

Note: This is Online Appendix 1 of Dube, M.P., Byaruhanga, C., Dorny, P., Dermauw, V. & Qekwana, D.N., 2024, 'Taenia saginata prevalence in cattle slaughtered at low throughput abattoirs in South Africa', *Onderstepoort Journal of Veterinary Research* 91(1), a2157. <https://doi.org/10.4102/ojvr.v91i1.2157>

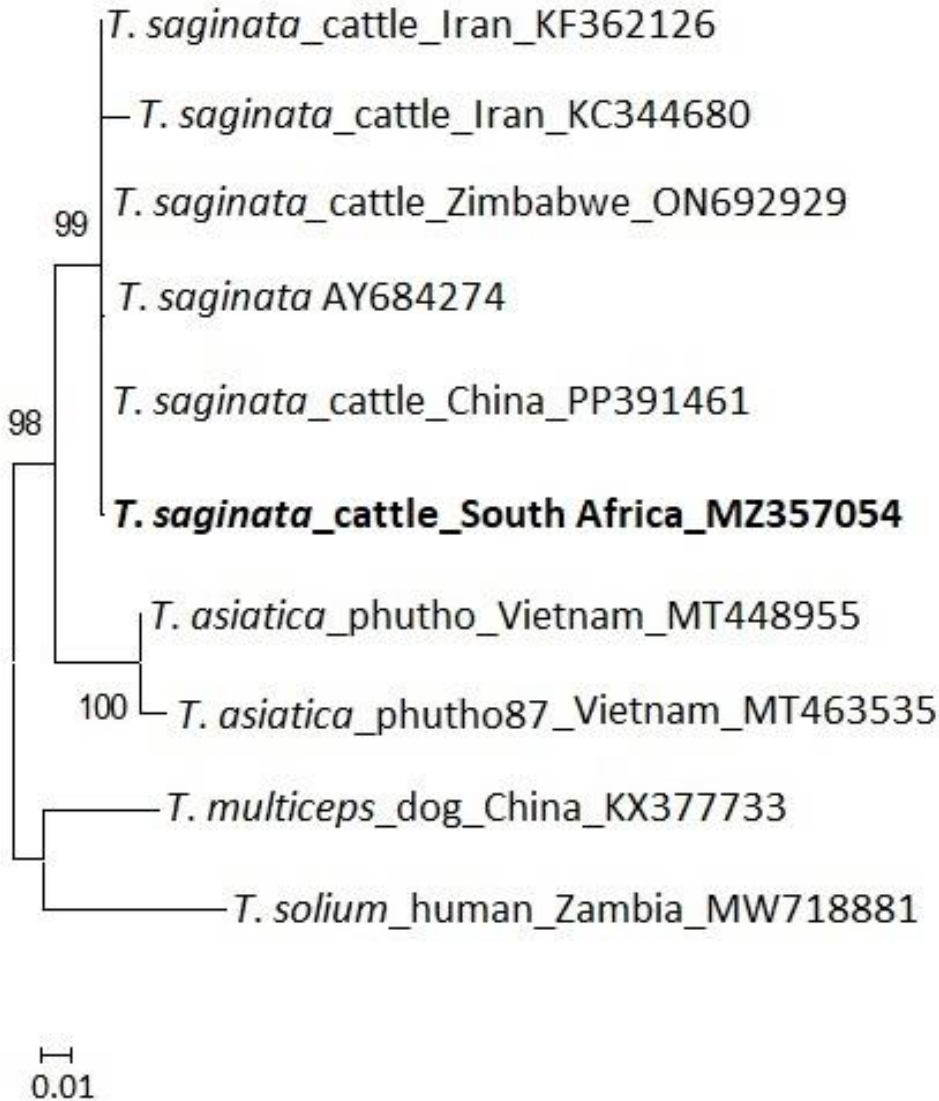


Figure S1. A *Taenia* species 12S rDNA maximum likelihood phylogenetic tree generated in Molecular Evolutionary Genetics Analysis software version 11 (Tamura et al., 2021). The obtained sequence is highlighted in bold. Numbers at the nodes denote bootstrap values, which are the percentage of replicate trees (n=1000) in which the analysed sequences grouped together. The associated dataset comprised 909 positions. The scale bar represents the average number of nucleotide substitutions per site. The tree was rooted using *T. multiceps* and *T. solium* 12S rDNA sequences from China and Zambia, respectively.