2 - 21.8%]	0.2263	0
JLXW01.1_Mtuberculosis	TS16_CVQQ01.1_M_aurum		19.7	[17.5 - 22.1%]	0.223	0
JLXW01.1_Mtuberculosis	TS17_CCAW01.1_M_austroafricanum		21.2	[18.9 - 23.6%]	0.2074	0
JLXW01.1_Mtuberculosis	TS18_ACFI01.1_M_avium_avium		30.3	[27.9 - 32.8%]	0.1406	0.12
JLXW01.1_Mtuberculosis	TS19_AGAR01.1_M_avium_paratuberculosis		30.7	[28.3 - 33.2%]	0.1385	0.14
JLXW01.1_Mtuberculosis	TS20_AYOC01.1_M_avium_silvaticum		30.7	[28.4 - 33.3%]	0.1381	0.14
JLXW01.1_Mtuberculosis	TS23_CSTD01.1_M_bohemicum		24.8	[22.5 - 27.3%]	0.1755	0.01
JLXW01.1_Mtuberculosis	TS27_GH1_Mbovis		22.1	[19.9 - 24.6%]	0.198	0
JLXW01.1_Mtuberculosis	TS30_FJNX01.1_M_brumae		20.4	[18.2 - 22.9%]	0.2149	0
JLXW01.1_Mtuberculosis	TS31_BCSY01.1_M_canariense		20.5	[18.3 - 22.9%]	0.2145	0
JLXW01.1_Mtuberculosis	TS32_GH1_Mcaprae		22	[19.8 - 24.5%]	0.1992	0
JLXW01.1_Mtuberculosis	TS33_BBUN01.1_M_celatum		22.5	[20.2 - 24.9%]	0.195	0
JLXW01.1_Mtuberculosis	TS35_CP010946.1_M_chelonae		19.4	[17.3 - 21.8%]	0.226	0
JLXW01.1_Mtuberculosis	TS36_MRBR01.1_M_chimaera		31.5	[29.1 - 34.1%]	0.134	0.2
JLXW01.1_Mtuberculosis	TS38_JYNL01.1_M_chlorophenicum		20.8	[18.5 - 23.2%]	0.2116	0
JLXW01.1_Mtuberculosis	TS39_NC_018027.1_M_chubuense		20	[17.8 - 22.4%]	0.2194	0
JLXW01.1_Mtuberculosis	TS40_AFWW02.1_M_colombiense		81.3	[78.4 - 83.9%]	0.0219	91.52
JLXW01.1_Mtuberculosis	TS41_CTEF01.1_M_conceptionense		21.1	[18.8 - 23.5%]	0.2085	0
JLXW01.1_Mtuberculosis	TS45_CCB01.1_M_cosmeticum		20.9	[18.7 - 23.3%]	0.21	0
JLXW01.1_Mtuberculosis	TS46_BBHD01.1_M_crocinum		22	[19.7 - 24.4%]	0.1996	0
JLXW01.1_Mtuberculosis	TS50_GH1_Melephantis		22.7	[20.4 - 25.2%]	0.1929	0
JLXW01.1_Mtuberculosis	TS54_CCAAY01.1_M_farcinogenes		20	[17.8 - 22.4%]	0.2193	0
JLXW01.1_Mtuberculosis	TS57_BBFT01.1_M_fluoranthenivorans		21.6	[19.3 - 24%]	0.2033	0
JLXW01.1_Mtuberculosis	TS58_CP014258.1_M_fortuitum_fortuitum		19.8	[17.6 - 22.2%]	0.2217	0
JLXW01.1_Mtuberculosis	TS59_BCSZ01.1_M_fortuitum_acetamidolyticum		20.7	[18.5 - 23.1%]	0.212	0
JLXW01.1_Mtuberculosis	TS62_GH1_Mfrederiksbergense		20.9	[18.6 - 23.3%]	0.2103	0
JLXW01.1_Mtuberculosis	TS64_AZYN01.1_M_gastri		22.5	[20.2 - 24.9%]	0.1948	0
JLXW01.1_Mtuberculosis	TS65_JAGZ01.1_M_genavense		23.7	[21.4 - 26.2%]	0.1843	0
JLXW01.1_Mtuberculosis	TS69_CP011883.2_M_haemophilum		22.4	[20.1 - 24.8%]	0.1957	0
JLXW01.1_Mtuberculosis	TS70_ARBU01.1_M_hassiacum		20.2	[18 - 22.6%]	0.2173	0
JLXW01.1_Mtuberculosis	TS76_BBG001.1_M_hodleri		23.3	[21 - 25.7%]	0.188	0
JLXW01.1_Mtuberculosis	TS78_FJVO01.1_M_houstonense		20.7	[18.5 - 23.2%]	0.2118	0
JLXW01.1_Mtuberculosis	TS79_CP011530.1_M_immunogenum		21.6	[19.3 - 24%]	0.2036	0
JLXW01.1_Mtuberculosis	TS81_FJVQ01.1_M_interjectum		25.8	[23.5 - 28.3%]	0.1681	0.01
JLXW01.1_Mtuberculosis	TS83_NC_016946.1_M_intracellulare		31.6	[29.2 - 34.1%]	0.1336	0.2
JLXW01.1_Mtuberculosis	TS85_NC_022663.1_M_kansasii		22.2	[20 - 24.7%]	0.1973	0
JLXW01.1_Mtuberculosis	TS89_GH1_Mkumamotoense		20.7	[18.4 - 23.1%]	0.2126	0
JLXW01.1_Mtuberculosis	TS90_BBKA01.1_M_kyrorinense		22	[19.7 - 24.4%]	0.1998	0
JLXW01.1_Mtuberculosis	TS99_CCBF01.1_M_mageritense		20.2	[18 - 22.6%]	0.2175	0
JLXW01.1_Mtuberculosis	TS106_GH1_Mminnesotense		20.1	[17.9 - 22.6%]	0.2182	0
JLXW01.1_Mtuberculosis	TS113_JMDW01.1_M_neoaurum		19.8	[17.6 - 22.2%]	0.2217	0
JLXW01.1_Mtuberculosis	TS114_CWKH01.1_M_neworleansense		20.1	[17.9 - 22.5%]	0.2183	0
JLXW01.1_Mtuberculosis	TS117_BCTA01.1_M_novocastrense		21	[18.8 - 23.5%]	0.2087	0
JLXW01.1_Mtuberculosis	TS118_JYNU01.1_M_obuense		20	[17.7 - 22.4%]	0.2203	0
JLXW01.1_Mtuberculosis	TS119_BBHE01.1_M_pallens		22.1	[19.9 - 24.6%]	0.1981	0
JLXW01.1_Mtuberculosis	TS125_GH1_Mparakoreense		21	[18.8 - 23.5%]	0.2088	0
JLXW01.1_Mtuberculosis	TS126_ADNV01.1_M_parascrofulaceum		26.8	[24.4 - 29.2%]	0.1617	0.02
JLXW01.1_Mtuberculosis	TS127_GH1_Mparaseoulense		26.1	[23.8 - 28.6%]	0.1659	0.02
JLXW01.1_Mtuberculosis	TS130_ANBO01.1_M_phlei		20.8	[18.6 - 23.2%]	0.2109	0
JLXW01.1_Mtuberculosis	TS131_GH1_Mphocaicum		20	[17.8 - 22.4%]	0.2196	0
JLXW01.1_Mtuberculosis	TS132_GH1_Mpinnipedii		22.1	[19.8 - 24.5%]	0.1986	0
JLXW01.1_Mtuberculosis	TS135_BCND01.1_M_pseudoshottsii		21.4	[19.2 - 23.8%]	0.2051	0
JLXW01.1_Mtuberculosis	TS138_BBHB01.1_M_pyrenivorans		23.5	[21.2 - 26%]	0.1859	0
JLXW01.1_Mtuberculosis	TS141_JROA01.1_M_rufum		20.9	[18.7 - 23.3%]	0.2103	0
JLXW01.1_Mtuberculosis	TS142_BBHF01.1_M_rutilum		24.1	[21.8 - 26.6%]	0.1811	0.01
JLXW01.1_Mtuberculosis	TS148_GH1_Msenuense		20.6	[18.4 - 23%]	0.2132	0
JLXW01.1_Mtuberculosis	TS149_GH1_Mseoulense		26.3	[24 - 28.8%]	0.1648	0.02
JLXW01.1_Mtuberculosis	TS150_CBMO01.1_M_septicum		20	[17.8 - 22.4%]	0.2197	0
JLXW01.1_Mtuberculosis	TS151_JTJW01.1_M_setense		20	[17.8 - 22.4%]	0.2201	0
JLXW01.1_Mtuberculosis	TS154_GH1_Mshinjukuense		23	[20.7 - 25.4%]	0.1907	0
JLXW01.1_Mtuberculosis	TS156_CBMJ02.1_M_simiae		23.2	[20.9 - 25.7%]	0.1886	0
JLXW01.1_Mtuberculosis	TS157_LN831039.1_M_smeigmatis		20.2	[17.9 - 22.6%]	0.218	0
JLXW01.1_Mtuberculosis	TS159_GH1_Mstomatepieae		23.6	[21.3 - 26.1%]	0.185	0
JLXW01.1_Mtuberculosis	TS162_BCTB01.1_M_thermoresistibile		20.1	[17.9 - 22.5%]	0.2185	0
JLXW01.1_Mtuberculosis	TS165_CCAU01.1_M_triplex		24.7	[22.4 - 27.2%]	0.1765	0.01
JLXW01.1_Mtuberculosis	TS167_NC_000962.3_M_tuberculosis		22.2	[19.9 - 24.6%]	0.1978	0
JLXW01.1_Mtuberculosis	TS170_BCRS01.1_M_vaccae		20.4	[18.2 - 22.9%]	0.2149	0
JLXW01.1_Mtuberculosis	TS171_NC_008726.1_M_vanbaalenii		20.3	[18.1 - 22.7%]	0.2166	0

Color Key	
dDDH Range	Interpretation†
80.0 - 100	Same species and subspecies
70.0 - 79.9	Same species, different subspecies
50.0 - 69.9	Different species
30.0 - 49.9	
0.0 - 29.9	

†Meier-Kolthoff et al., 2014

JLXW01.1_Mtuberculosis	TS172_CCBG01.1_M_vulneris	20.1	[17.9 - 22.5%]	0.2185	0
JLXW01.1_Mtuberculosis	TS175_NC_021715.1_M_yongonense	31.3	[28.9 - 33.8%]	0.1354	0.18
JLXW01.1_Mtuberculosis	TS176_CP010271.1_M_saopaulense	19.4	[17.2 - 21.7%]	0.2272	0
JLXW01.1_Mtuberculosis	TS177-450_CP003324.1_M_paraintracellulare	31.4	[29 - 33.9%]	0.1347	0.19
JLXW01.1_Mtuberculosis	TS178-3_NZ_AP014547.1_M_abscessus_masilliense	19.3	[17.1 - 21.7%]	0.2277	0
JLXW01.1_Mtuberculosis	TS179_CVTB01.1_M_malmesburyense	20.2	[18 - 22.6%]	0.2173	0
JLXW01.1_Mtuberculosis	TSOUT1_BAFO02.1_Nocardia_asteroides	19.3	[17.1 - 21.7%]	0.2277	0