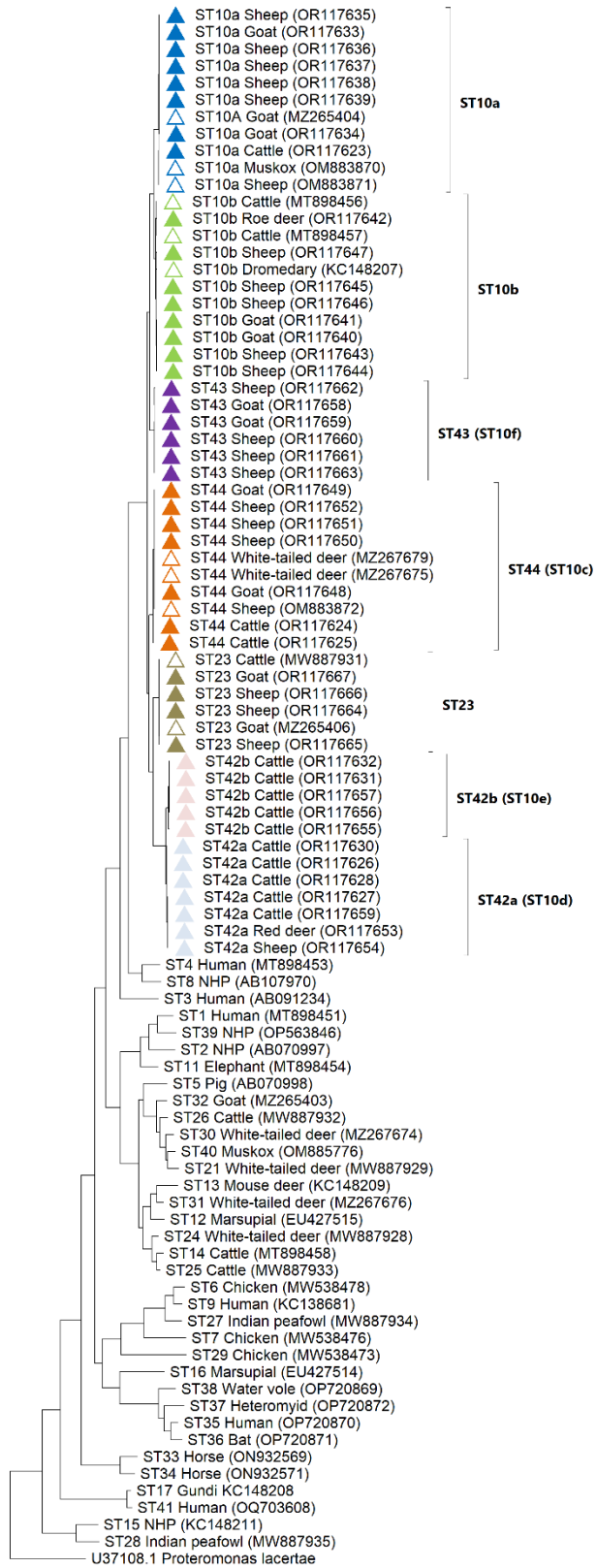


SUPPORTING INFORMATION

Division of *Blastocystis* ST10 into three new subtypes: ST42-ST44 by Monica Santin, Ana Figueiredo, Aleksey Molokin, Nadja George, Pamela C. Köster, Alejandro Dashti, David González-Barrio, David Carmena, Jenny G. Maloney

Figure S1. Phylogenetic relationships among *Blastocystis* full-length *SSU* rRNA gene nucleotide sequences generated in the present study (represented with a filled triangle), representative reference sequences of the accepted subtypes (Table 1), and *Proteromonas lacertae* used as outgroup taxon to artificially root the tree. Analysis was inferred using the Maximum Likelihood method with genetic distances calculated using the Kimura 2-parameter model. This analysis involved 92 nucleotide sequences, and there were a total of 1982 positions in the final dataset.



0.050