Supplementary figures

Community sequencing on a natural experiment reveals little influence of host species and timing but a strong influence of compartment on the composition of root endophytes in three annual Brassicaceae

Jose G. Maciá-Vicente^{1*}, Bora Nam², Marco Thines^{1,2,3*}

¹Institute of Ecology, Evolution and Diversity, Goethe University Frankfurt, Max-von-Laue-Str. 13, Frankfurt am Main 60438, Germany

²Biodiversity and Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, Frankfurt am

Main 60325, Germany

³LOEWE Centre for Translational Biodiversity Genomics (TBG), Georg-Voigt-Str. 14-16, 60325 Frankfurt am Main, Germany

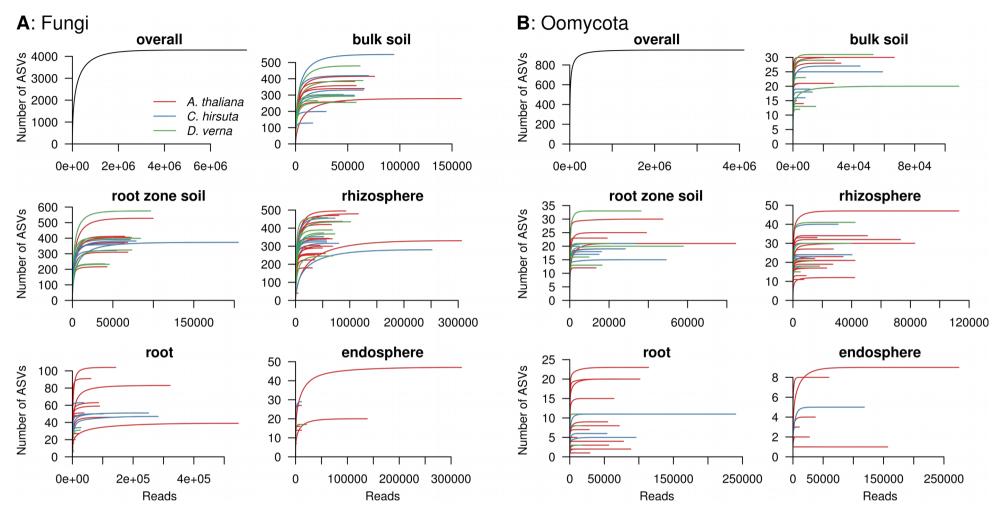


Figure S1. Rarefaction curves of ASVs accumulation with sequence reads, for the fungal ITS (A) and the oomycete cox2 gene (B) datasets.

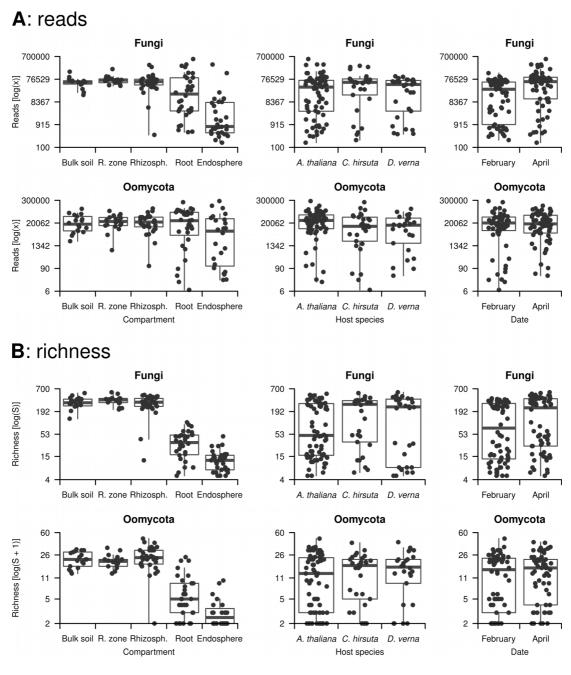


Figure S2. Reads (**A**) and ASVs richness (**B**) values obtained by Illumina MiSeq sequencing across the factors considered in this study. Box-and-whisker plots summarize the distribution of each measurement (median, interquartile range, and range) per factor, and points show individual values per sample.