

**Supplementary Table 1.** Overview of sequencing data and OTU analysis for bacterial and fungal endophyte samples ( $n = 18$ )

Sample type	Total input reads	After Q30 filtering	After DADA2 denoising	After removal of chimeric reads	Total OTUs	After removing undesired taxa	After removing OTUs < 3 reads	OTUs collapsed to genus level	No. of OTUs			OTUs collapsed to genus level			Average no. of reads per sample	No. of OTUs used in analysis
									Root	Stem	Leaf	Root	Stem	Leaf		
Bacteria	4,214,060	3,551,853 (84.28%)	3,512,818 (83.35%)	3,052,582 (72.43%)	1,651	1,145	230	90	228	89	98	89	47	57	169,587	230
Fungi	4,134,835	3,114,211 (75.31%)	3,070,207 (74.2%)	2,586,606 (62.5%)	2,787	861	181	53	177	156	172	53	46	53	88,144	181

OTU, operational taxonomic unit.