Maximum likelihood reconstruction of the whole-genome phylogeny of 81 Ct sequences from the Bijagós Islands, 48 Ct sequences from Rombo and 38 Ct reference strains. Bijagós Ct sequences (n=81) were mapped to Ct A/HAR-13 using SAMtools [55]. SNPs were called as described by Harris et al. [4]. Phylogenies were computed with RAxML [62] from a variable sites alignment using a GTR+gamma model and are midpoint rooted. The scale bar indicates evolutionary distance. Bijagós Ct sequences in this study are coloured BLACK and reference strains are coloured by tissue localization (RED=Ocular, GREEN=Urogenital, BLUE=LGV). Branches are supported by >90% of 1000 bootstrap replicates. Branches supported by 80-90% (ORANGE) and <80% (BROWN) bootstrap replicates are indicated.