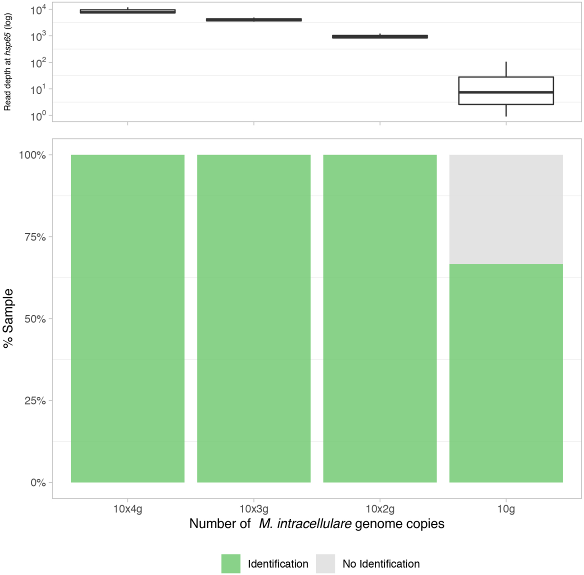

Supplementary Figure S2. Limit of detection (LOD) of Deeplex Myc-TB for NTM identification. (Top) Read depth at hsp65 versus the number of input genomes of a *M. intracellulare* strain. Median values as well as 25-75% quartiles are shown. (Bottom) LOD was measured as the fraction with (green) or without (grey) correct identification in three independent replicated analyses of 10, 10^2, 10^3, 10^4 *M. intracellulare* genome copies.