

Fig S1

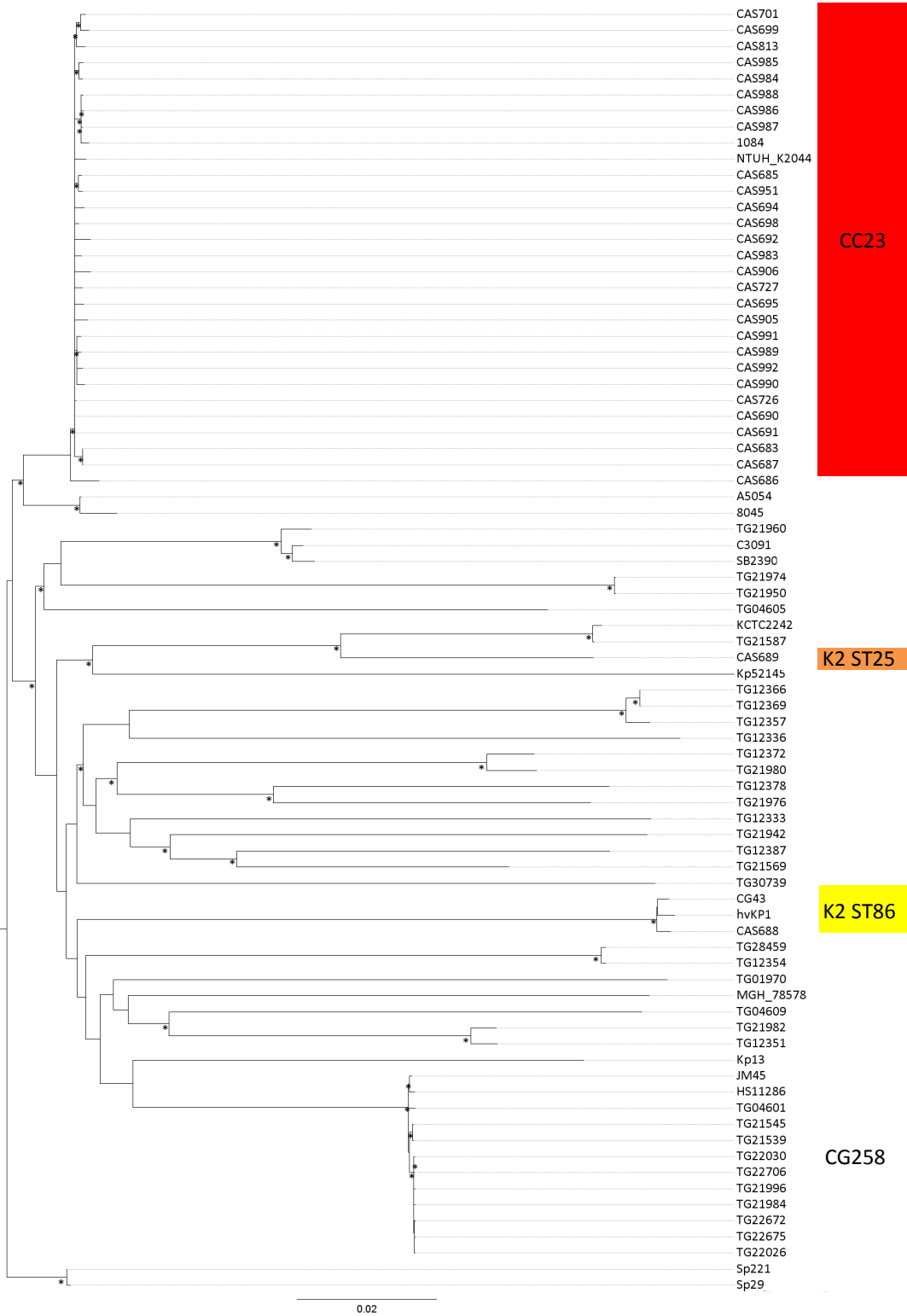


FIG S1 Rooted maximum-likelihood phylogeny of 80 *K. pneumoniae* isolates after recombination filtering by Gubbins (34). Hypervirulent clonal lineages (ST14, CC23, and ST86) are marked with shadings.