

Figure S4: GDM model fitting for all FEF (not just Pezizomycotina). Unlike the GDM model for only Pezizomycotina (Figure 3), evapotranspiration was not a significant predictor variable when all FEF were considered. However, the majority of our samples were composed of over 90% Pezizomycotina, and 90% of our samples had over 50% of reads assigned to Pezizomycotina. Other variables like those shown on this figure were similar between the two GDM models. Variables explaining less than 2% of community dissimilarity are not shown.

