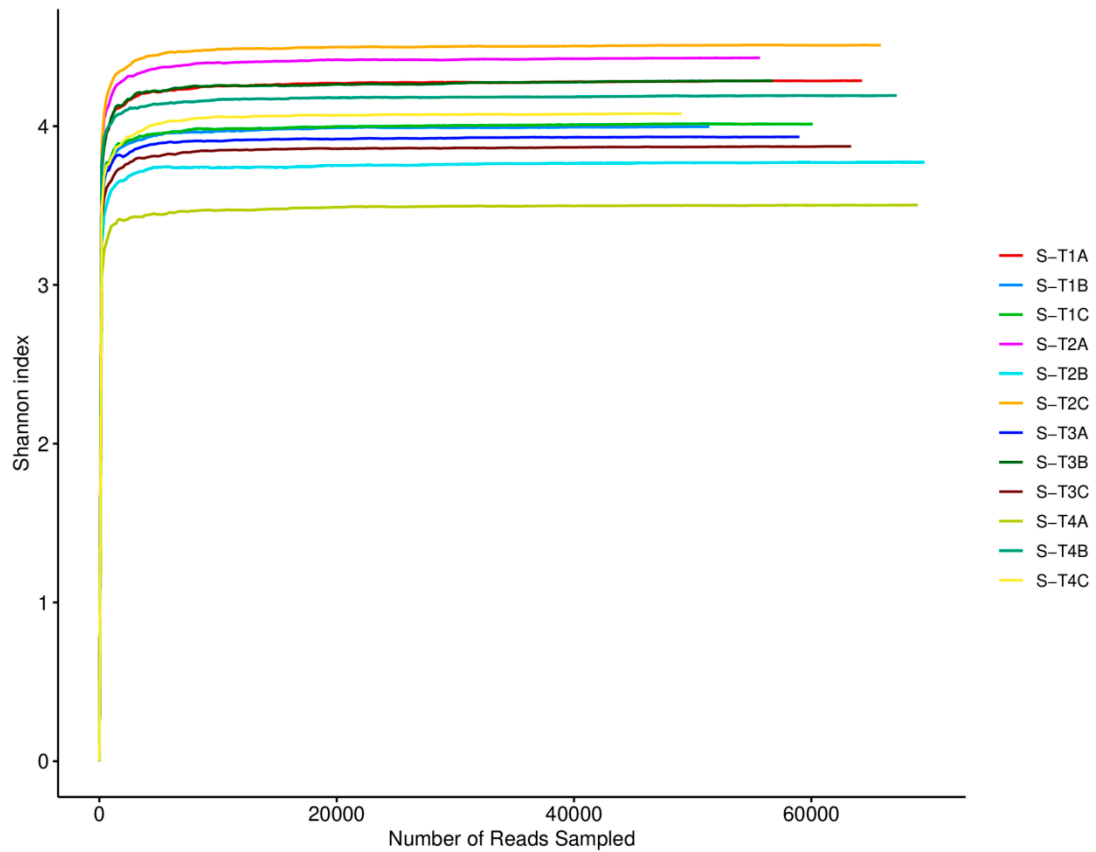
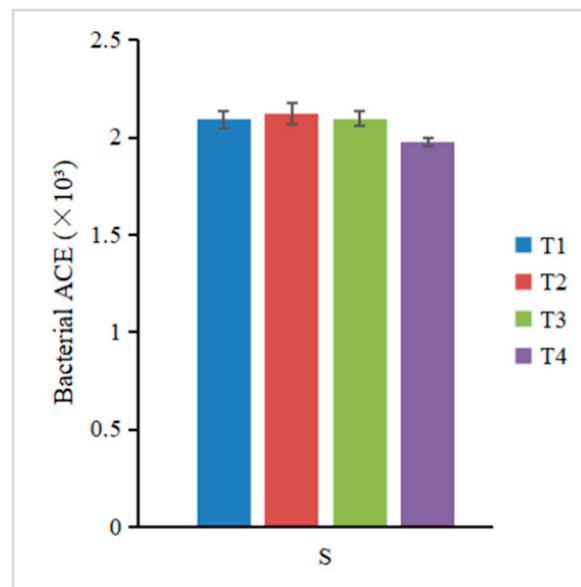


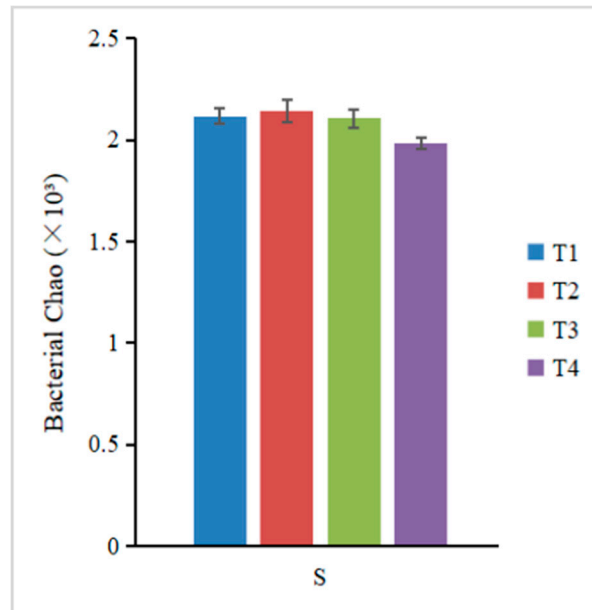
**Supplementary Fig. S1** Bacterial shannon curve based on V3-V4 regions of the 16S rRNA for high-throughput sequencing analysis



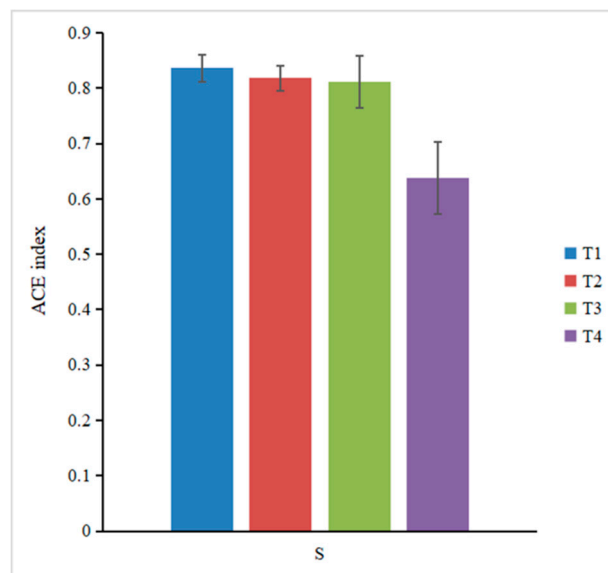
**Supplementary Fig. S2** Fungal shannon curve based on 1-2 regions of ITS for high-throughput sequencing analysis



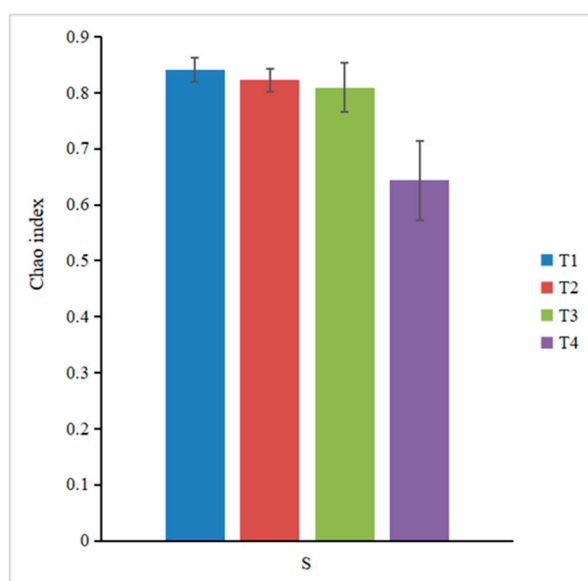
**Supplementary Fig. S3** Bacterial richness (abundance-based coverage estimator, ACE) in rhizosphere soil



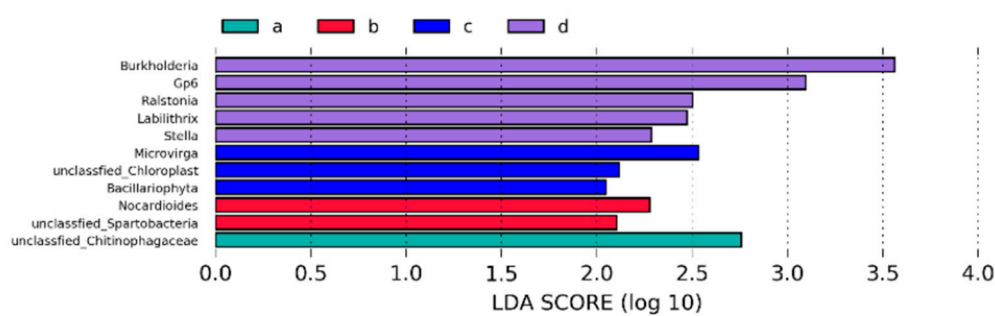
**Supplementary Fig. S4** Bacterial chao index in rhizosphere soil



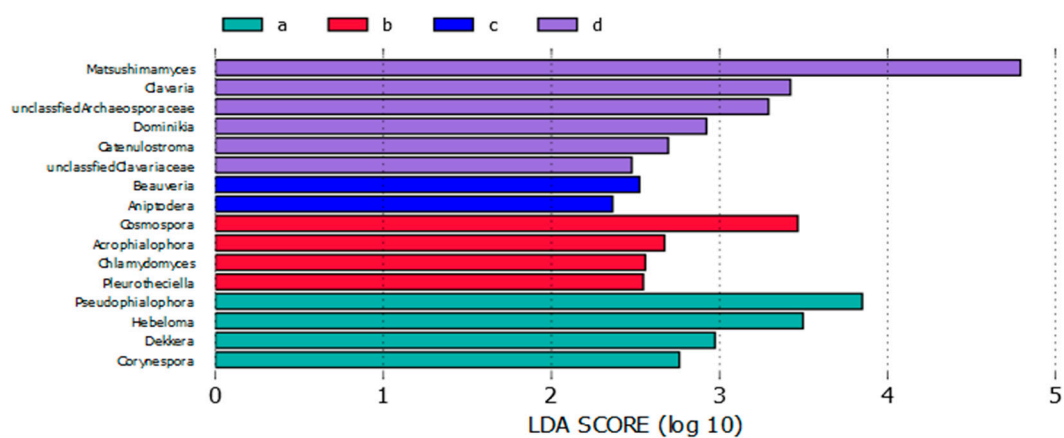
**Supplementary Fig. S5** Fungal richness (abundance-based coverage estimator, ACE) in rhizosphere soil



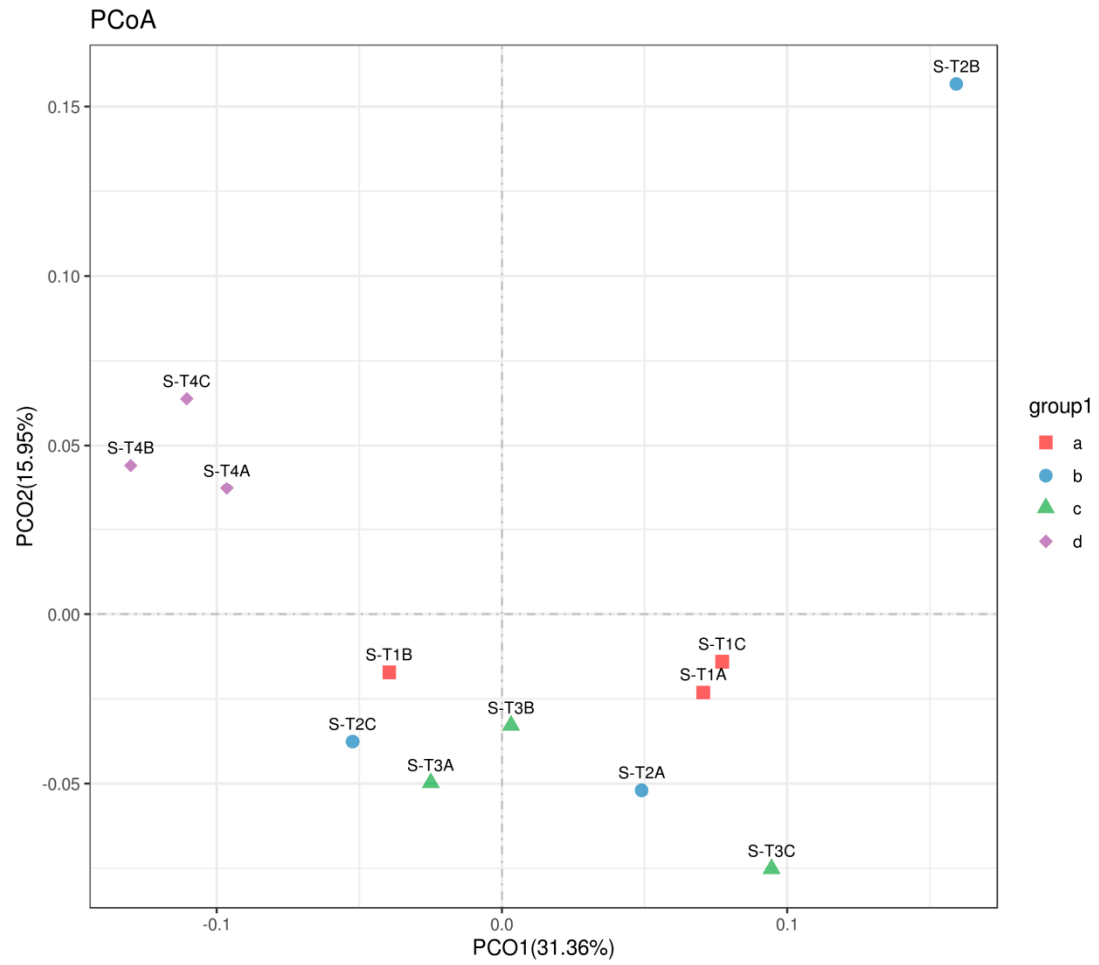
**Supplementary Fig. S6** Fungal chao index in rhizosphere soil



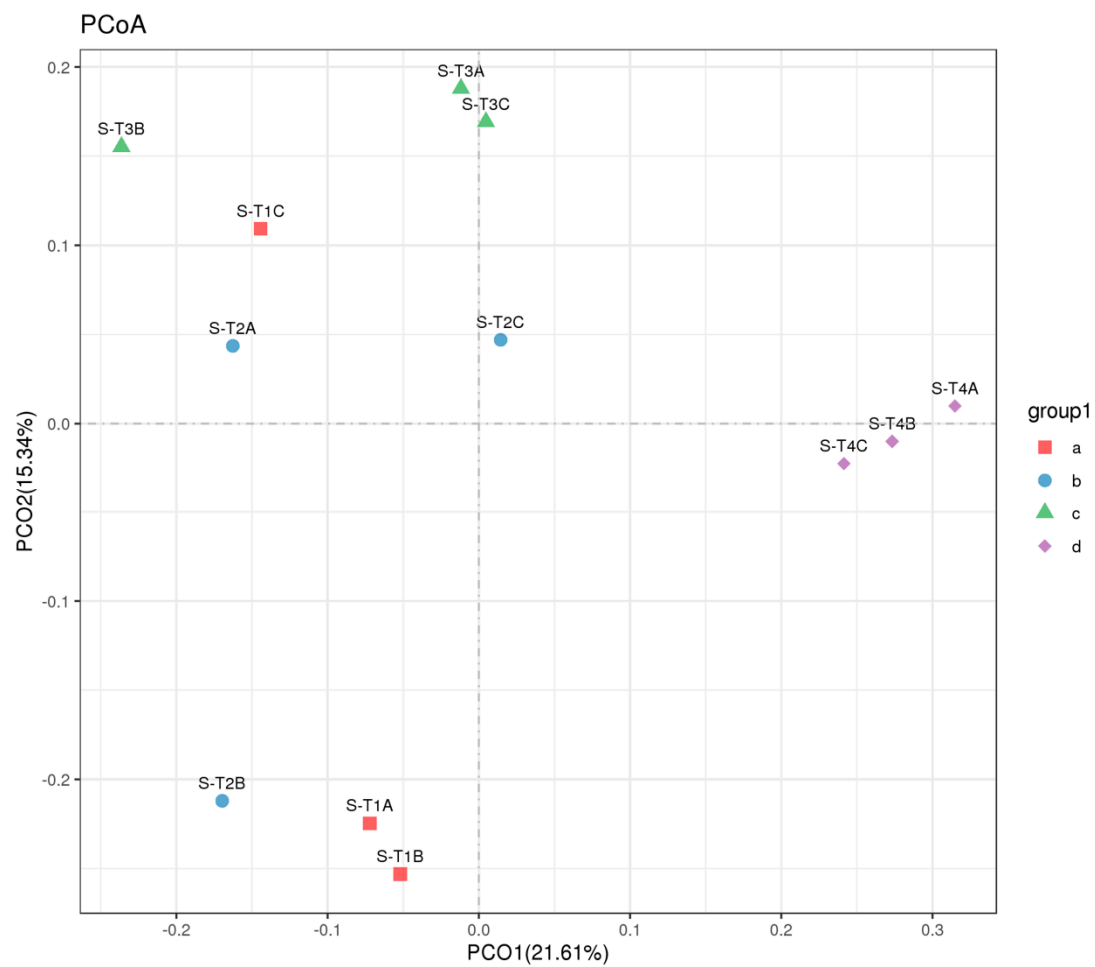
**Supplementary Fig. S7** Bar diagram of the linear discriminant analysis (LDA) distribution (LDA score threshold:  $\geq 2$ ) with soil bacterial communities



**Supplementary Fig. S8** Bar diagram of the linear discriminant analysis (LDA) distribution (LDA score threshold:  $\geq 2$ ) with soil fungal communities



**Supplementary Fig. S9** Principal coordinates analyses (PCoA) were performed based on the soil bacterial OTU distributions using Bray-Curtis distance (a: T1; b: T2; c: T3; d: T4)



**Supplementary Fig. S10** Principal coordinates analyses (PCoA) were performed based on the soil fungus OTU distributions using Bray-Curtis distance