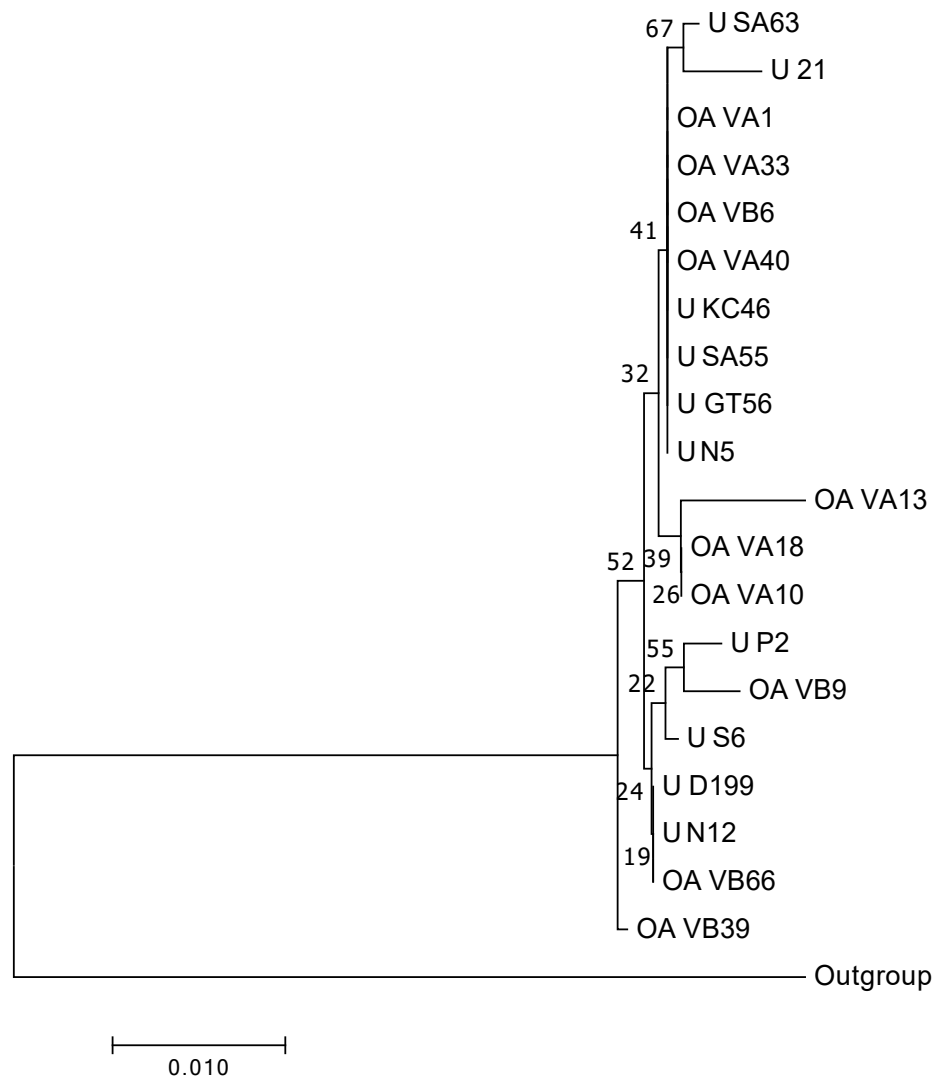


## Supplementary Figure S1



**Figure S1.** Phylogenetic tree analyzing the urban and orang asli isolates of *Blastocystis* sp. ST3 inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.10769462 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Urban isolates are indicated with ‘U’ and orang asli isolates indicated with ‘OA’. The outgroup used were partial-length 18S rDNA of *Blastocystis* sp. ST 2.