



Supplementary Figure S2. Maximum Likelihood (ML) phylogeny of *Metarhizium* fungi as reconstructed from a concatenation of EF1A-RPB1-RPB2 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 >50 %. The size bar corresponds to 0.5 % sequence divergence; branches drawn as dashed lines are not to scale. A concatenation of the orthologous sequences from the *M. acridum* type strain has been used as outgroup.