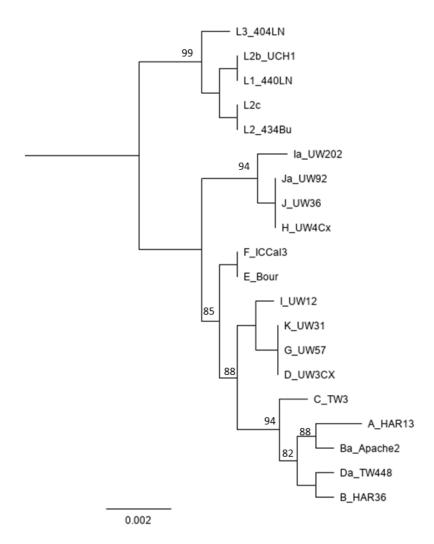
Supplementary Figures



Supplementary Fig 1. Concatenated *trp*RBA phylogenetic tree of 21 *Ct* reference strains constructed by FastTree with a Generalized Time-Reversible model based on a MAFFT alignment of *trp*RBA sequences (see Methods). Both were executed in Geneious (https://www.geneious.com). The tree scale indicates the distance between the sequences and the branch length indicates the number of substitutions that have occurred in that branch.