

Supplementary Figure S1. One of four most parsimonious trees inferred from the 16S rRNA sequence data for *Burkholderia kirstenboschensis* sp. nov. and other *Burkholderia* species. The tree depicted is 484 steps long with consistency, retention and homoplasy indices of 0.37, 0.61 and 0.63, respectively. Bootstrap values ($\geq 50\%$) are indicated at the branches and type strains of the species *Burkholderia cepacia* and *B. vietnamiensis* were used as outgroup. The scale bar indicates the number of nucleotide changes per site. The type strain and GenBank accession numbers for each species are listed in brackets.

16S rRNA

