

Supplementary figures

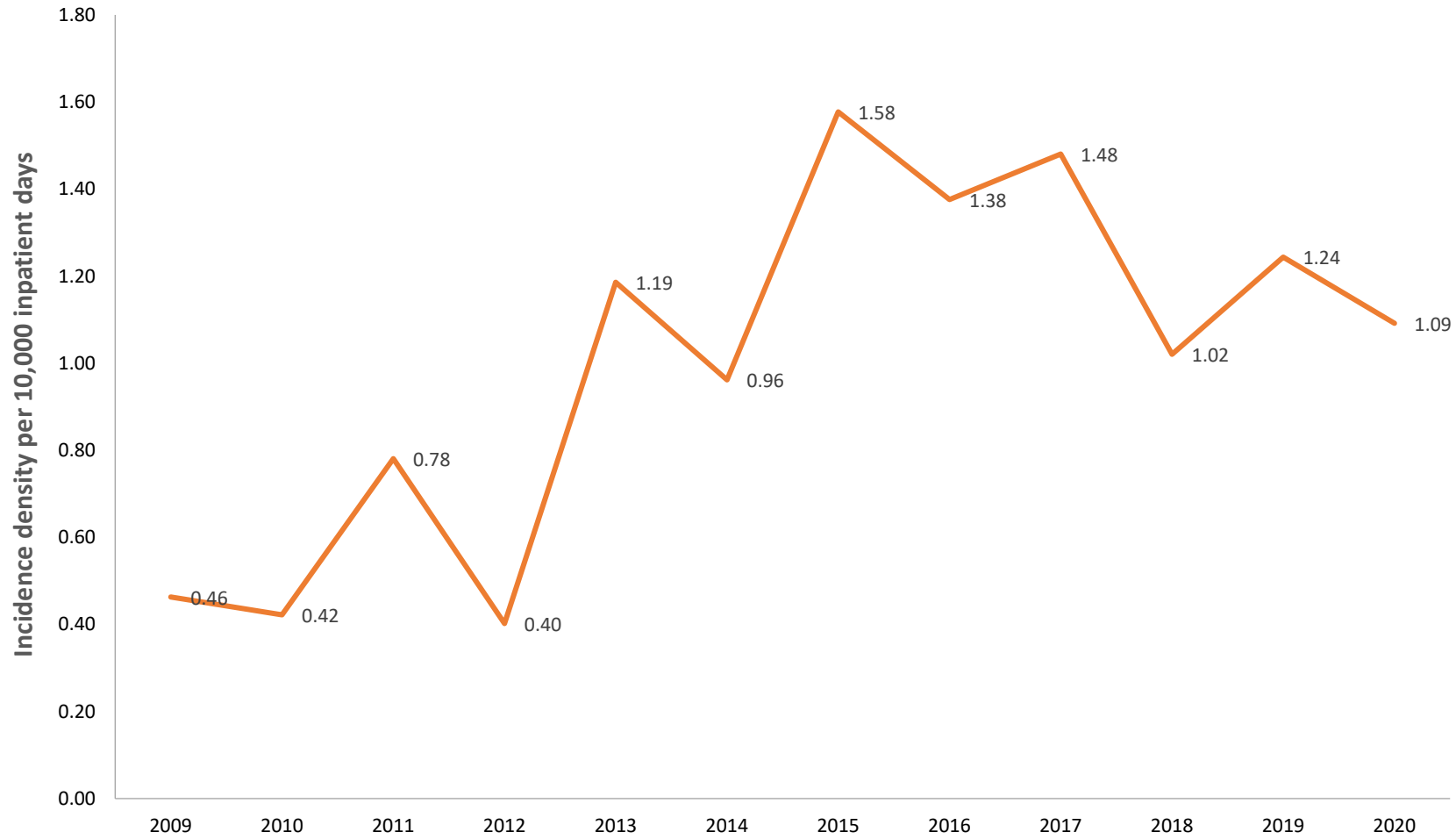


Figure 1. Incidence density trends of clinical carbapenem-resistant *K. pneumoniae* from 2009 – 2020

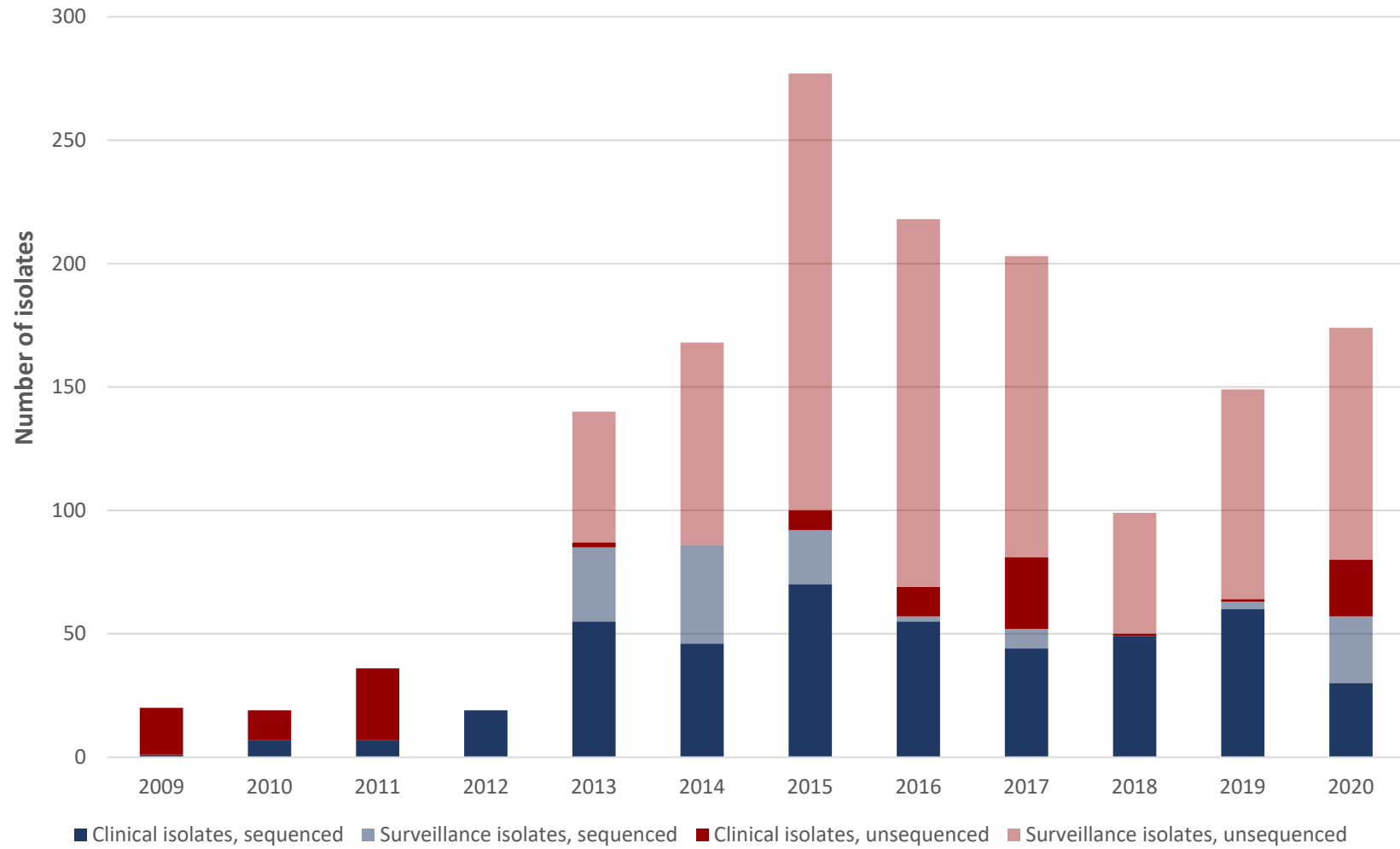


Figure 2. Number of carbapenem-resistant isolates collected and sequenced from 2009 – 2020



Figure 3a Core SNP phylogenetic tree of CG14/15 genomes with pairwise SNP distance matrix. The maximum-likelihood tree of CG14/15 was inferred from mapping 79 genomes to reference EC1155. The scale bar indicates the number of substitutions per site. CG, clonal group; SNP, single nucleotide polymorphism; ST, sequence type.

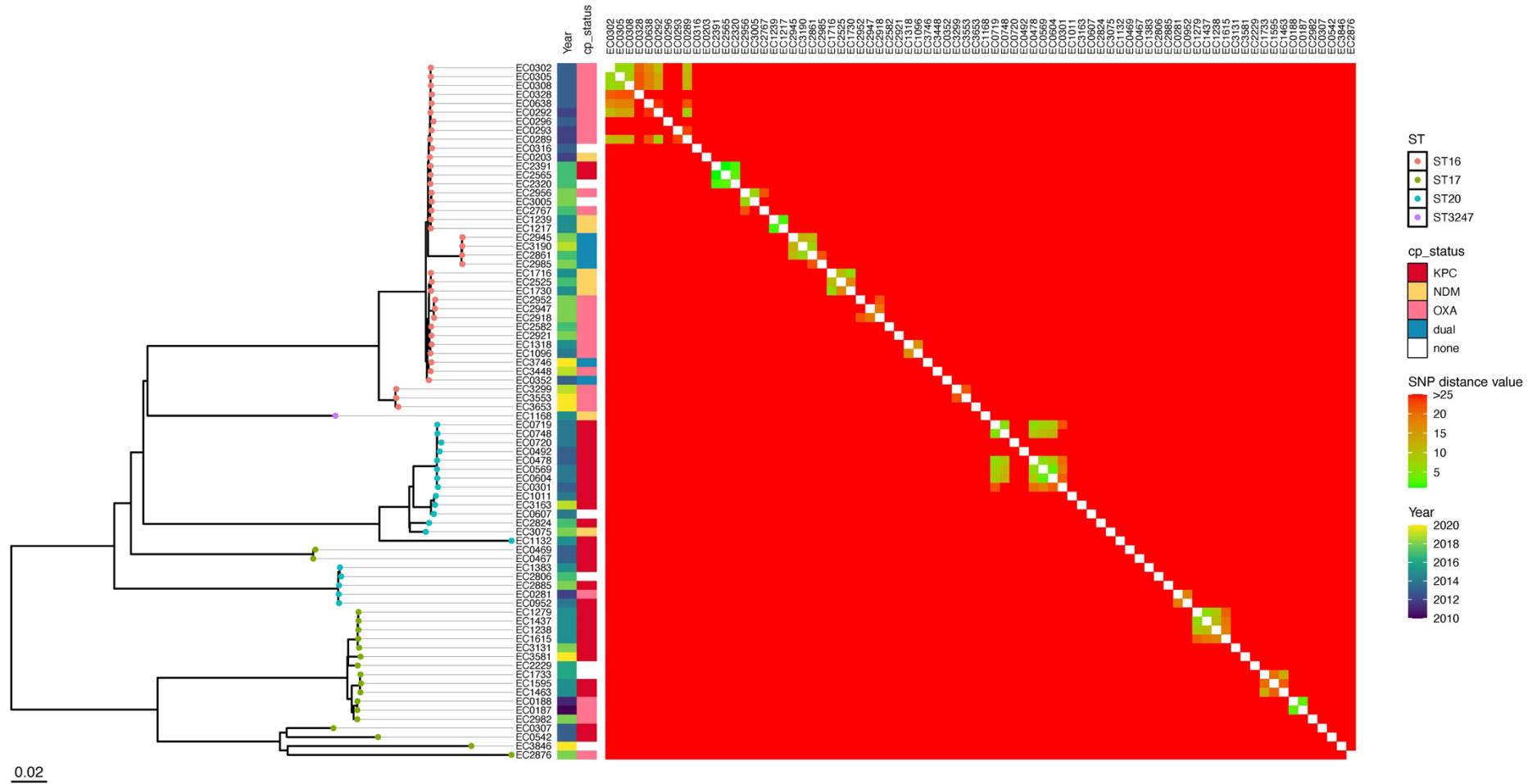
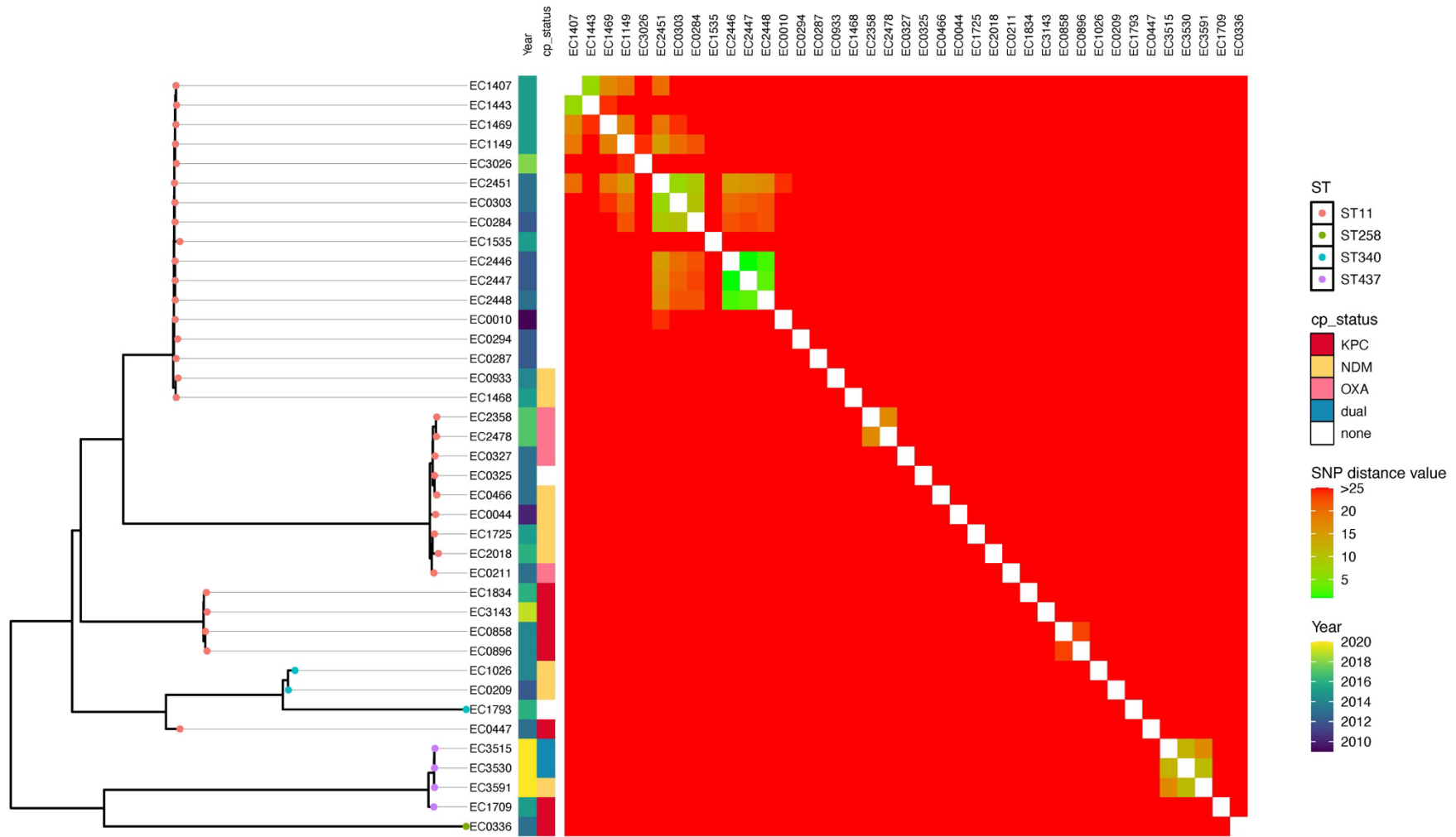


Figure 3b. Core SNP phylogenetic tree of CG17/20 genomes with pairwise SNP distance matrix. The maximum-likelihood tree of CG17/20 was inferred from mapping 78 genomes to reference EC0720. The scale bar indicates the number of substitutions per site. CG, clonal group; SNP, single nucleotide polymorphism; ST, sequence type.



0.03

Figure 3c. Core SNP phylogenetic tree of CG258 genomes with pairwise SNP distance matrix. The maximum-likelihood tree of CG258 was inferred from mapping 39 genomes to reference EC3204. The scale bar indicates the number of substitutions per site. CG, clonal group; SNP, single nucleotide polymorphism; ST, sequence type.

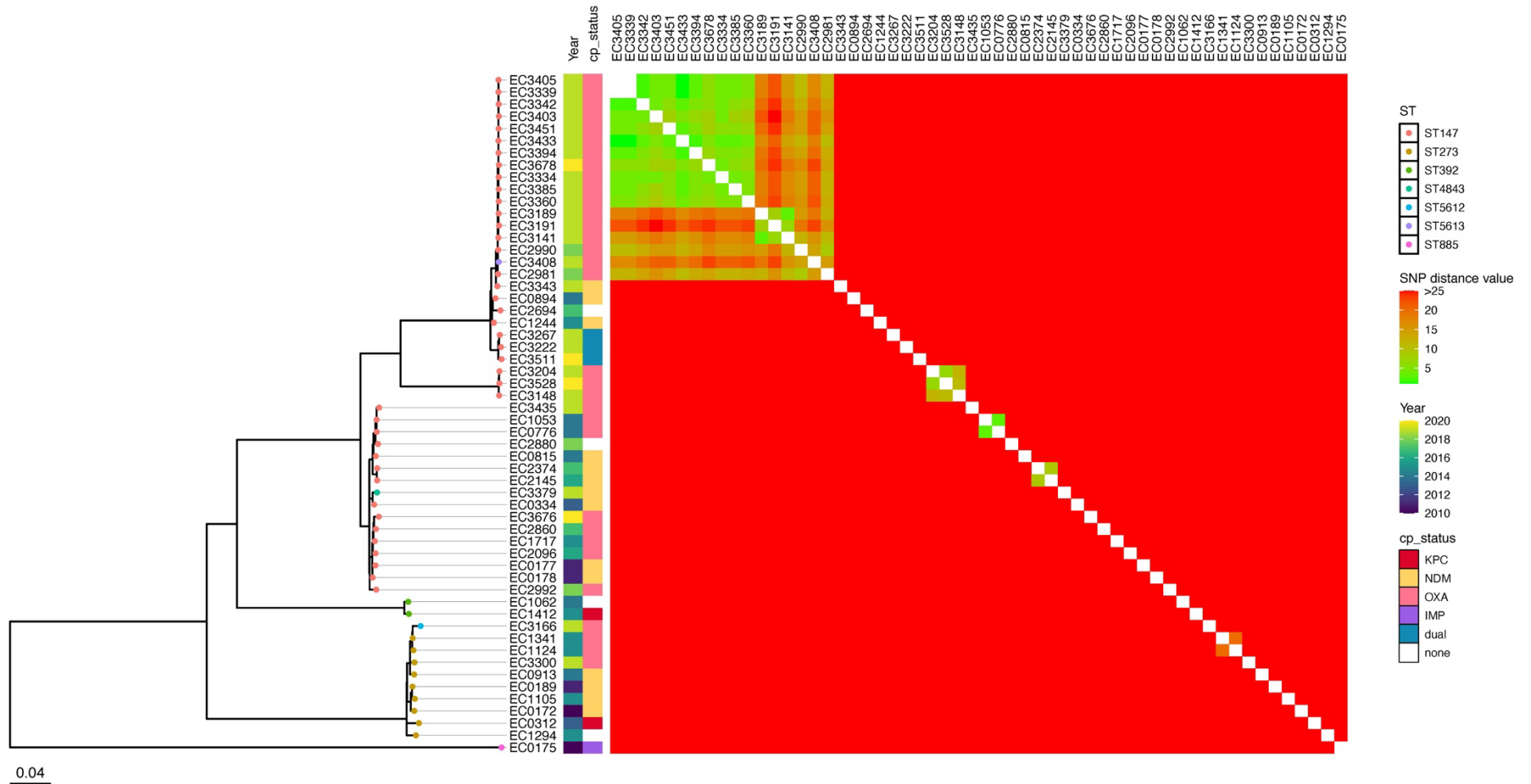


Figure 3d. Core SNP phylogenetic tree of CG147 genomes with pairwise SNP distance matrix. The maximum-likelihood tree of CG147 was inferred from mapping 56 genomes to reference EC0325. The scale bar indicates the number of substitutions per site. CG, clonal group; SNP, single nucleotide polymorphism; ST, sequence type.

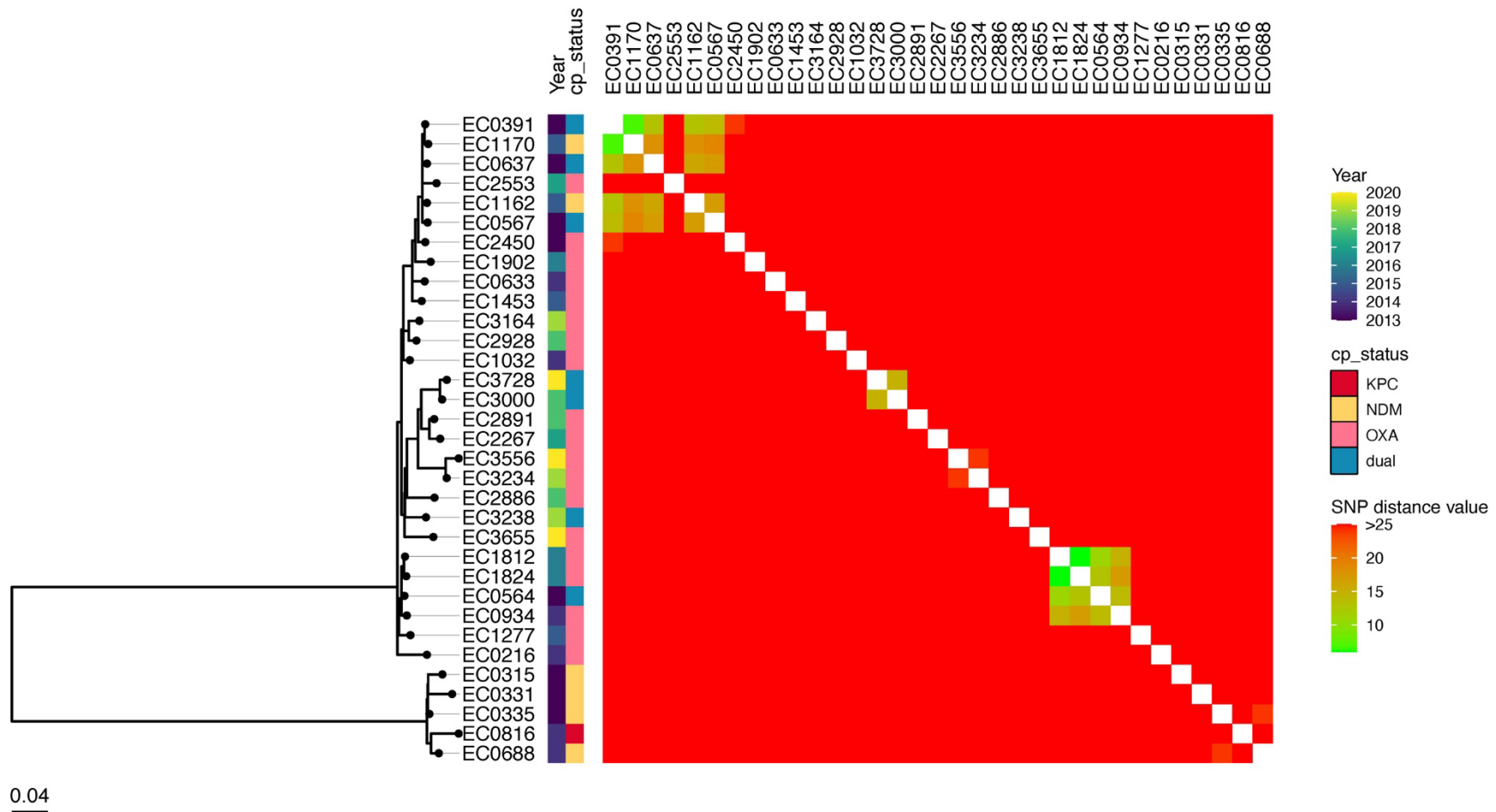


Figure 3e. Core SNP phylogenetic tree of ST231 genomes with pairwise SNP distance matrix. The maximum-likelihood tree of ST231 was inferred from mapping 33 genomes to reference EC2886. The scale bar indicates the number of substitutions per site. CG, clonal group; SNP, single nucleotide polymorphism; ST, sequence type.