Table S1. Data sets used for the analyses

Data set	Analysis	Genomes	Markers and data information
Myc19	Phylogenetic reconstruction	The 19 mycobacteria proteomes ($n = 19$) Data Set	Concatenation of 1,011 aligned protein sequences (1:1 orthologs; 364,491 amino acid positions) Data Set MYC amino acid substitution matrix
Myc18	Gain and death analysis	The Myc19 data set, excluding *M. abscessus* ($n = 18$)	14,108 ortholog groups (or gene families; N:N and N:M relationships)