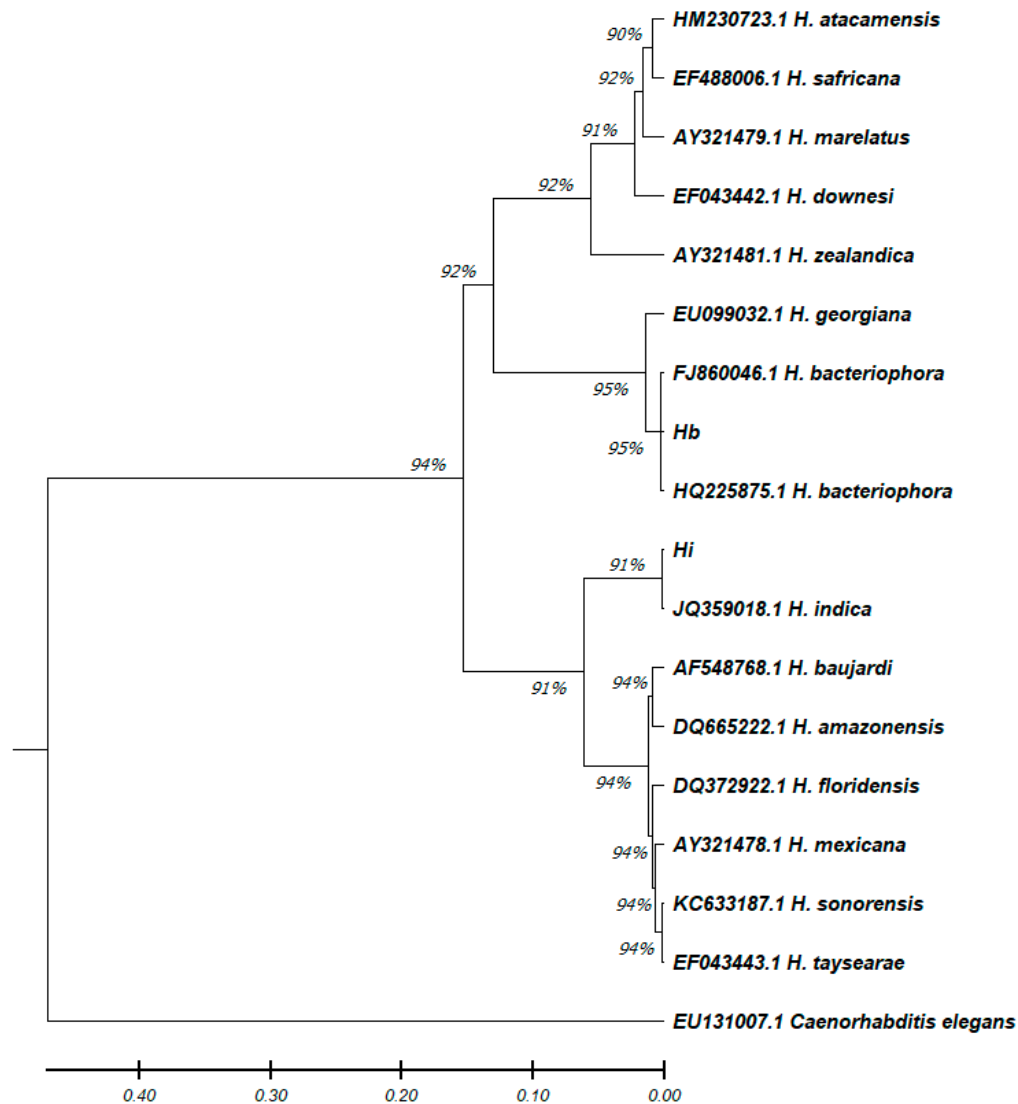


Figure S1

Phylogenetic relationships of entomopathogenic nematode cultured populations identified in the genus *Steinernema* (*Sf*, *S. feltiae*, NCBI accession #OQ998935 ; *Sc*, *S. carpocapsae*, OQ998952) based on Sanger's sequencing results of the ITS1, ITS2 region of rDNA, as inferred by the Maximum Likelihood method and Tamura-Nei model. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. All reference sequences are indicated by the NCBI accession numbers in the phylogenetic tree. The reference sequences were employed to confirm the right identification of each read in the phylogram. *C. elegans* was used as a global outgroup.



**Figure S2**

Phylogenetic relationships of entomopathogenic nematode cultured populations identified in the genus *Heterorhabditis* (*Hb*, *H. bacteriophora*, NCBI accession #OQ998912; *Hi*, *H. indica*, OQ998942) based on Sanger's sequencing results of the ITS1 and ITS2 region of rDNA, as inferred by the Maximum Likelihood method and Tamura-Nei model. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. All reference sequences are indicated by the NCBI accession numbers in the phylogenetic tree. The reference sequences were employed to confirm the right identification of each read in the phylogram. *C. elegans* was used as a global outgroup.