



Figure 1. Phylogenetic tree of the 100 most abundant OTUs in the 16S rDNA sequencing data. The tree is rooted at the top and shows the relationships between the OTUs. The OTUs are labeled with their accession numbers and the number of reads. The tree is divided into two main clades: Bacteria and Eukarya. The Bacteria clade is further divided into several phyla, including Proteobacteria, Firmicutes, and Actinobacteria. The Eukarya clade is divided into several phyla, including Ascomycota, Basidiomycota, and Chytridiomycota. The tree is color-coded by phylum: Proteobacteria (red), Firmicutes (green), Actinobacteria (blue), Ascomycota (orange), Basidiomycota (purple), and Chytridiomycota (brown). The tree is rooted at the top and shows the relationships between the OTUs. The OTUs are labeled with their accession numbers and the number of reads. The tree is divided into two main clades: Bacteria and Eukarya. The Bacteria clade is further divided into several phyla, including Proteobacteria, Firmicutes, and Actinobacteria. The Eukarya clade is divided into several phyla, including Ascomycota, Basidiomycota, and Chytridiomycota. The tree is color-coded by phylum: Proteobacteria (red), Firmicutes (green), Actinobacteria (blue), Ascomycota (orange), Basidiomycota (purple), and Chytridiomycota (brown).

