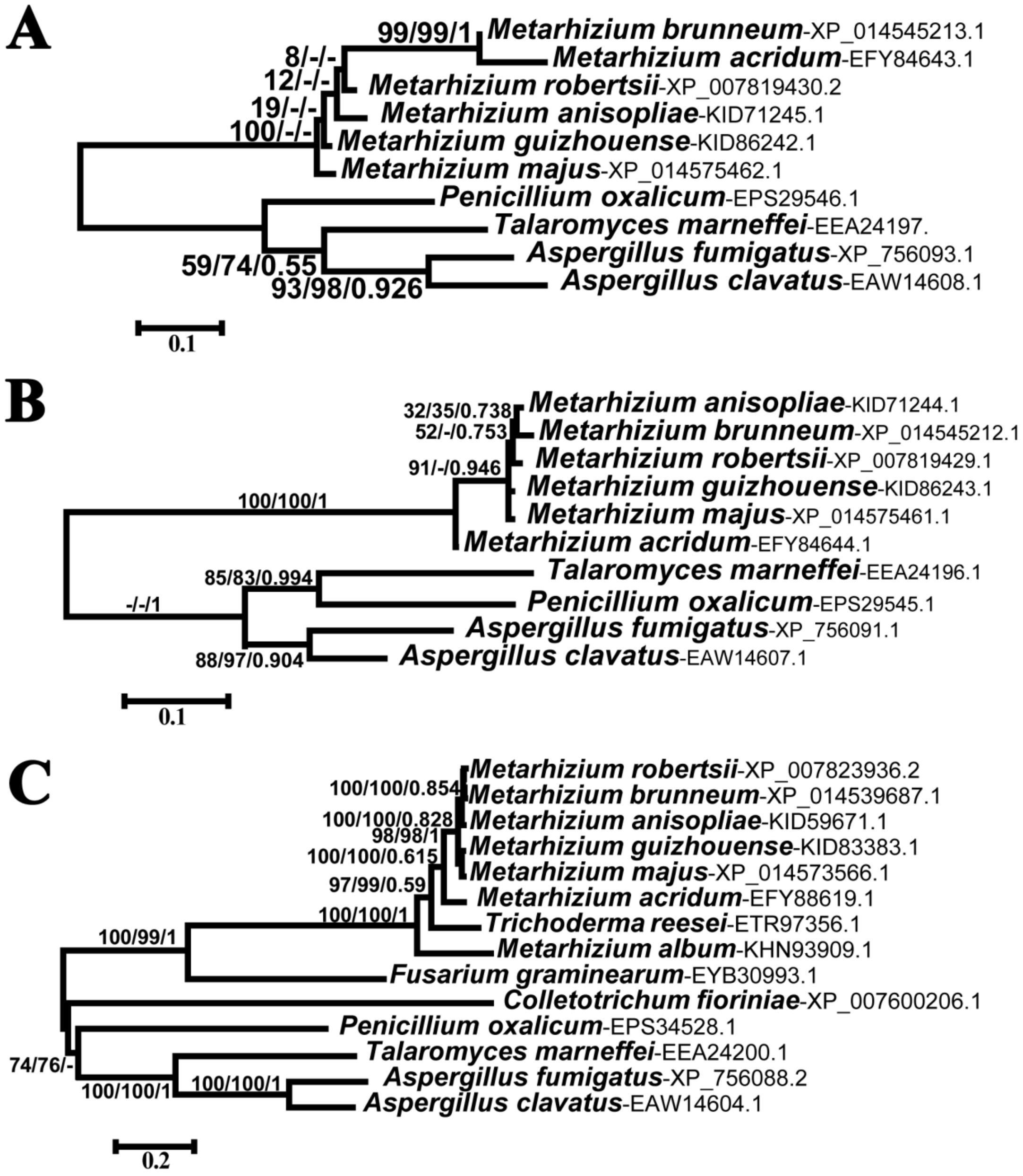

**S8 Fig:** Phylogenetic analyses of Arp1 (**A**), Arp2 (**B**) and Abr2 (**C**) in *Metarhizium* and other fungi that have gene clusters similar to *Pks1-gc* or *Pks2-gc*. Numbers at nodes represent bootstrap values of Maximum Likelihood (left), Neighbor-Joining (middle) and Bayesian posterior probabilities (right). Hyphen (-) indicates no support value in the corresponding method. The scale bar corresponds to the estimated number of amino acid substitutions per site.