

This figure displays a highly branched phylogenetic tree, likely generated using a maximum likelihood or Bayesian inference method. The tree is rooted at the top left and branches downwards. The nodes are labeled with species names, predominantly starting with 'Chabira_GBG63270' and 'Chabira_GBG63271'. The branches are color-coded: red for the main lineage and black for the side branches. The scale bar at the bottom left indicates a genetic distance of 0.16667. The tree shows a complex pattern of relationships, with many branches leading to species that are closely related to the main lineage. The species names are truncated, showing only the first few characters of the species name.

0.16667