



**Fig. S1. Flowchart of the study population.** <sup>a</sup>Population including *M. tuberculosis*, *M. marinum*, *M. goodii*, and *M. szulgai*. <sup>b</sup>Population including *M. chelonae*, *M. abscessus*, *M. neoaurum*, *M. immunogenum*, *M. haemophilum*, and *M. intracellulare*. NTM, nontuberculous mycobacterium; RD1, regions of difference 1.