



**S7 Fig:** Phylogenetic analysis of KS domains in the PKSs analyzed in Fig 1A and additional 18 PKSs in *M. robertsii*. The Genbank accession number for each full-length amino acid sequence of each PKS is shown after the species name. The clade containing *Metarhizium*'s PKS1s is highlighted in pink, PKS2s highlighted in red and additional *M. robertsii* PKSs in blue. Numbers at nodes represent the bootstrap values of Maximum Likelihood (left), Neighbor-Joining (middle), and the Bayesian posterior probabilities (right). A hyphen (-) indicates no support value in the corresponding method. The scale bar corresponds to the estimated number of amino acid substitutions per site.