

Figure S1. Sequencing depth and rarefaction assessment of bacterial ASVs across the six lake-water samples. (a) Number of reads assigned to ASVs retained after the taxonomic filtering described in the Methods. Values above bars indicate the number of retained reads per sample. (b) Relationship between observed ASV richness and richness after rarefaction. The dashed diagonal line represents equality between observed and rarefied richness. (c) Sample-based rarefaction curves showing the accumulation of rarefied ASVs with increasing sequencing depth. Curves approaching an asymptote indicate that additional sequencing would be expected to recover relatively few additional ASVs under the analytical conditions used. Sample labels identify the lake and sampling event.

Figure S2. Exploratory maximum-likelihood phylogenetic placement of *Mycobacterium* ASVs detected in samples from Tota and Fúquene. The analysis included ASV sequences assigned to *Mycobacterium* and reference 16S rRNA gene sequences from named species. Branch-support values are shown at the corresponding nodes. Sequences identified in this study are highlighted in blue. Species names associated with reference sequences indicate phylogenetic affinity only and should not be interpreted as definitive species-level assignments because the analysis was based on the V3–V4 region of the 16S rRNA gene.

Table S1. Complete metataxonomic classification and relative abundance of ASVs detected in the six-freshwater lake-water samples analyzed. Taxonomic assignments are reported at the available ranks, with unresolved classifications indicated as unclassified or NA. Relative abundances are presented for each individual sample.

Table S2. Reference *Mycobacterium* sequences included in the exploratory phylogenetic analysis. The table lists the taxonomic identification of each reference sequence and its corresponding GenBank accession number.