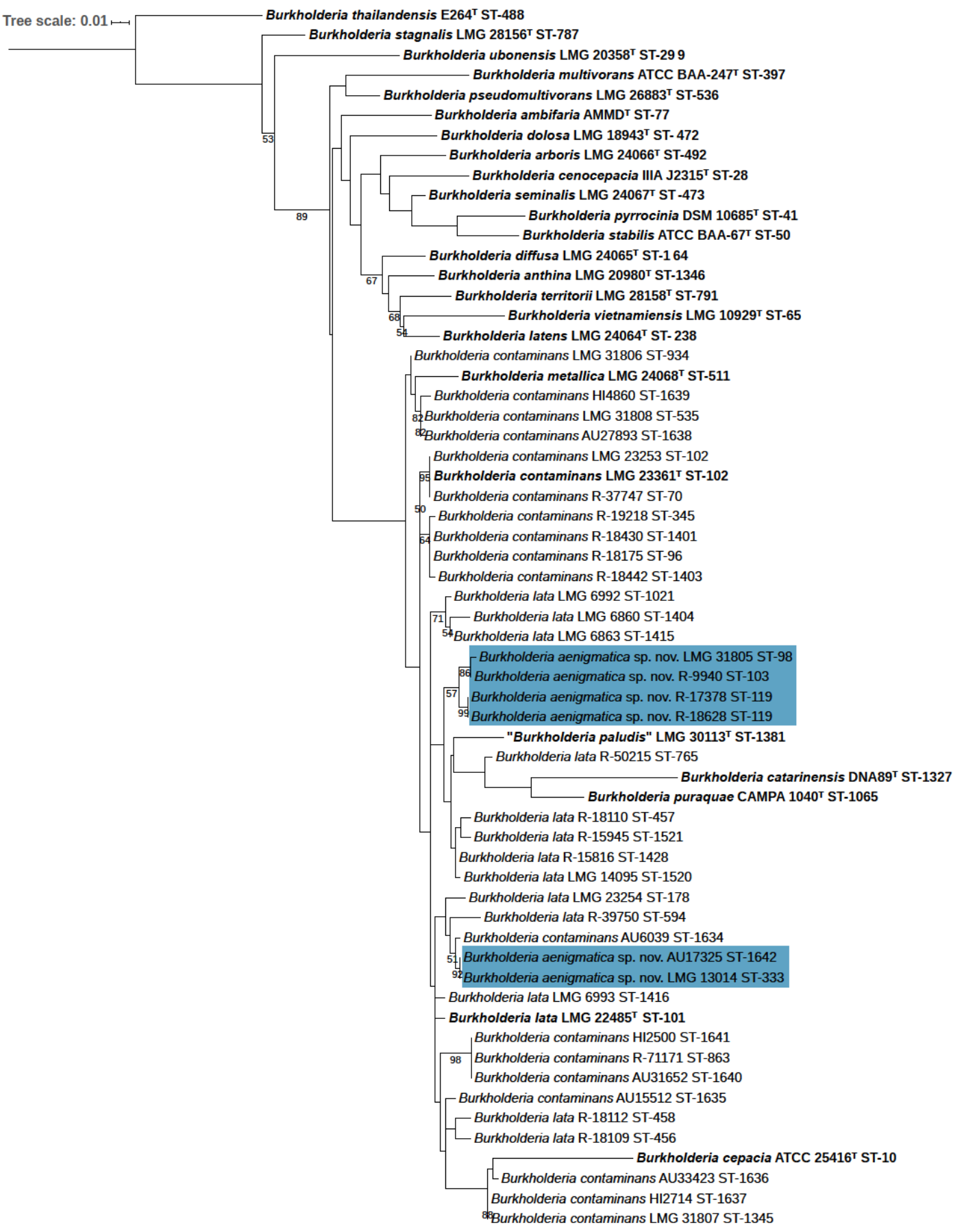


Tree scale: 0.01



Supplementary Figure 1. Phylogenetic tree based on partial *recA* sequences of the 61 *Burkholderia* strains examined in the present study. Sequences (663 bp) were aligned based on their amino acid sequences and phylogeny was inferred using the Maximum Likelihood method and GTRCAT substitution model in RAxML. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches if greater than 50%. *Burkholderia thailandensis* E264^T was used as outgroup. The scale bar indicates the number of substitutions per site. Type strains of validly named Bcc species are shown in bold character type. Strains that were reclassified into the novel species *Burkholderia aenigmatica* sp. nov. are marked in blue.