



**Supplementary Figure S1.** A dendrogram of the 16S sequence from four NTM isolates recovered from a lung infection using the Neighbor-Joining algorithm in MEGA X software. The 16S rRNA tree, generated through a phylogenetic approach with sequences of reference strains, identified the

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strains indicated in a red box. We used ML and T92+G+I with an MP guide tree to perform the phylogenetic construction, with the robustness of the bootstrapping set at 500 pseudo-replicates. See also reference 17.