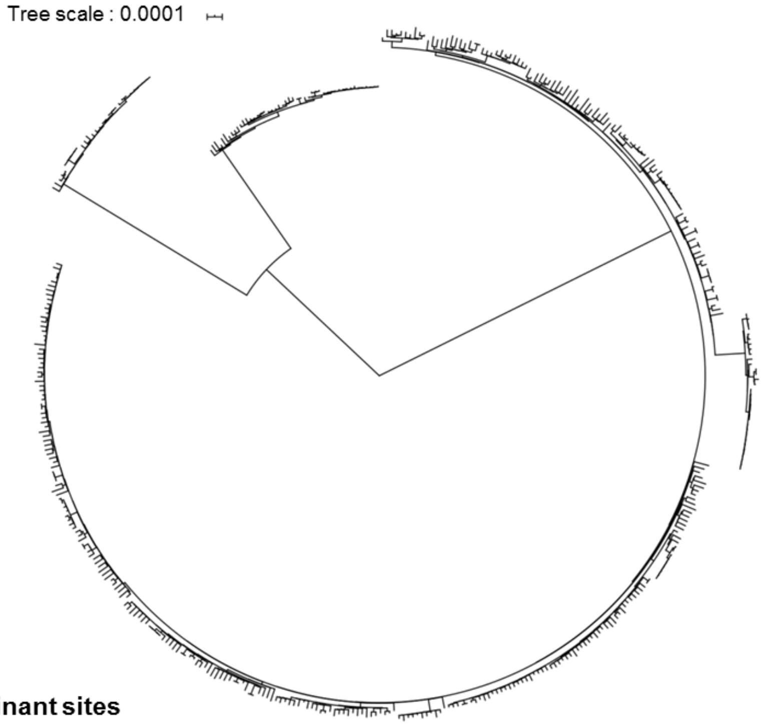
A) Including recombinant sites



B) Without recombinant sites

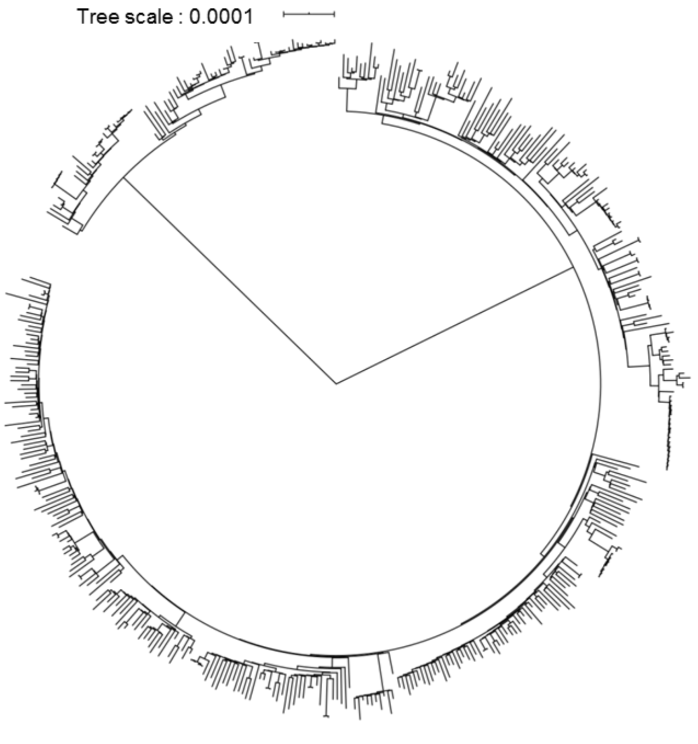


Figure S1: Comparison of Maximum likelihood trees of multiple sequence alignments including (A) and without (B) recombinant sites. Both trees were calculated from concatenated cgMLST sequences present in all 451 ST45 isolates. For tree B, all genes containing possible recombination sites were purged from the alignment.