

Figure S1: Additional dendrograms constructed using Jaccard and Sokal & Sneath coefficients as distance measures and weighted neighbor joining and UPGMA as dendrogram generation algorithms.

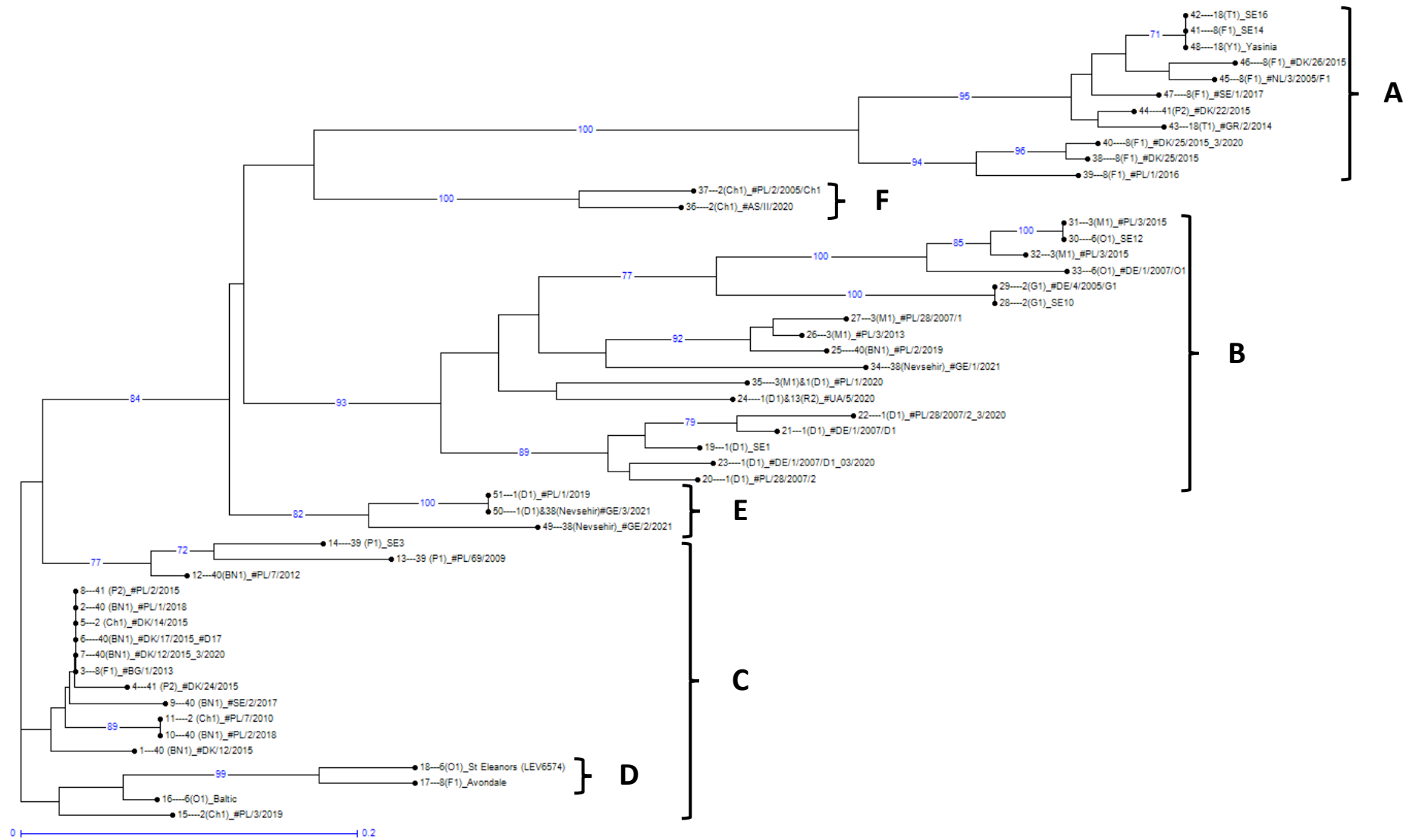


Figure S1a: Weighted Neighbor-Joining dendrogram based on the Jaccard dissimilarity index for the 51 isolates using 73 marker-alleles. A bootstrap analysis with 1000 replicates was applied and values above 70% are shown at the branches.

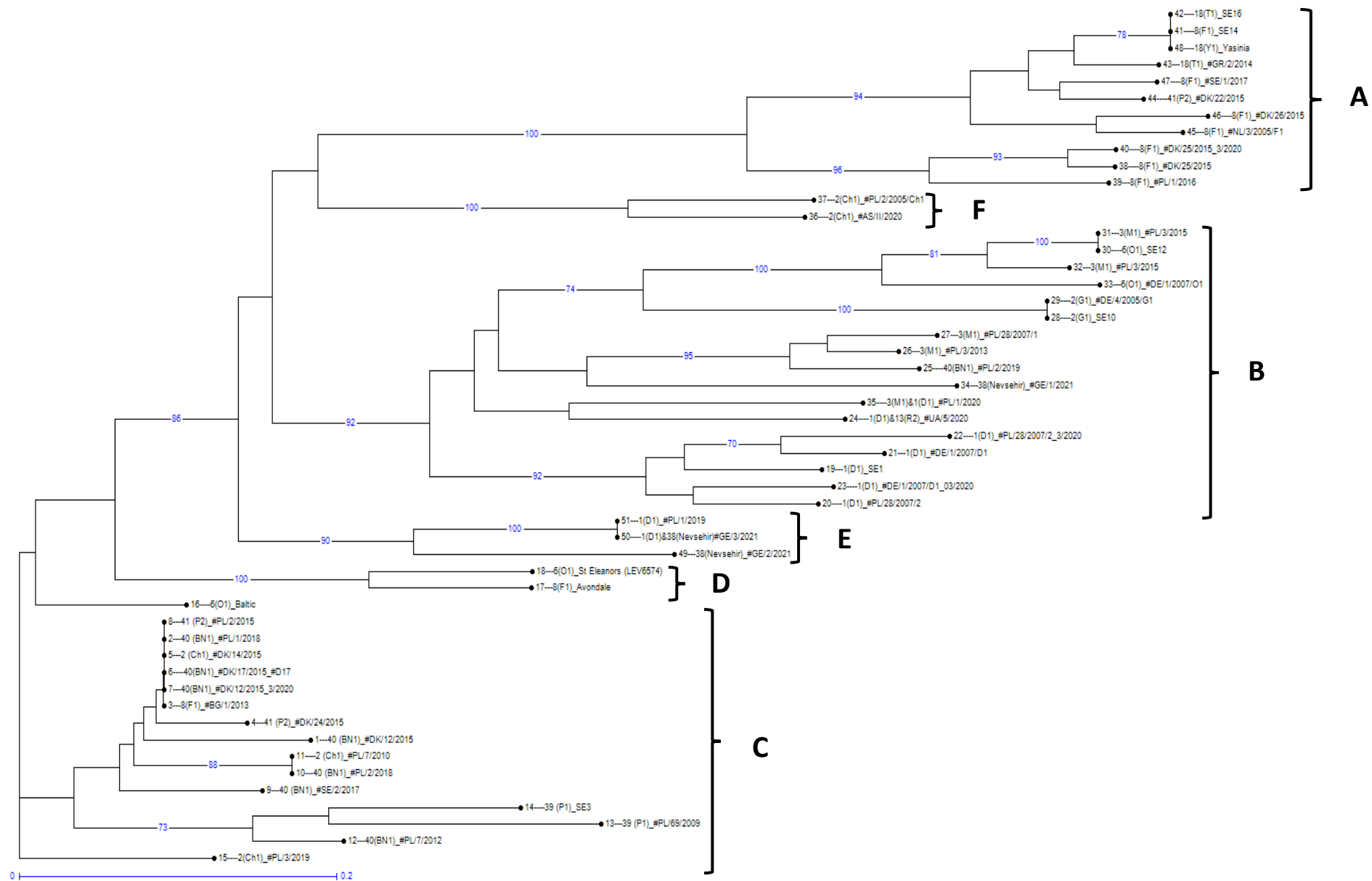


Figure S1b: Weighted Neighbor-Joining dendrogram based on the Sokal & Sneath dissimilarity index for the 51 isolates using 73 marker-alleles. A bootstrap analysis with 1000 replicates was applied and values above 70% are shown at the branches.

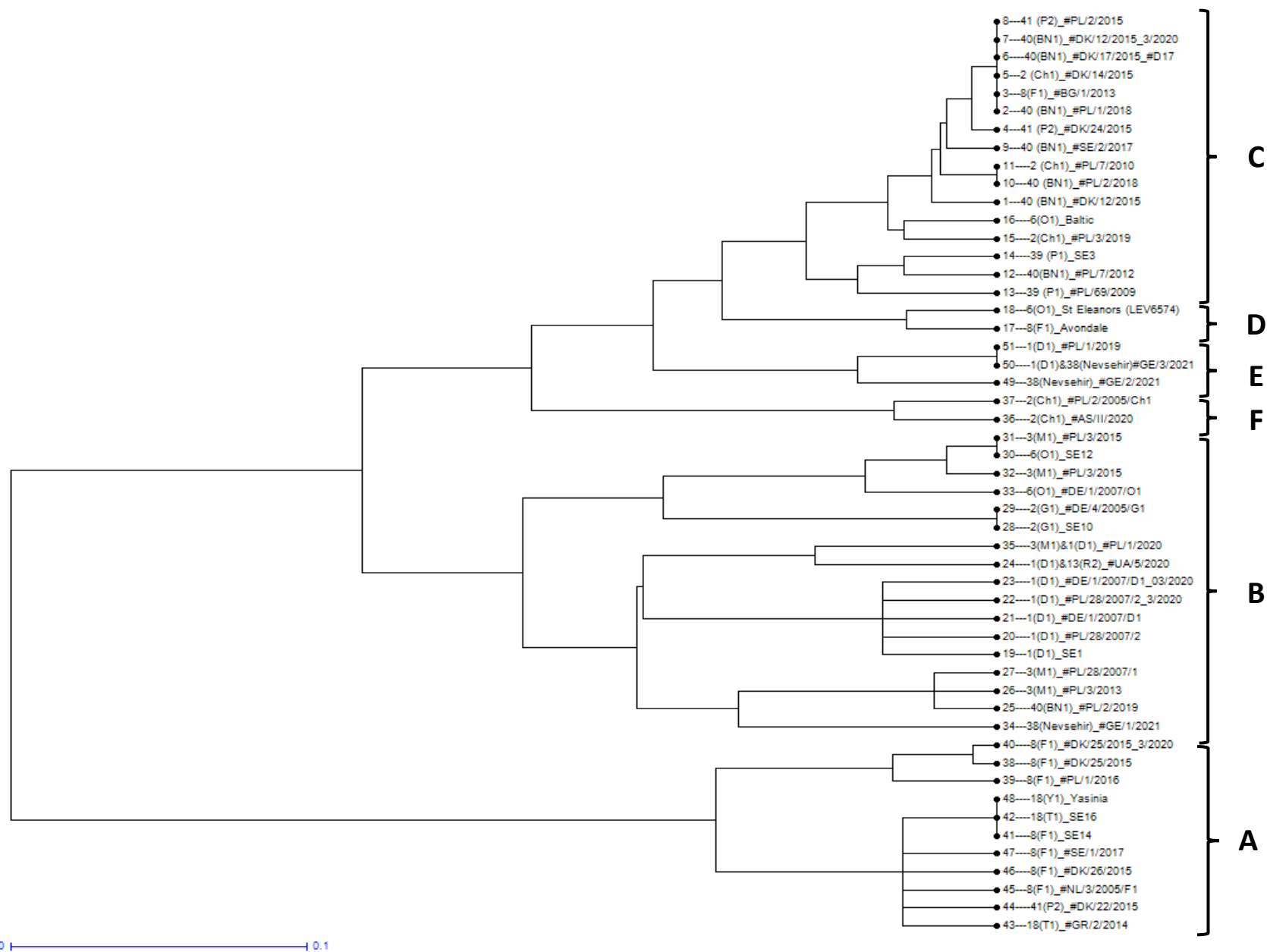


Figure S1c: UPGMA dendrogram based on the Dice dissimilarity index for the 51 isolates using 73 marker-alleles.

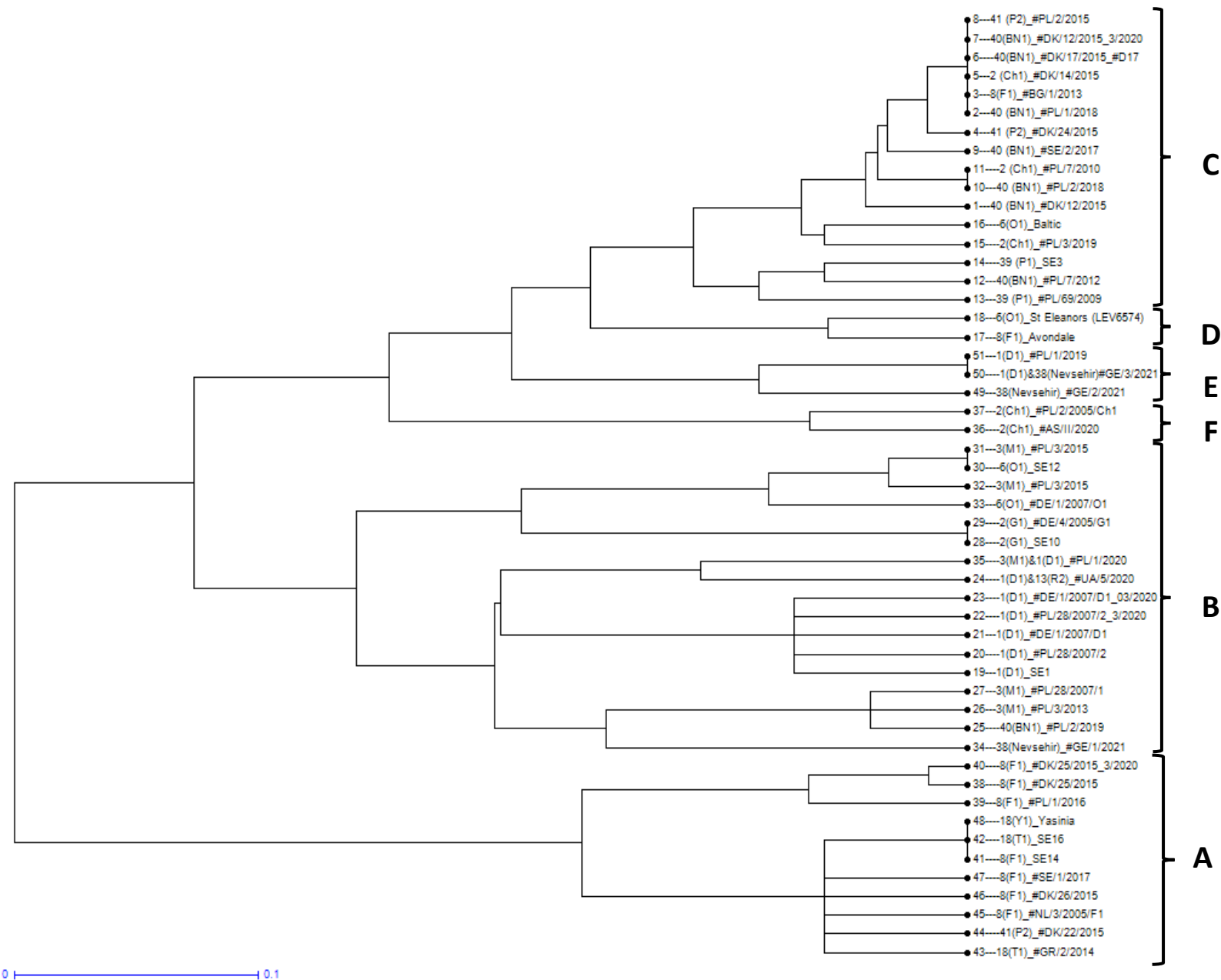


Figure S1d: UPGMA dendrogram based on the Jaccard dissimilarity index for the 51 isolates using 73 marker-alleles.

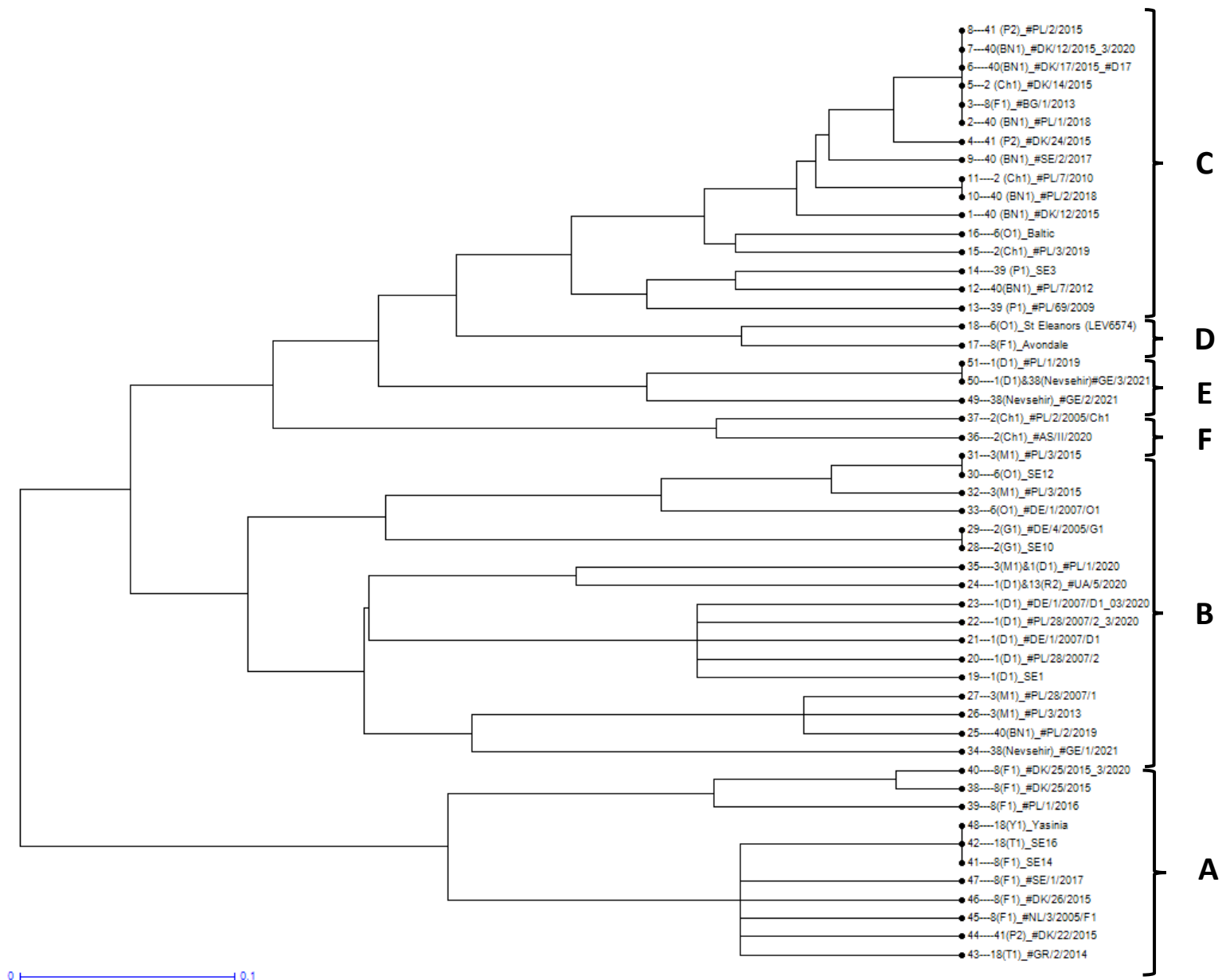


Figure S1e: UPGMA dendrogram based on the Socal & Sneath dissimilarity index for the 51 isolates using 73 marker-alleles.