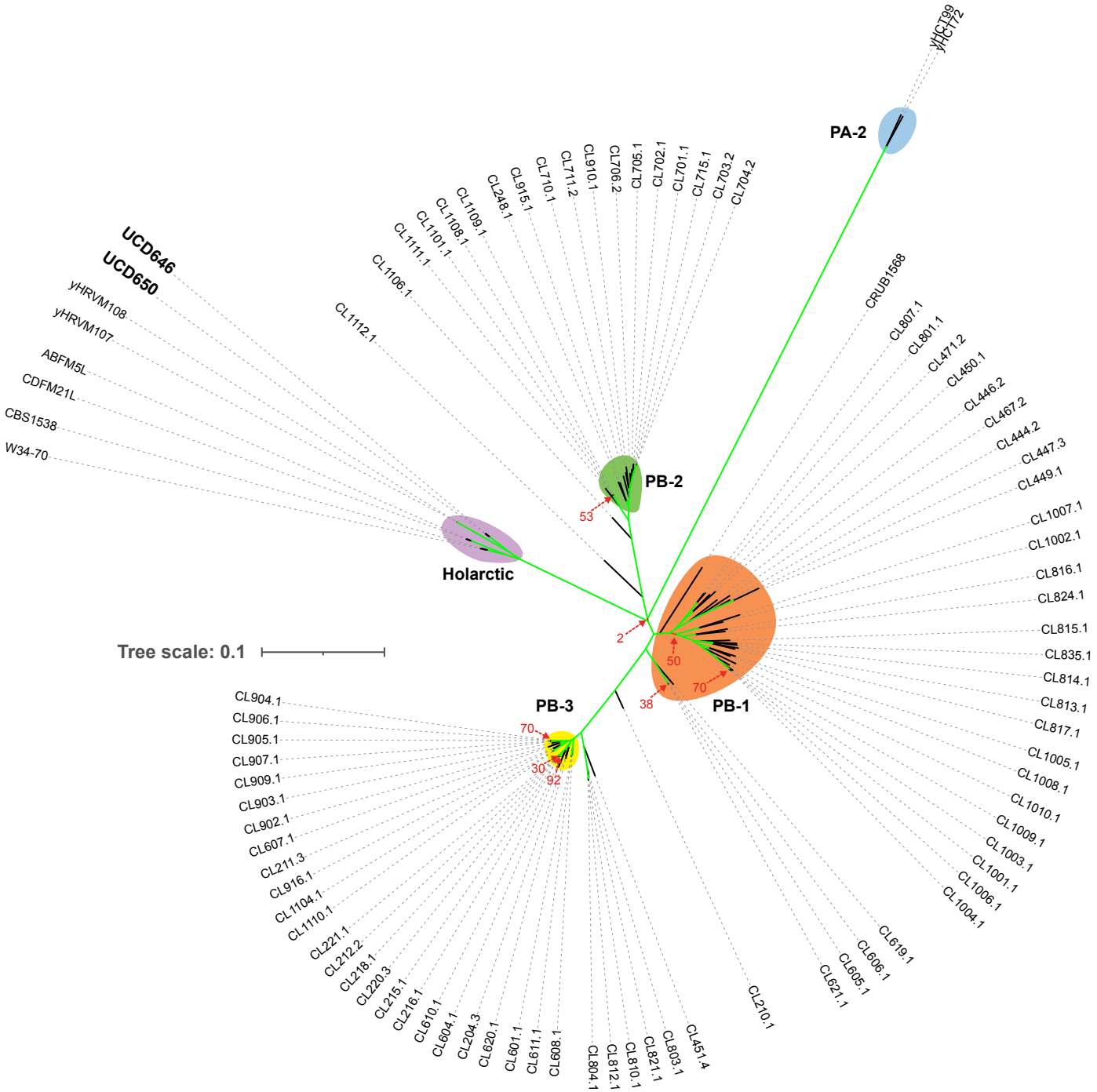

Supplementary Fig. 1. Estimated phylogeny of 89 *S. eubayanus* and two *S. pastorianus* strains. The tree was constructed with RAxML using the GTRGAMMA model of nucleotide substitution, using a concatenated SNP alignment. Coloured shapes highlight distinct populations identified previously (Nespolo et al. 2020), and the two UCD isolates are highlighted in bold. All branches in the Holarctic clade have a support value of 100. Support values < 100 are labelled with red arrows.