

**Supplementary Figure 1. (a)** Root-to-tip regression analysis performed using a maximum likelihood tree of *Candida auris* genomes from Kenyan isolates clustering to Clade III. R-squared value = 0.55. **(b)** Marginal posterior distributions for the date of the most recent common ancestor (TMRCA) of *C. auris* Clades I, II, III and IV, analysis performed by BEAST under distinct models and mutation rates.