



**Figure S1.** Rarefaction curves illustrating the sequencing depths in the roots of tomato plants. The vertical lines indicate a minimum (21,357 sequences) number of detected sequences. Zero-P: red, low-P: blue, and high-P: green.

**Figure S2.** A neighbor-joining tree of partial SSU rDNA sequences obtained from tomato roots based on the p-distances method, with the tree rooted by *Saccharomyces cerevisiae* as an outgroup. Bootstrap values (only values > 70 were shown) were estimated from 1000 replicates. Representative sequences in each ASV from roots were incorporated in this study.

