



Figure S1. Phylogenetic trees of β -tubulin genes constructed by maximum likelihood analyses based on an alignment of cDNA positions 1 and 2. Coloured operational taxonomic units represent individual or groups of sequences that differ in their position between this tree and the trees presented in Figure 1. The nomenclature of the genes follows the suggestion made by Roose et al. [43]. Branch support is given as SH-aLRT support (%) / aBayes support / ultrafast bootstrap support (%). Several support values for grouping of very closely related ascarid β -tubulin genes are not shown. In all these cases, the SH-aLRT support was 0%. The scale bars indicate a distance of 0.1 substitutions per site.