Typing of *Legionella* strains isolated from environmental samples in Crete, Greece, during the period 2004–2011

**Supplementary Figure 1** | Separate phylogenetic trees of 16S rRNA (a) and *mip* (b) genes. The evolutionary history was inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1,000 replicates is taken to represent the evolutionary history of the taxa analyzed. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. Isolates with identical gene sequences are represented once and can be identified by the four digit isolate number at the end.