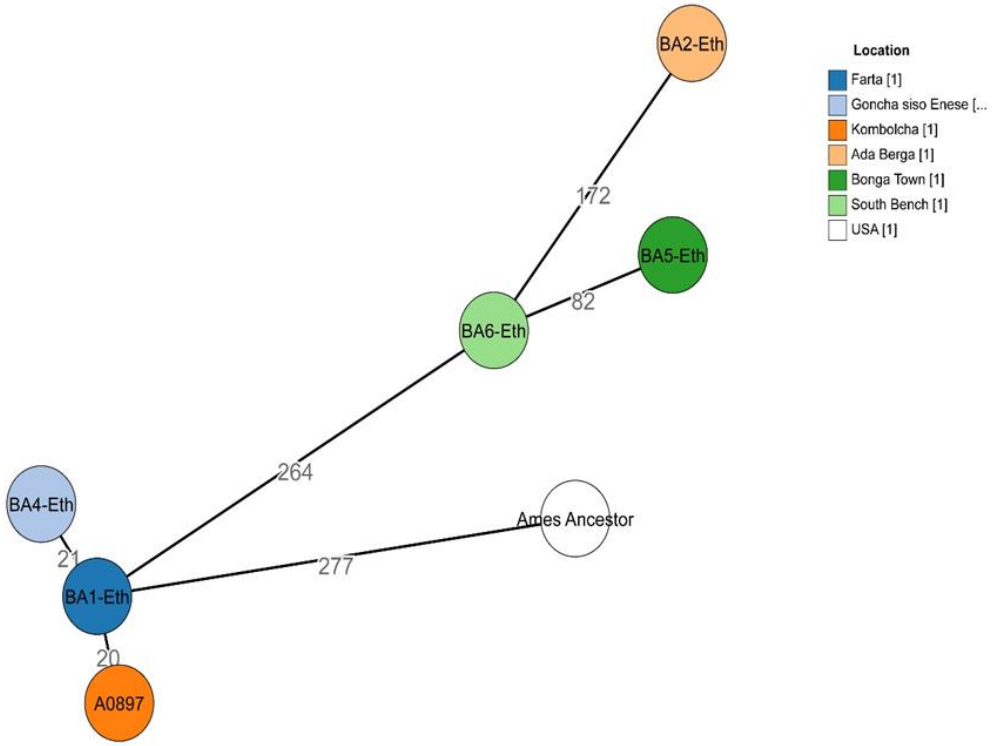


Figure S1. A minimum-spanning tree of six Ethiopian *B. anthracis* strains, constructed using cgMLST whole genome analysis. The legend specifies the geographical location associated with each sequence, with the Ames Ancestor strain represented by a white circle. Numbers indicate allelic differences between samples.