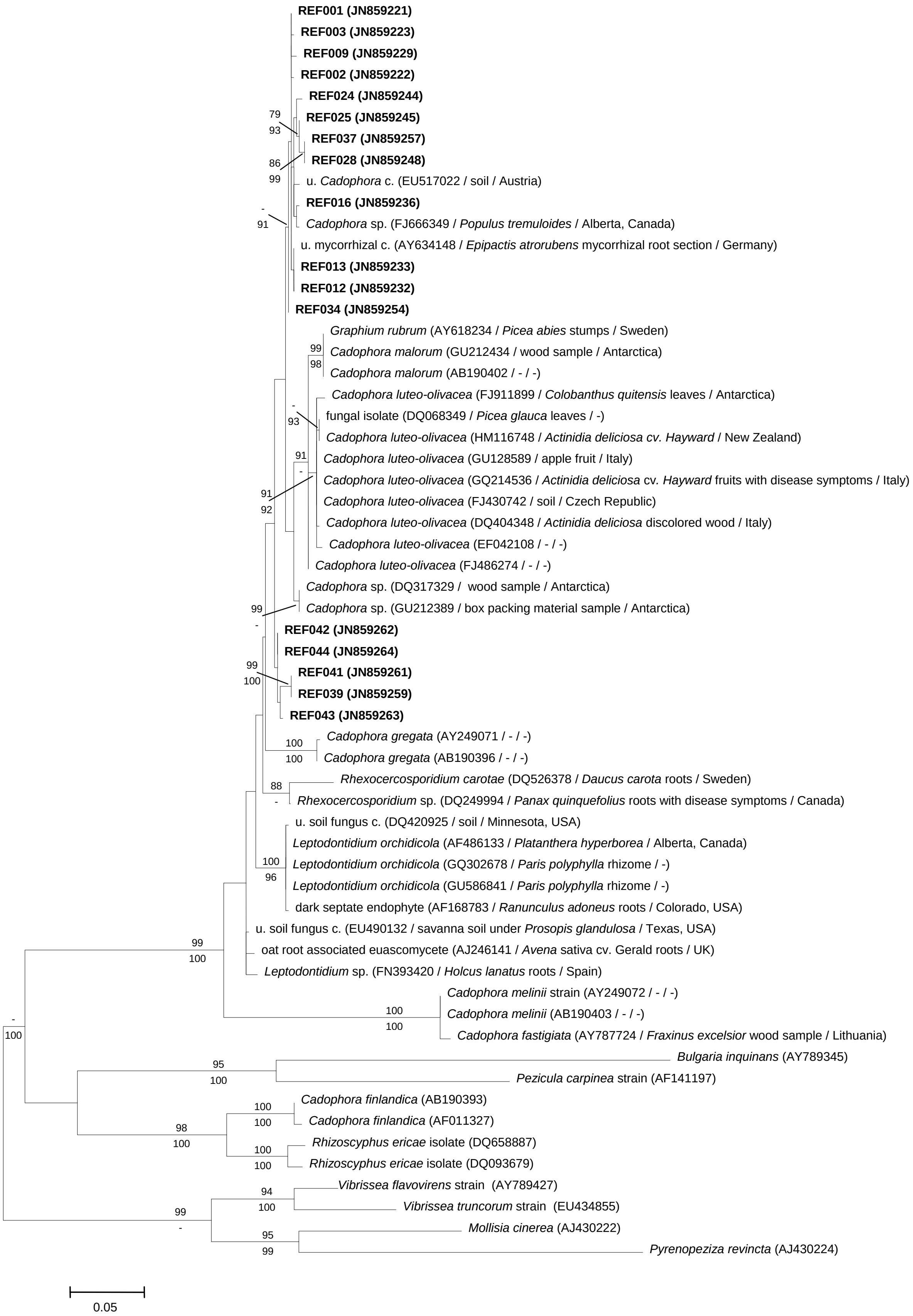

Figure S3 The maximum likelihood (ML) tree of the ITS sequences of representatives of group DSE-1 and similar sequences from GenBank. Sequences obtained in this study are shown in bold. *Pyrenopeziza revincta* (AJ4302224) was used as outgroup. Accession number, isolation source and geographic origin of sequences from public databases are shown. NJ bootstrap (not shown below 70%) values are above and the Bayesian posterior probabilities as percentage (not shown below 90%) are below the branches. Abbreviations: uncultured (u.), clone (c.). Bar = 0.05 expected change on one nucleotide.