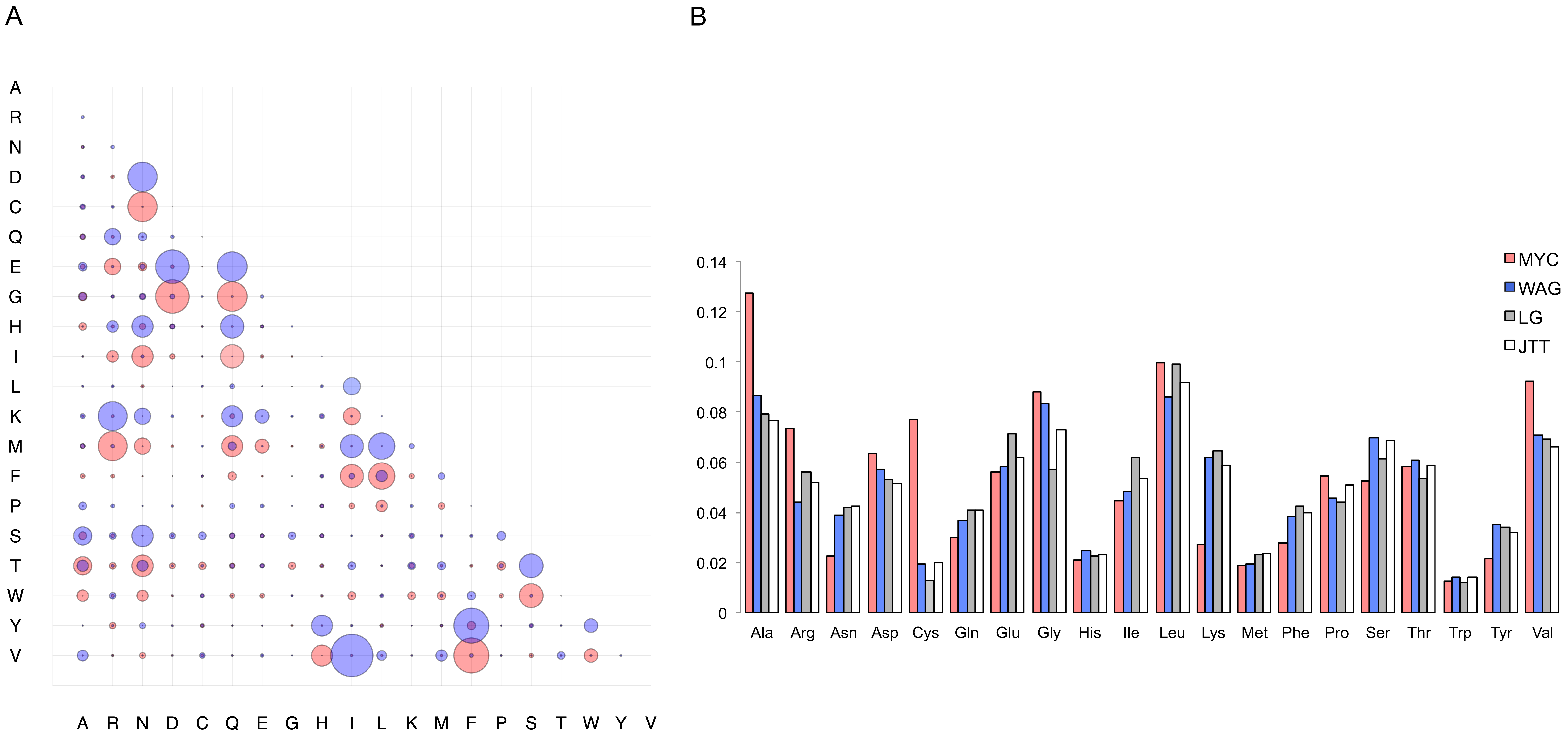
Supplementary Figures

FIG. S1. Properties of the GTR MYC amino acid substitution matrix and comparison with other matrices. (A) Bubble plot of the exchangeability rate differences between the WAG (blue) and MYC (red) amino acid substitution matrices. (B) Comparison of amino acid frequencies among different matrices (MYC, WAG, LG, JTT).

FIG. S2. Topological differences between the phylogenetic reconstruction based on the concatenate of protein alignments and the commonly used bacterial marker locus 16S rRNA. Incongruences between trees are represented as red circles connected with red lines. Putative 16S rRNA duplications are indicated with red arrows (concatenated alignment-based tree) connected with red circles (16S rRNA tree). Values on the nodes indicate the bootstrap support values expressed as the proportion (%) of bootstrap trees that agree with a given bipartition on the best ML tree.

FIG. S3. Number of genes estimated in ancestral nodes under the four branch-specific gain and death rate models. GD-GR-ML, global rates model; GD-PR-ML, pathogenic lineage-specific rates model; GD-PRl-ML, GD-PR-ML model + *M. leprae* specific rates model; GD-FR-ML, free rates model.

Fig. S1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D
C
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V
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B
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
MYC
WAG
LG
JTT
Ala
Arg
Asn
Asp
Cys
Gln
Glu
Gly
His
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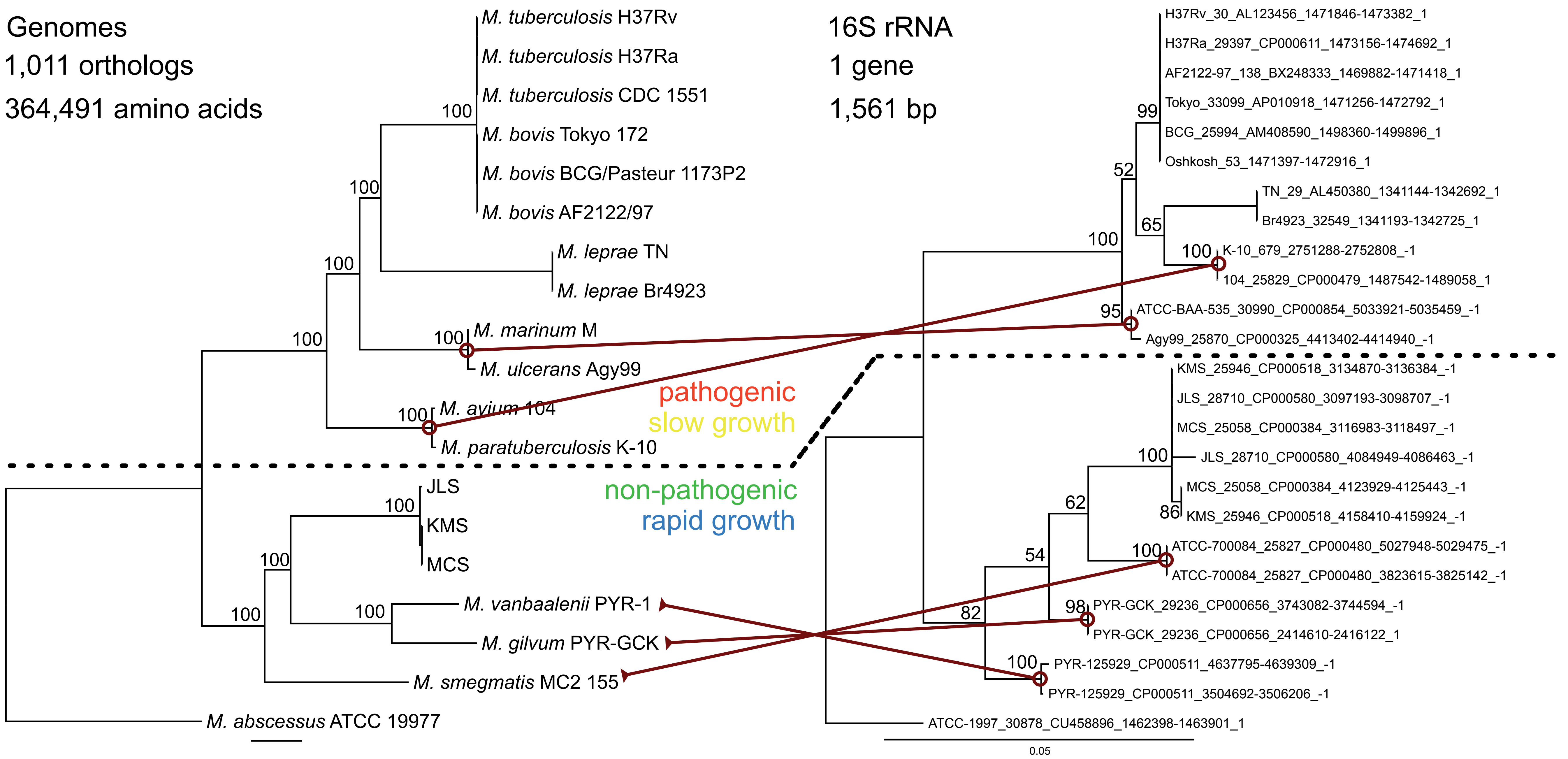
Leu
Lys
Met
Phe
Pro
Ser
Thr
Trp
Tyr
Val

Fig. S2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M. bovis AF2122/97
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M. leprae Br4923
M. marinum M
M. ulcerans Agy99
M. avium 104
M. paratuberculosis K-10
JLS
KMS
MCS
M. vanbaalenii PYR-1
M. gilvum PYR-GCK
M. smegmatis MC2 155
M. abscessus ATCC 19977
100
100
100
100
100
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100
100
100
100
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slow growth
non-pathogenic
rapid growth
16S rRNA
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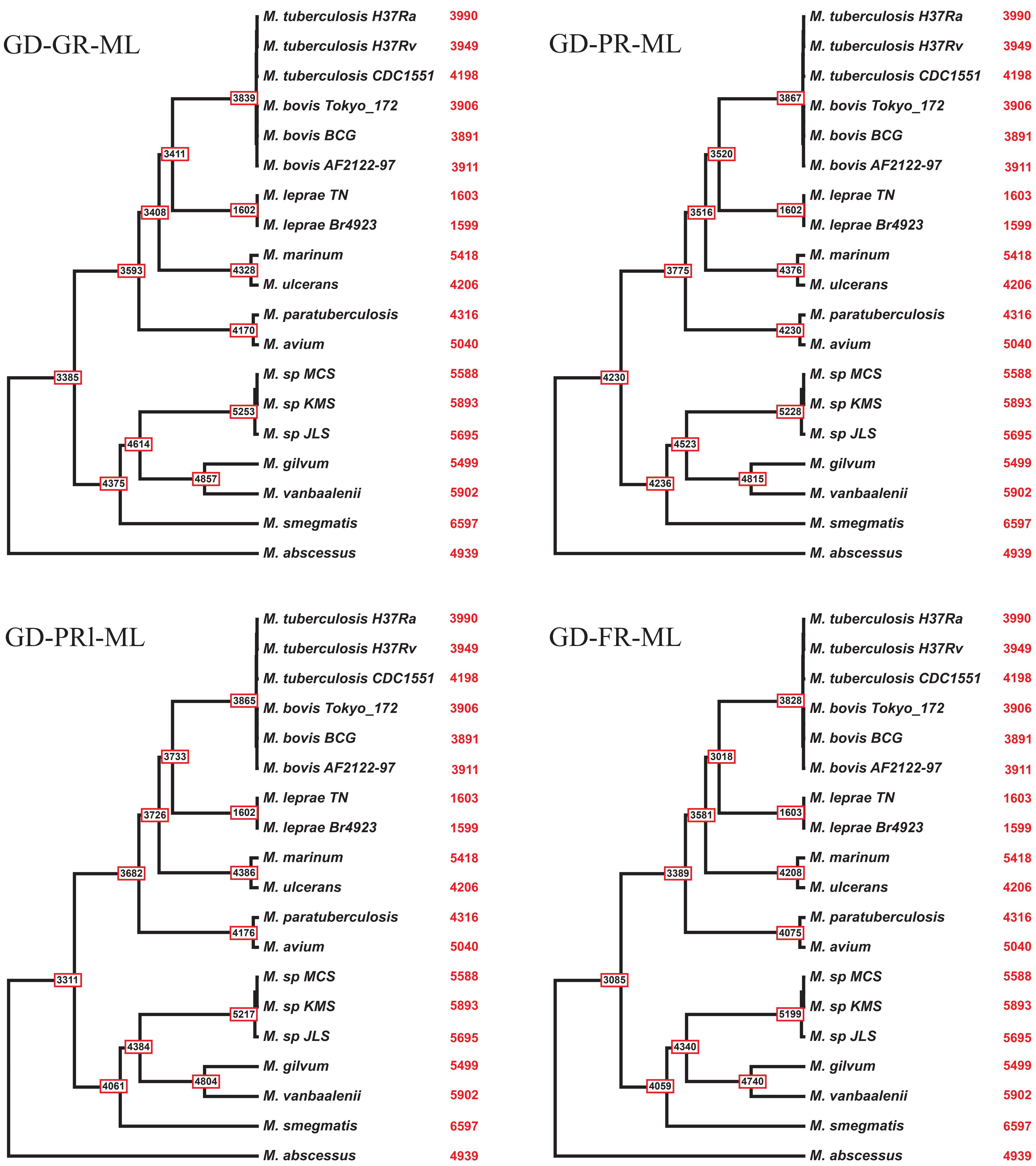
Fig. S3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M. bovis AF2122-97 3911
M. leprae TN 1603
M. leprae Br4923 1599
M. marinum 5418
M. ulcerans 4206
M. paratuberculosis 4316
M. avium 5040
M. sp MCS 5588
M. sp KMS 5893
M. sp JLS 5695
M. gilvum 5499
M. vanbaalenii 5902
M. smegmatis 6597
M. abscessus 4939
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GD-PR-ML
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