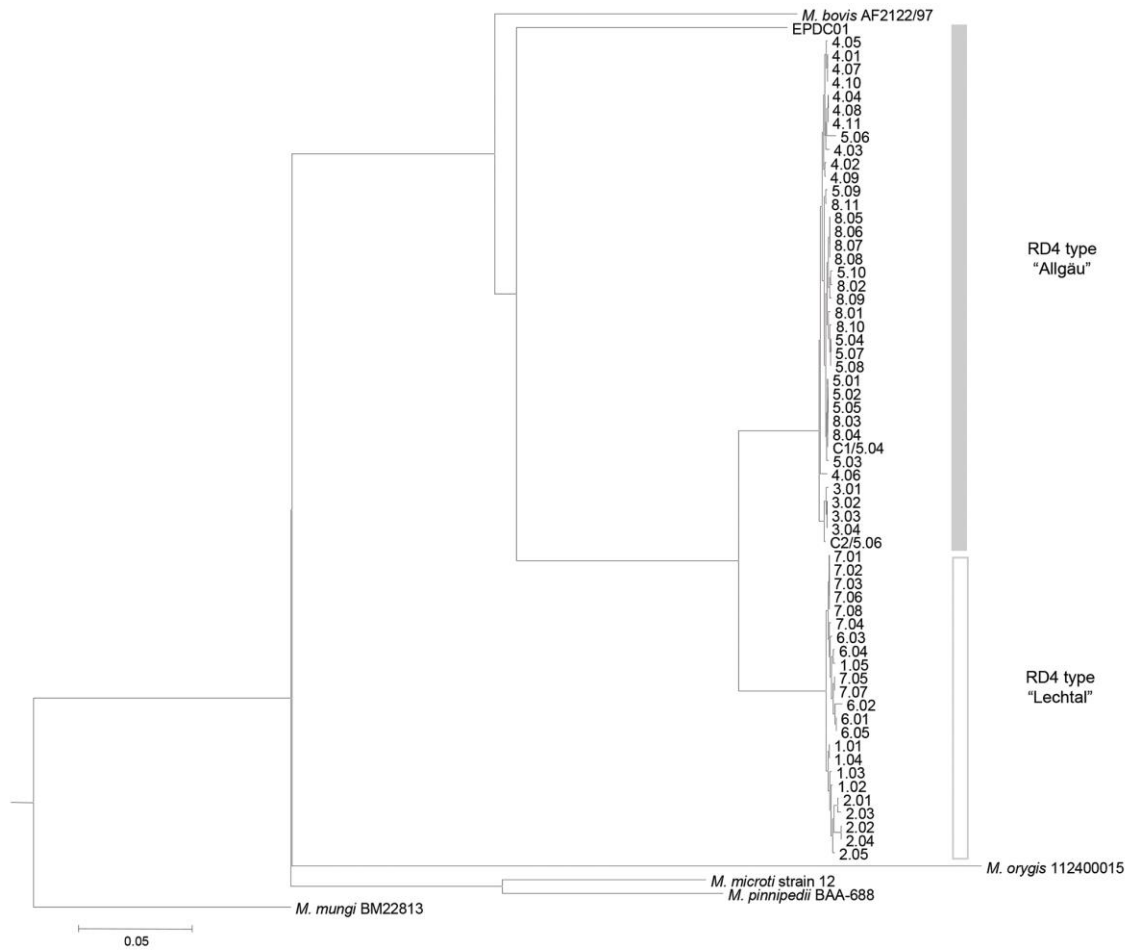


# *Mycobacterium caprae* Infection in Captive Borneo Elephant, Japan

## Technical Appendix



**Technical Appendix Figure.** Phylogenetic tree of isolate EPDC01 from a captive Borneo elephant with *Mycobacterium caprae* infection, Japan, 2016, and 61 *Mycobacterium caprae* strains (Allgäu and Lechtal types) in Broeckl et al. (1). Short reads of *M. caprae* strains were assembled by CLC Genomics Workbench, version 9.5.1 (<https://www.qiagenbioinformatics.com/solutions/functional->

genomics/?gclid=EAlalQobChMlvvGL3L7T2wIVTSOBCh2FAAKtEAAYASAAEgKLVvD\_BwE) before analysis. Core single nucleotide polymorphisms of all 13 strains, including reference *M. tuberculosis* complex strains (*M. bovis*: AF2122/97 [GenBank accession no. NC\_002945.4], *M. orygis*: 112400015 [NZ\_APKD000000000.1], *M. pinnipedii*: BAA-688 [MWXB000000000.1], *M. microti*: strain 12 [CP010333.1], and *M. mungi*: BM22813 [NZ\_LXTB000000000.1]) were determined and used for tree construction based on neighbor-joining by kSNP3 (2). Scale bar = nucleotide substitutions per site.

## References

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2. Gardner SN, Slezak T, Hall BG. kSNP3.0: SNP detection and phylogenetic analysis of genomes without genome alignment or reference genome. *Bioinformatics.* 2015;31:2877–8. [PubMed http://dx.doi.org/10.1093/bioinformatics/btv271](http://dx.doi.org/10.1093/bioinformatics/btv271)