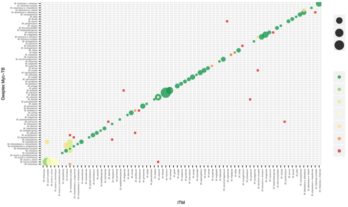

Supplementary Figure 3. Identification of nontuberculous mycobacterial species by Deeplex Myc-TB versus reference identification. Deeplex Myc-TB results were based on *hsp65* best match analysis, complemented by specific SNP detection in 16S (*rrs*) and 23S rDNA (*rrl*) targets for *M. kansasii* and *M. chelonae* strains, while reference identification was based on *rpoB* and/or 16S rDNA Sanger sequencing results, phenotypic profiling and/or type strain status. The number of isolates studied per taxon (complex, species or subspecies) is proportional to associated circle sizes. FM-A, FM-C: Full match at same taxonomic level (complex, species or subspecies), FM-B: Full match at (sub)species level but with a clonal mix identified by Deeplex, M-D: Match at complex level, sublevel provided by Deeplex, M-E: Match at complex level, sublevel provided by the reference, M-F: Match at complex level, different subspecies, PM: Partial match, several possible species identified by Deeplex, NM: No match. Nontuberculous mycobacterial taxa are ordered phylogenetically, according to Tortoli *et al.* 2019.