



Supplementary Figure 4. Maximum likelihood tree reconstruction using PKS KS-domains from Zoopagomycota and Mucoromycota genomes. The maximum likelihood phylogenetic was reconstructed using the KS-domains from Kroken et al. (2013) and the KS 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 50%. Cluster names represent the groups assigned to each KS-domain clade.