

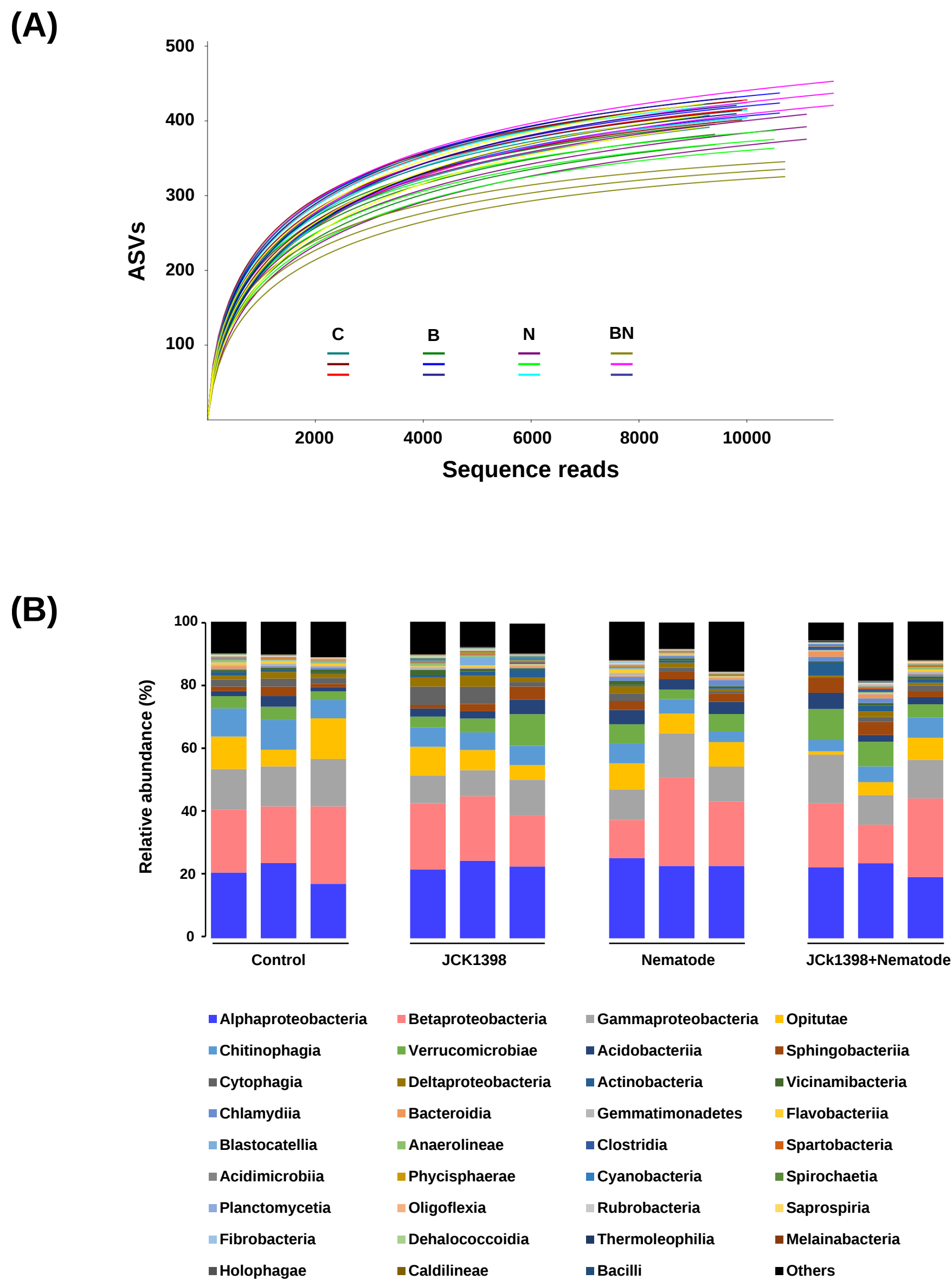


Figure S1. (A) Rarefaction curves demonstrating the alpha diversity of the rhizosphere microbiota based on amplicon sequence variants (ASVs) derived from 16S rRNA gene sequences. Curves with 95% confidence intervals indicate sufficient sequencing depth for all treatments. (B) Stacked bar plot showing the relative abundance of major bacterial classes in the rhizosphere of pine seedlings across treatments, highlighting shifts in microbial community composition. Treatments include control, *B. subtilis* JCK-1398, *B. xylophilus*, and the combination of *B. subtilis* and *B. xylophilus*.

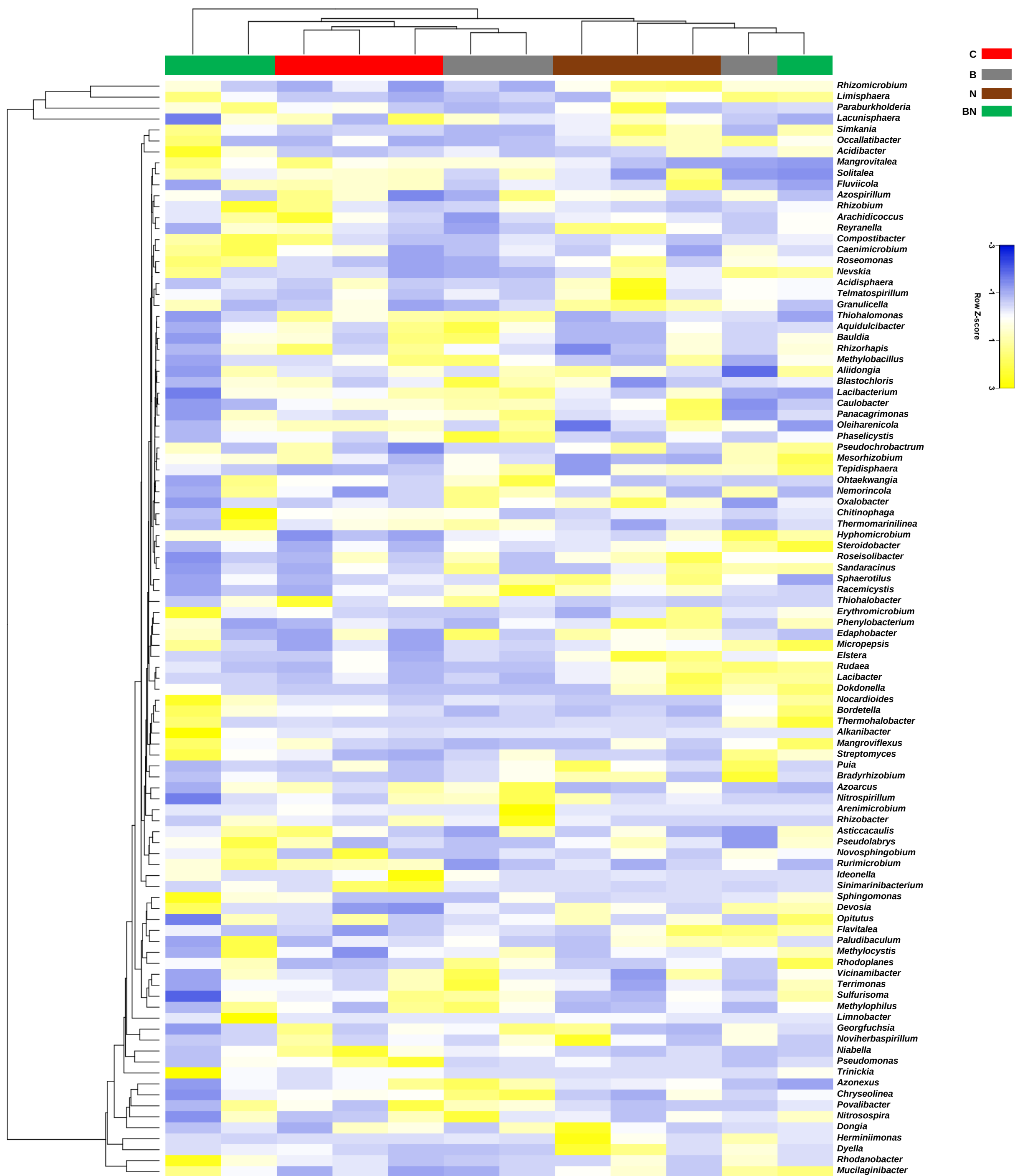


Figure S2. Heatmap of the top 100 bacterial genera in the rhizosphere, clustered using Manhattan distance and hierarchical clustering based on the average linkage method. Z-scores represent standardized relative abundances of each genus, with distinct patterns of abundance between treatments. Treatments: C (control), B (*B. subtilis* JCK-1398-treated), N (*B. xylophilus*-inoculated), and BN (combined treatment with bacteria and nematodes).

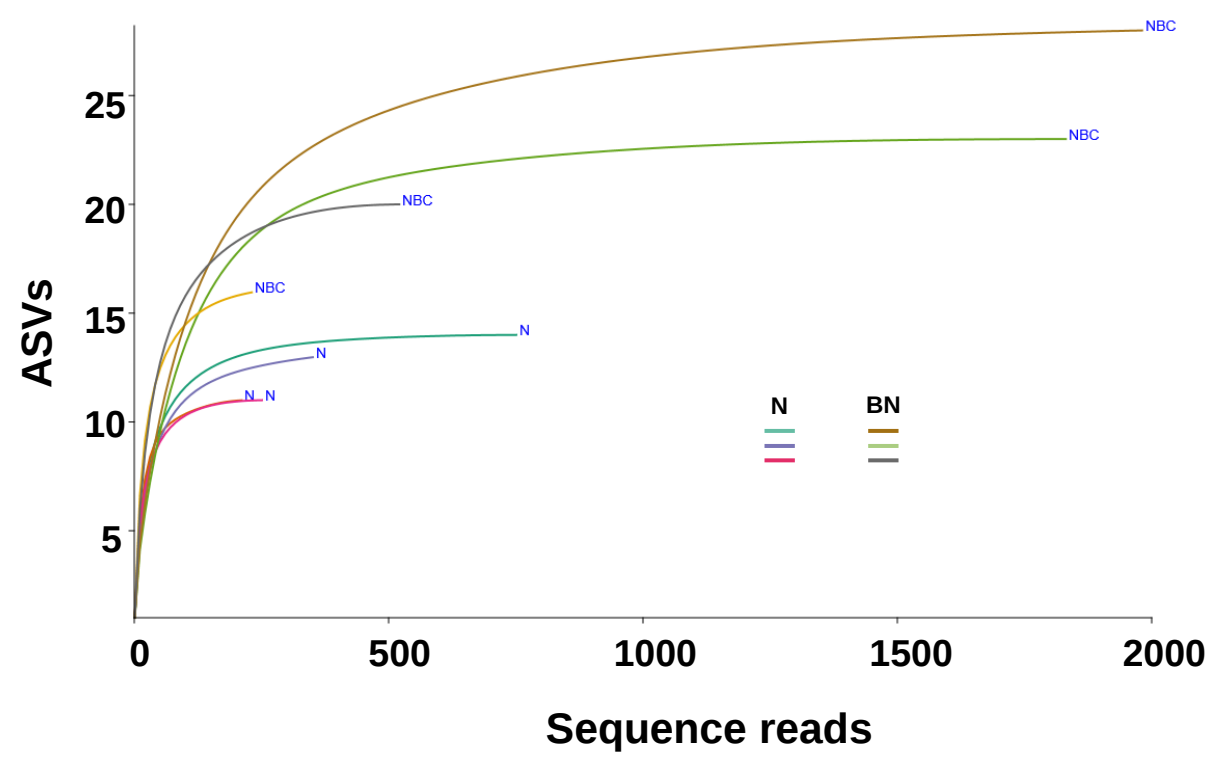


Figure S3. Rarefaction curves depicting the alpha diversity of the microbiota associated with *Bursaphelenchus xylophilus* nematodes, based on amplicon sequence variants (ASVs) obtained from 16S rRNA gene sequencing. The sequencing depth is sufficient for all treatments. N represents nematodes isolated from untreated pine seedlings, while BN denotes nematodes from seedlings treated with *B. subtilis* JCK-1398.