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**Supplementary Figure 3. Genome-wide FST analysis of the two most closely related clades (Clades I and III).** **(a, b)** Genome-wide FST analyses revealed substantial interspecific divergence and reproductive isolation between *C. auris* Clades I and III and small regions with FST values close to zero. **(c)** Phylogenetic analysis of selected genes revealed that these regions in isolates from Clades I and III are intermixed in a monophyletic clade.