



Supplementary Figure 1. Maximum likelihood tree reconstruction using NRPS A-domains from Zoopagomycota and Mucoromycota genomes. The maximum likelihood phylogenetic was reconstructed using the A-domains from Bushley et al. (2010) and the A-domains predicted for all genomes used in this report. Numbers above each branch represent bootstrap values after 1,000 replicates when support is greater than 70%. Cluster names represent the groups assigned to each A-domain clade.