



Figure S1. Phylogenetic relatedness between one ST446 outbreak 2 isolate (KpII) and the remaining ST16 outbreak and environmental isolates (KpI).

Midpoint rooted phylogeny estimated from the alignment of 12,190 core SNPs identified from or ST446 (*Klebsiella quasipneumoniae*) isolate and nine ST16 isolates (*Klebsiella pneumoniae*) in our study, together with a global collection of 36 ST16 *K. pneumoniae*. The bolded tips highlight the isolates from our study. The scale bar represents nucleotide substitutions per site.