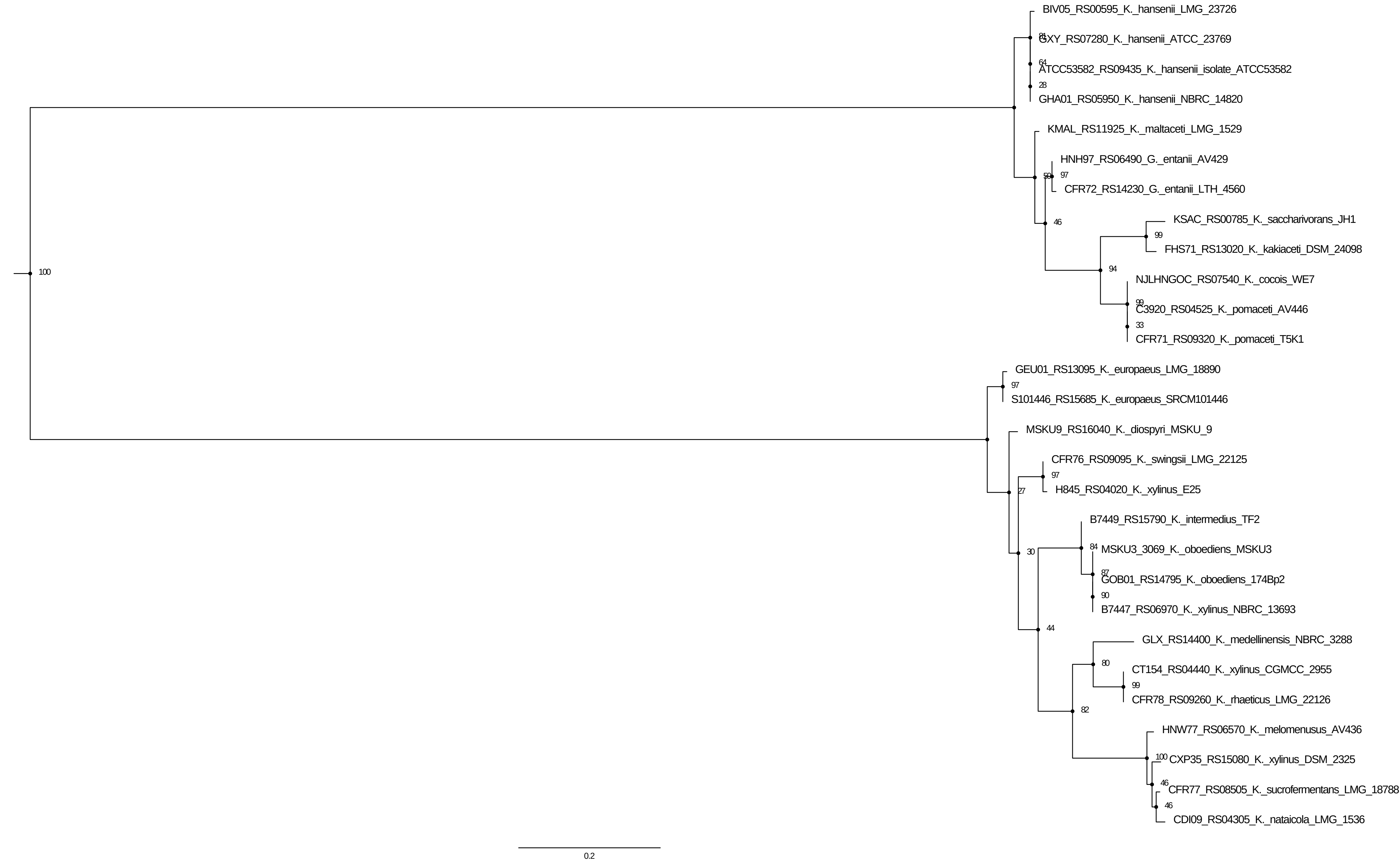
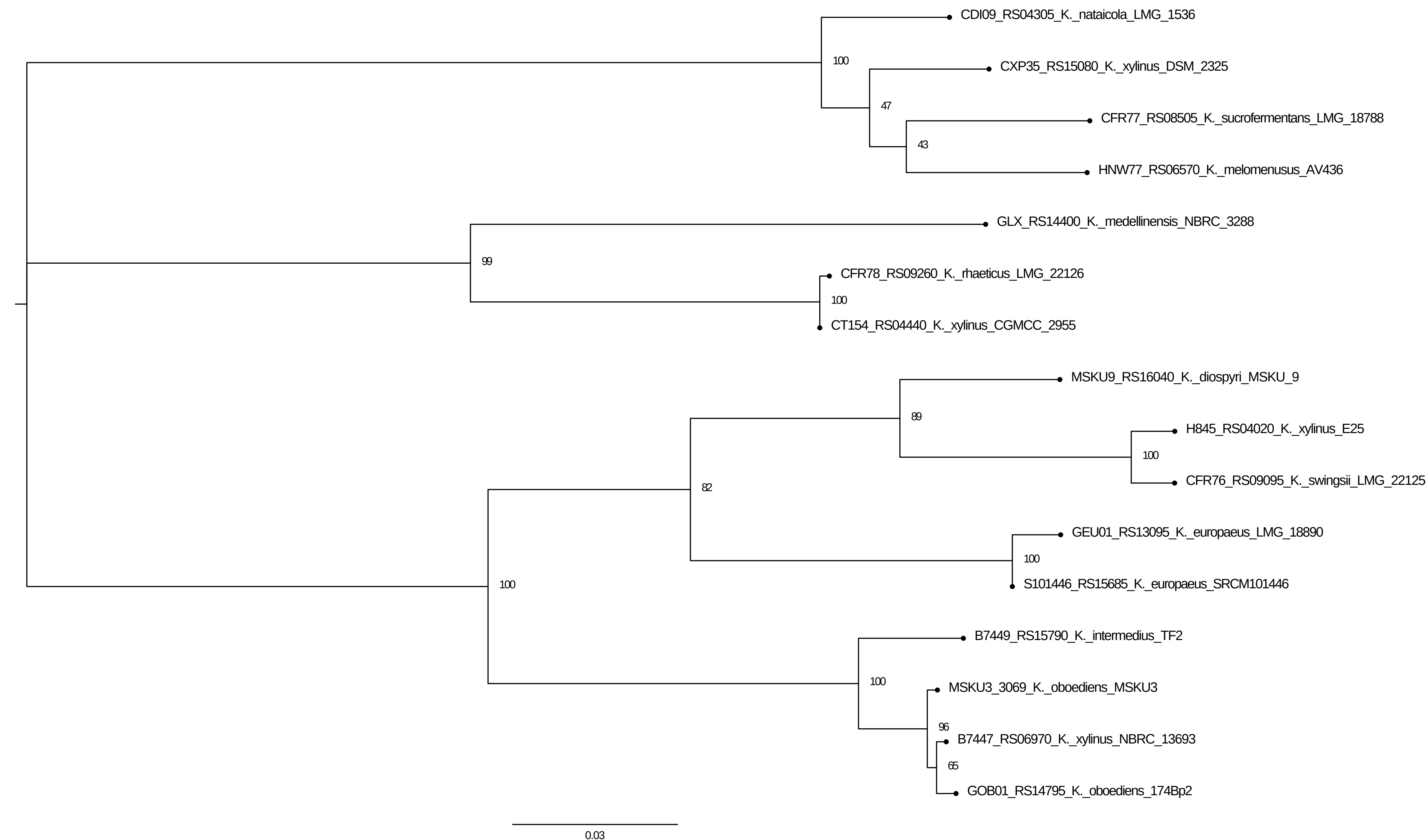


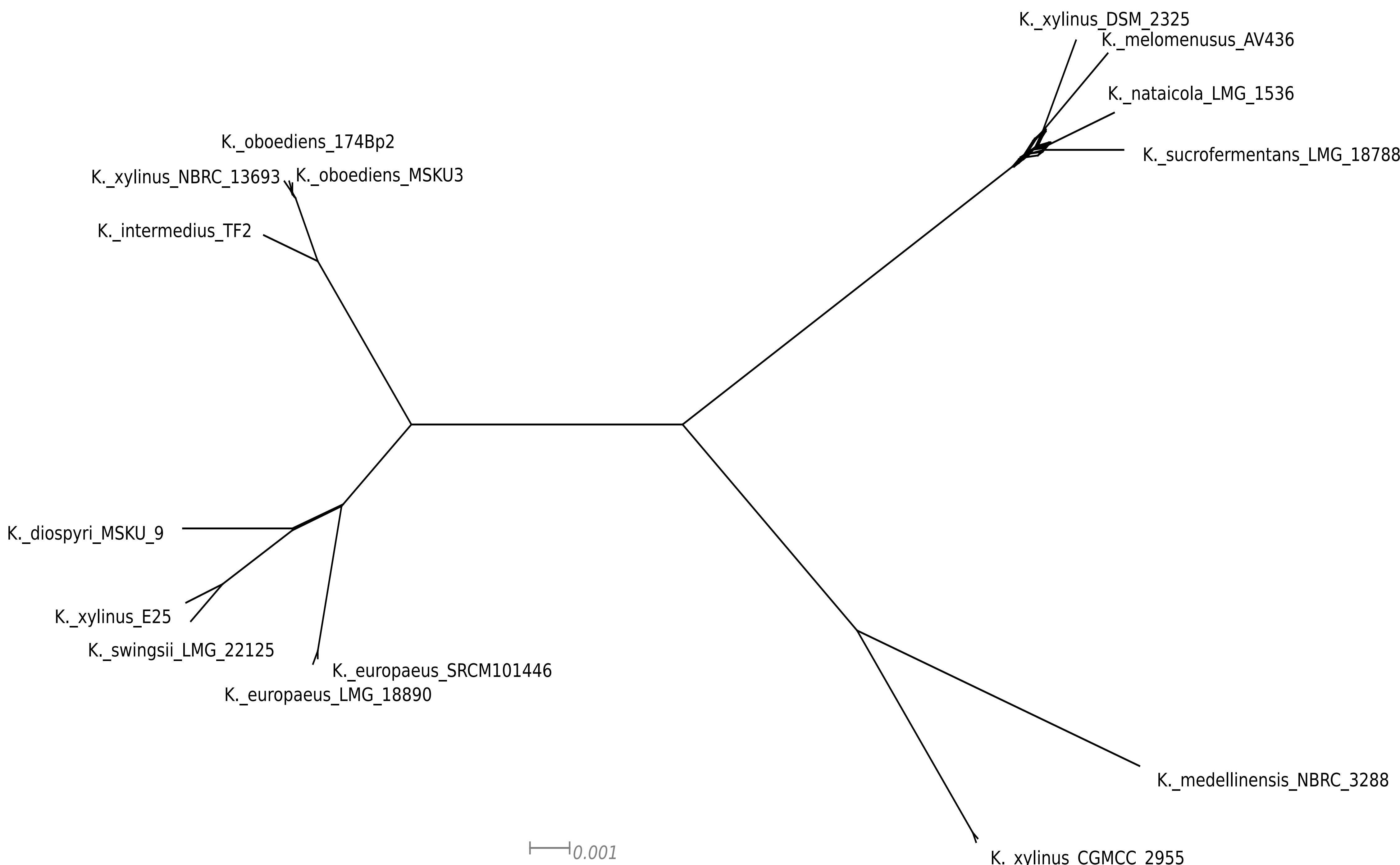
A



B



C



Supplementary figure 1. Divergence and putative horizontal gene transfer of acetan-like loci in *Komagataeibacter*. **A:** phylogeny of *Komagataeibacter* AceH as deduced by PhyML using LG substitution table and 1000 bootstrap replicates. The lower cluster corresponds to the archetypal *K. xylinus* E25 locus, while the upper groups the AceH belonging to the newly found locus. **B:** *aceH* gene phylogeny of *K. xylinus* E25 type acetan locus reconstructed using GTR model and 1000 bootstrap replicates. *K. xylinus* loci are dispersed among several well resolved clusters. **C:** Supernetwork analysis of 17 gene trees of the 16 *Komagataeibacter* strains harboring the archetypal *K. xylinus* locus. All the trees are essentially very similar implying the locus was transferred as a unit several times.