



Supplementary Figure S6. Maximum Likelihood (ML) phylogeny of *Metarhizium* fungi as reconstructed from a concatenation of 5TEF, DUF895 (MzIGS3) and rIGS-ID800 marker sequences. Terminal branches are labelled by genus, species and strain designations; “TYPE” denotes the nomenclatural type strain of a species. Numbers on branches indicate bootstrap support percentages. The size bar corresponds to 1 % sequence divergence; branches drawn as dashed lines are not to scale. Concatenations of the orthologous sequences from the *M. majus* and *M. guizhouense* type strains have been used as outgroup.