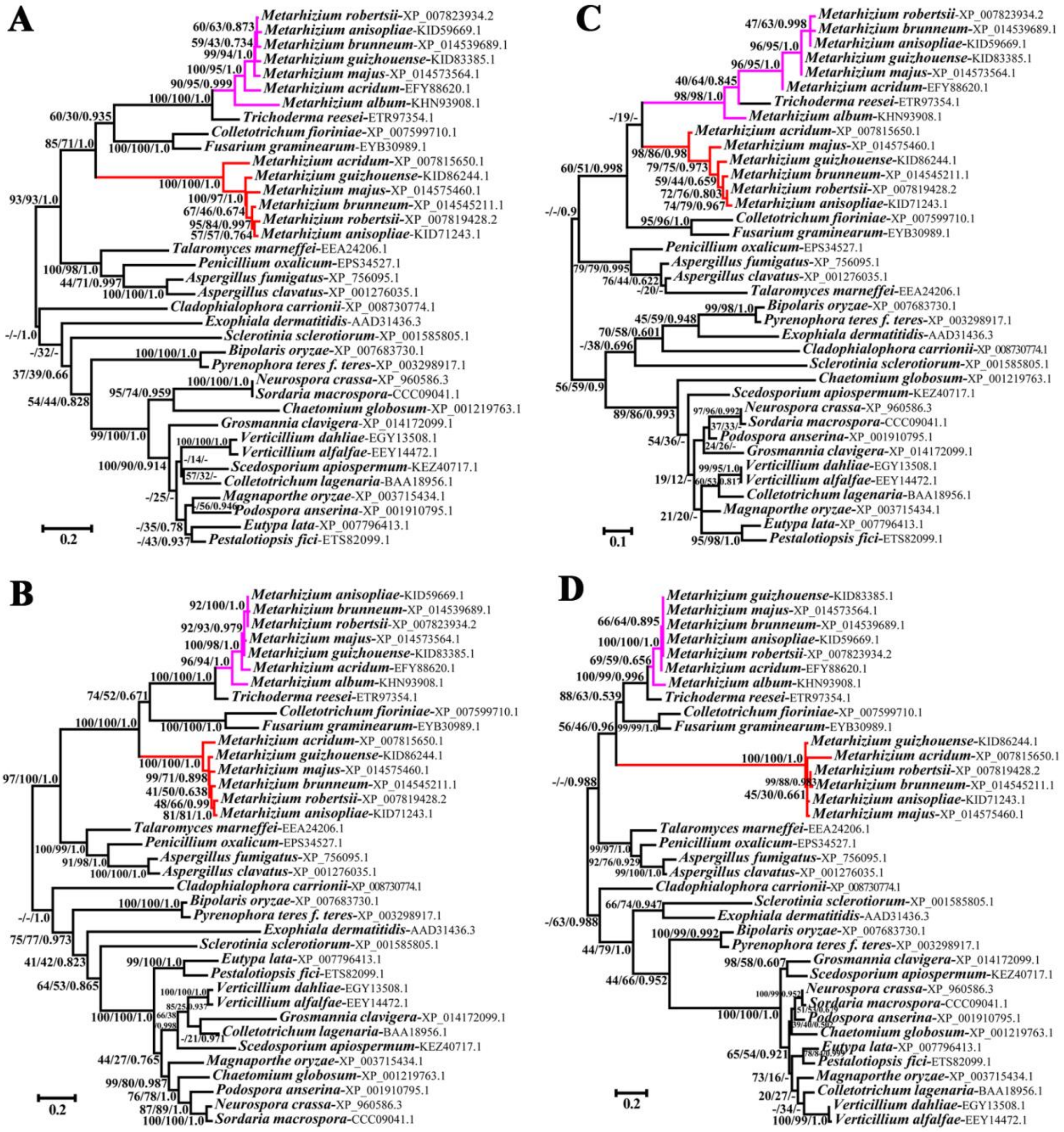

S2 Fig: Phylogenetic analysis of domains in the PKSs analyzed in Fig 1. (**A**) AT domain; (**B**) PP-binding domain, (**C**) PS-DH domain, (**D**) TE domain. The Genbank accession number for each full-length amino acid sequence of each PKS is shown after the species name. The clade containing *Metarhizium* PKS1s is highlighted in pink, PKS2s highlighted in red. 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.