Figure S1. A SNP-derived maximum likelihood phylogenetic tree (midpoint rooted) of K.pneumoniae isolates belonging to clonal group (CG) 101, including ST101 and ST2502, constructed using Snippy and IQ-tree (see the Methods section) and using K. pneumoniae DG5544 as reference genome. Bootstrap-based branch support values, obtained from 100 replicate trees, are indicated as branch labels. Branches showing bootstrap values lesser than 50 were collapsed. The scale bar shows substitutions per nucleotide position. Colored squares give provide details about the origin of analyzed strains (AOUC, Florence Careggi Universitary Hospital; LTACRF, long-term acute-care rehabilitation facility), the isolation month referring to study period (2016) and about the patients' room numbers. Sublineages (SL) A and B of ST101 isolates are also indicated by red boxes.