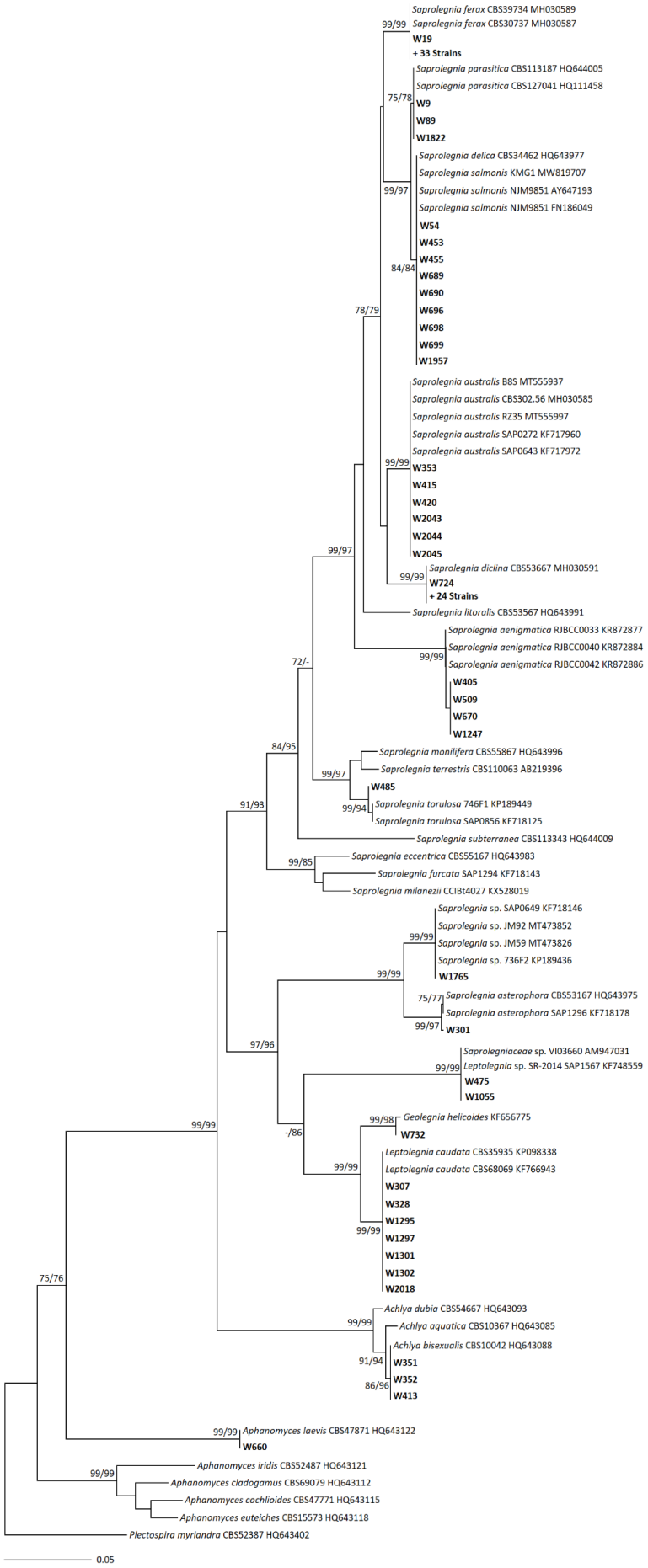Supplementary Figure S2. Phylogenetic tree of *Saprolegniales* species from the minimum evolution analysis based on internal transcribed spacer (ITS) rDNA sequences. Bootstrapping values (minimum evolution BP/maximum likelihood BP) higher than 70 % were given above or below the branches (1,000 replicates). The strains obtained from this study are shown in bold. The scale bar equals the number of nucleotide substitutions per site.