

Figure S5 Proportion of the ‘reactive’ OTUs from one type of habitat (aquatic –blue-, terrestrial –brown-, and phyllosphere –green-) detected in a different type of ecosystem as a function of the depth of sequencing for the 3 comparisons (see legend) Rarefaction depth is plotted on a log scale (base 10). For these analyses, the OTU table with the 3 deeply sequenced samples was randomly subsampled to 100000, 500000, 1000000, 1500000, and 2000000 sequences per sample.

