Supplementary file for the article:

Holovachov O, Haenel Q, Bourlat SJ, Jondelius U. Taxonomy assignment approach determines the efficiency of identification of OTUs in marine nematodes. *Royal Society Open Science.*

Supplementary Figure 1. Barcoding region used in this study – generalized secondary structure model of the 90% consensus sequence (excluding rare insertions) based on combined data from secondary-structure-based alignment of reference sequences and mothur-based alignment of OTU sequences (444 sequences in total). Helices (6-10, 10/e1, 11-14) are according to [63]. Variable regions V1 and V2 are labelled according to [64].