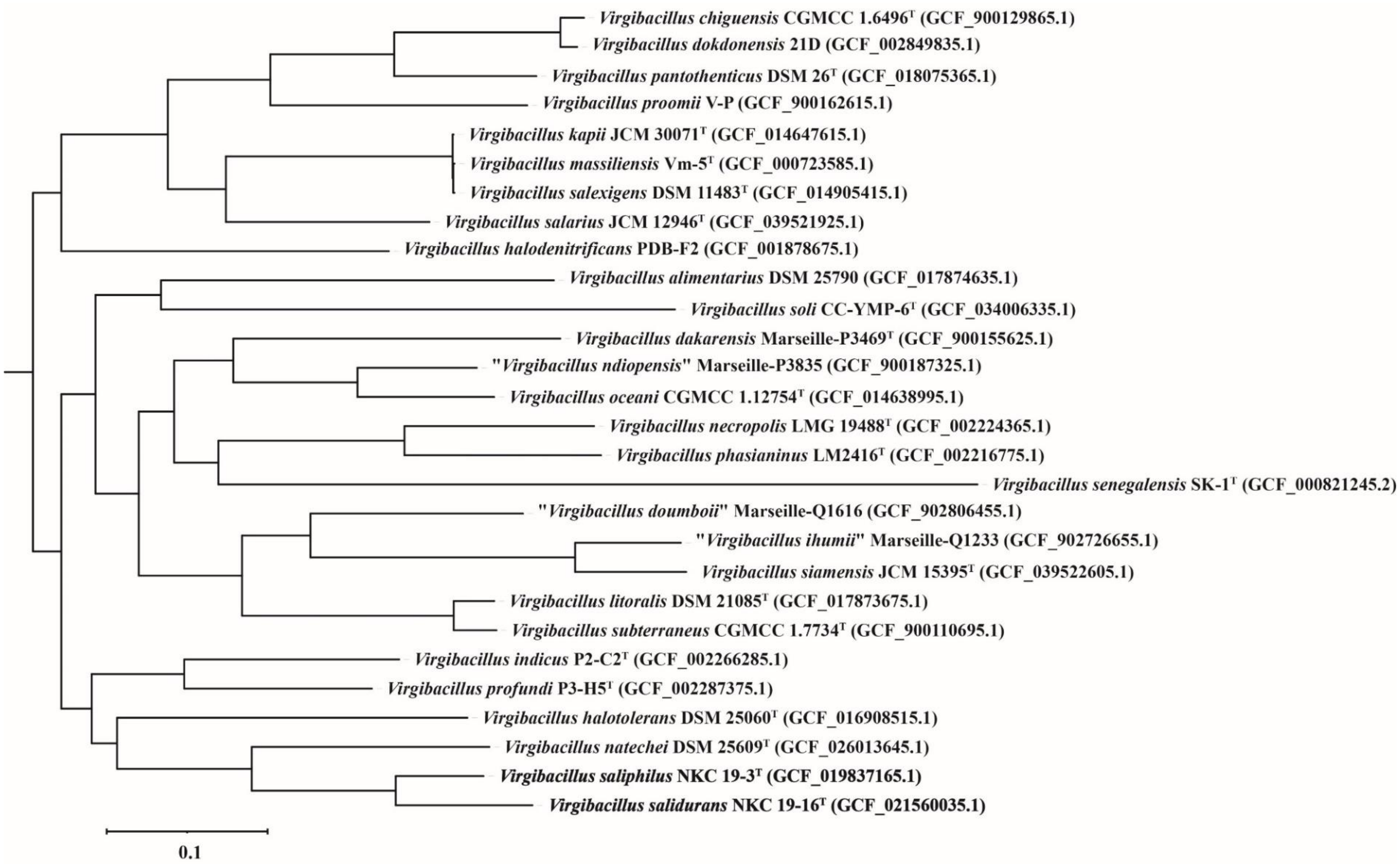

Fig. S4. Core-genome-based phylogenetic tree of the genus *Virgibacillus*. The tree represents the evolutionary relationships among 28 species within the genus Virgibacillus, constructed using alignments of core-genome sequences derived from pan-genome analysis. The core-genome consists of highly conserved genes shared across all analyzed genomes, providing a robust framework for resolving phylogenetic relationships. Scale bar 0.1 indicates the number of substitutions per site in the core-genome alignment.